

Haddad, M
10/6/9323 Page 1
Seq ID 1#4-6

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: January 20, 2006, 17:33:55 ; Search time 116.923 Seconds
(without alignments)
300.628 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192
Perfect score: 80
Sequence: 1 HKDEVIKEVQEFYKDTYNKL.....LETFTVKSCPDAIKEVFNK 80
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 2443163 seqs, 439378781 residues
Word size : 0
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries
Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	80	100.0	227	2	AAR86834 Human CD9
2	80	100.0	227	5	ABT78366 Amino aci
3	80	100.0	227	5	AAE14636 Human CD9
4	80	100.0	227	6	ABU05057 Human exp
5	80	100.0	227	6	ABU05060 Human exp
6	80	100.0	227	7	ABW00436 Human CD9
7	80	100.0	227	7	ADK69862 Human CD9
8	80	100.0	227	8	AD119366 Human CD9
9	80	100.0	227	9	AEAR9005 Human CD9
10	80	100.0	228	2	AAK27525 Metastasi
11	80	100.0	228	4	ABBA4581 Human wou
12	80	100.0	228	6	ABU05059 Human exp
13	80	100.0	228	6	ABU05052 Human exp
14	80	100.0	228	6	ABU05048 Human exp
15	80	100.0	228	6	ABU05056 Human exp
16	80	100.0	228	6	ABU05049 Human exp
17	80	100.0	228	6	ABU05050 Human exp
18	80	100.0	228	6	ABU05053 Human exp
19	80	100.0	228	7	ABW01519 Protein #
20	80	100.0	228	7	ADD89037 TAT278. 1
21	80	100.0	228	7	ADG32002 Human hom
22	80	100.0	228	8	ADJ57558 Human CD9
23	80	100.0	228	8	ADL26782 Human CD9
24	80	100.0	228	8	ADL82853 Human PRO

25	80	100.0	225	8	ADP23088 PRO polyp
26	80	100.0	228	8	Adr73450 Human CD9
27	80	100.0	228	9	Adv70263 Tumor-ase
28	80	100.0	228	9	Adv97163 Human CD9
29	80	100.0	228	9	ADY19604 PRO polyp
30	80	100.0	228	9	ADY14362 PRO polyp
31	80	100.0	228	9	AEB98450 Human CD9
32	80	100.0	275	3	AAB43936 Human can
33	80	100.0	275	3	AAG75156 Human col
34	80	100.0	275	6	ABU05055 Human exp
35	80	100.0	275	6	ABU05054 Human exp
36	47	58.8	79	2	AAW35851 Human CD9
37	47	58.8	79	6	ABU05058 Human exp
38	43	53.8	454	4	ABG14067 Novel hum
39	40	50.0	209	4	AAG76051 Human col
40	38	47.5	38	8	ADJ57561 Human CD9
41	32	40.0	80	6	ABP76310 Human GEN
42	30	37.5	30	6	ABU05051 Human exp
43	25	31.2	25	8	ADJ57562 Human CD9
44	22	27.5	24	8	ADJ57578 Human CD9
45	18	22.5	18	8	ADJ57563 Human CD9
46	15	18.8	226	7	ADB85281 Rat G9 su
47	13	16.2	226	4	ABB44580 Mouse wou
48	13	16.2	226	5	ABB57234 Mouse isc
49	13	16.2	226	9	ADV25799 Mouse CD9
50	13	16.2	226	9	AEAS5045 Mouse CD9
51	13	16.2	226	9	AEAS5045 Mouse CD9
52	10	12.5	10	6	ABU03385 Human exp
53	8	10.0	33	5	ABP43064 Human ova
54	8	10.0	303	5	ABP40370 Staphyloc
55	8	10.0	303	8	ADSO4987 Staphyloc
56	7	8.8	58	5	ABU51670 Helicobac
57	7	8.8	100	3	AAW25679 Soybean c
58	7	8.8	100	3	AAW25679 Soybean c
59	7	8.8	103	9	ADZ22202 Full leng
60	7	8.8	246	8	ADK67412 Plant ful
61	7	8.8	321	7	ABO77257 Pseudomon
62	7	8.8	516	4	AAU35716 Helicobac
63	7	8.8	516	4	AAU35716 Helicobac
64	7	8.8	589	6	ADA35614 Acinetoba
65	7	8.8	608	6	ABR40692 Zea maye
66	7	8.8	679	8	ADK66425 Plant ful
67	7	8.8	770	7	ABO78119 Pseudomon
68	7	8.8	781	7	ABO80180 Pseudomon
69	7	8.8	827	8	ADY07562 Plant ful
70	7	8.8	855	8	ADY07562 Plant ful
71	7	8.8	1020	6	ABU30092 Protein e
72	7	8.8	1104	7	ABR82748 Cold- and
73	7	8.8	1104	7	ADG32553 Murine TR
74	7	8.8	1140	4	ABB64675 Drosophill
75	7	8.8	1196	7	ADC94317 E. faecili
76	7	8.8	2444	4	ABB71807 Drosophill
77	6	7.5	9	6	ABR67406 Human pro
78	6	7.5	16	2	AAW31082 Amino aci
79	6	7.5	18	9	ADV67376 Amino aci
80	6	7.5	20	8	ADI95249 OSPF-rela
81	6	7.5	20	8	ADI95250 OSPF-rela
82	6	7.5	25	9	ADY28634 Novel mod
83	6	7.5	25	9	ADY28635 Novel mod
84	6	7.5	29	7	ADG14386 Cytochrom
85	6	7.5	31	7	ADD49210 Human HMG
86	6	7.5	33	6	ABJ18835 Human Bcl
87	6	7.5	37	7	ADP13922 Human end
88	6	7.5	42	3	AAW54485 Arabidops
89	6	7.5	43	5	AAO15500 Porphyra
90	6	7.5	62	5	ABP26527 Streptoco
91	6	7.5	62	8	ABO58008 Human gen
92	6	7.5	66	5	AAO15501 Porphyra
93	6	7.5	68	2	AAW98521 H. pylori
94	6	7.5	69	2	AAW98521 H. pylori
95	6	7.5	69	2	AAW98521 H. pylori
96	6	7.5	71	7	ADP14031 Human end
97	6	7.5	72	4	AAW83932 Human imm

98	6	7.5	72	4	ABG07225	Abg07225 Novel hum	171	6	7.5	123	4	AAO12084	Aao12084 Human pol
99	6	7.5	73	6	ABM73013	Abm73013 Staphyloc	172	6	7.5	125	4	AAU30896	Aau30896 Novel hum
100	6	7.5	74	5	AAH86173	Aah86173 Human imm	173	6	7.5	125	8	ADJ49997	Adj49997 Oil-assoc
101	6	7.5	74	5	ABP00618	Abp00618 Human ORF	174	6	7.5	125	8	ADJ49693	Adj49693 Oil-assoc
102	6	7.5	75	7	ABO66297	Ab066297 Klebsiell	175	6	7.5	126	8	ADJ49738	Adj49738 Oil-assoc
103	6	7.5	76	7	ADC94793	Adc94793 E. faeciu	176	6	7.5	127	8	ADP30103	Adp30103 Human sec
104	6	7.5	78	8	ADX74566	Adx74566 Plant ful	177	6	7.5	129	7	ADC00424	Adc00424 Enterohae
105	6	7.5	78	8	ADX74707	Adx74707 Plant ful	178	6	7.5	130	3	AG221210	Ag221210 Arabidops
106	6	7.5	81	7	ADD49202	Add49202 Human HMG	179	6	7.5	137	3	AAH38546	Aah38546 Human sec
107	6	7.5	85	5	AAO15498	Aao15498 Porphyra	180	6	7.5	141	9	ADY17158	Ady17158 PRO polyp
108	6	7.5	85	7	ADG14378	Adg14378 Cytochrom	181	6	7.5	143	4	RAA50141	Raa50141 Human bra
109	6	7.5	88	3	AAQ21211	Aaq21211 Arabidops	182	6	7.5	143	4	AAO10767	Aao10767 Human pol
110	6	7.5	88	7	ADD49206	Add49206 Human HMG	183	6	7.5	143	5	ABP00599	Abp00599 Human ORF
111	6	7.5	90	3	AB281899	Ab281899 Human HMG	184	6	7.5	144	6	ABP99886	Abp99886 Breast sp
112	6	7.5	90	4	ABG26793	Abg26793 Novel hum	185	6	7.5	144	7	ADC00619	Adc00619 Enterohae
113	6	7.5	90	5	AAO18887	Aao18887 Human ova	186	6	7.5	144	8	ADF85949	Adf85949 Human bre
114	6	7.5	90	6	ABU54863	Abu54863 Human ova	187	6	7.5	144	8	ADR94685	Adr94685 Novel S.
115	6	7.5	90	7	ADD49207	Add49207 Human HMG	188	6	7.5	144	9	AEA58555	Aea58555 Streptoco
116	6	7.5	90	8	ADO31118	Ado31118 N-end rul	189	6	7.5	146	4	AAU03698	Aau03698 Group B S
117	6	7.5	90	8	ADO31119	Ado31119 N-end rul	190	6	7.5	147	9	AEA28577	Aea28577 Stress co
118	6	7.5	90	8	ADP30101	Adp30101 Human sec	191	6	7.5	149	8	ADP99119	Adp99119 C. albica
119	6	7.5	90	8	ABM80042	Abm80042 Tumour-as	192	6	7.5	151	6	ABG74905	Abg74905 Human epi
120	6	7.5	90	8	ABM81597	Abm81597 Tumour-as	193	6	7.5	152	7	ADC00817	Adc00817 Enterohae
121	6	7.5	90	8	ABM80446	Abm80446 Tumour-as	194	6	7.5	153	4	AAU52790	Aau52790 Propionib
122	6	7.5	90	8	ADV70076	Adv70076 HLP-3P21	195	6	7.5	153	6	ABM49309	Abm49309 Propionib
123	6	7.5	91	6	ABU21061	Abu21061 Protein e	196	6	7.5	156	9	ABM90952	Abm90952 M. xanthu
124	6	7.5	92	2	AAW25678	Aaw25678 Soybean c	197	6	7.5	159	9	ADX38816	Adx38816 Human can
125	6	7.5	92	4	AAU46197	Aau46197 Propionib	198	6	7.5	161	5	ABG93444	Abg93444 Ehrlichia
126	6	7.5	92	6	ABM42716	Abm42716 Propionib	199	6	7.5	161	5	AAU73241	Aau73241 Human gra
127	6	7.5	92	8	ABM80011	Abm80011 Tumour-as	200	6	7.5	164	8	ADK16925	Adk16925 Nancarcha
128	6	7.5	93	5	ABG61520	Abg61520 Iron upta	201	6	7.5	165	4	RAO04331	Rao04331 Human pol
129	6	7.5	93	6	ABU01464	Abu01464 S. pneumo	202	6	7.5	165	8	ADO00803	Ado00803 Human dm
130	6	7.5	96	6	ADK75074	Adk75074 Plant ful	203	6	7.5	166	5	ABP32211	Abp32211 Human ORF
131	6	7.5	97	9	ADZ22210	Adz22210 Full leng	204	6	7.5	167	4	RAU69483	Rau69483 Human pur
132	6	7.5	97	9	ADZ22200	Adz22200 Full leng	205	6	7.5	169	7	ADH85764	Adh85764 Enterococ
133	6	7.5	98	8	ADY24162	Ady24162 Plant ful	206	6	7.5	170	8	ADN99424	Adn99424 Novel hum
134	6	7.5	98	8	ADX73597	Adx73597 Plant ful	207	6	7.5	171	3	AAQ21209	Aaq21209 Arabidops
135	6	7.5	98	8	AUX90899	Aux90899 Plant ful	208	6	7.5	173	3	AAH16715	Aah16715 Bacteriop
136	6	7.5	98	9	ADM85981	Adm85981 Coffea ca	209	6	7.5	175	4	ABG23712	Abg23712 Novel hum
137	6	7.5	99	8	ADX75277	Adx75277 Plant ful	210	6	7.5	175	9	ADU40601	Adu40601 Novel hum
138	6	7.5	100	8	ADK47228	Adk47228 Streptoco	211	6	7.5	175	9	AEA20954	Aea20954 Novel hum
139	6	7.5	100	8	ABM81534	Abm81534 Tumour-as	212	6	7.5	180	3	AAV99663	Aav99663 Human GTP
140	6	7.5	101	7	ADC00724	Adc00724 Enterohae	213	6	7.5	180	7	ADI40624	Adi40624 Human pur
141	6	7.5	101	8	ADX74479	Adx74479 Plant ful	214	6	7.5	181	4	AAE03650	Aae03650 Human ext
142	6	7.5	102	4	AAU42900	Aau42900 Propionib	215	6	7.5	183	6	ABU01866	Abu01866 S. pneumo
143	6	7.5	102	4	ABG26794	Abg26794 Novel hum	216	6	7.5	183	8	ADS43039	Ads43039 Bacterial
144	6	7.5	102	6	ABM39419	Abm39419 Propionib	217	6	7.5	186	7	ADB64005	Adb64005 Human pro
145	6	7.5	102	7	ADC00521	Adc00521 Enterohae	218	6	7.5	188	5	ABB50051	Abb50051 Listeria
146	6	7.5	103	4	ABG11216	Abg11216 Novel hum	219	6	7.5	188	6	ABM67739	Abm67739 Photorhab
147	6	7.5	103	8	ADX73610	Adx73610 Plant ful	220	6	7.5	192	8	ADM87685	Adm87685 Human EST
148	6	7.5	103	8	ADX77283	Adx77283 Plant ful	221	6	7.5	194	7	ABO63259	Ab063259 Klebsiell
149	6	7.5	104	4	ABG11523	Abg11523 Novel hum	222	6	7.5	195	6	ADB12771	Adb12771 Vigna ung
150	6	7.5	104	7	ADD01190	Add01190 Human nuc	223	6	7.5	196	7	ADF05019	Adf05019 Bacterial
151	6	7.5	104	8	ADK74802	Adk74802 Plant ful	224	6	7.5	201	7	ABM85631	Abm85631 Human pro
152	6	7.5	105	8	ADX92298	Adx92298 Plant ful	225	6	7.5	207	5	ABP39643	Abp39643 Staphyloc
153	6	7.5	105	9	ADW76459	Adw76459 Chestnut	226	6	7.5	207	8	ADS05706	Ads05706 Staphyloc
154	6	7.5	105	9	ADY52137	Ady52137 Phormidiu	227	6	7.5	207	9	ADX38835	Adx38835 Human can
155	6	7.5	106	4	ABG23711	Abg23711 Novel hum	228	6	7.5	210	4	RAE04375	Rae04375 Mouse can
156	6	7.5	109	5	ABP41531	Abp41531 Human ova	229	6	7.5	211	8	ADX75631	Adx75631 Plant ful
157	6	7.5	109	7	ADC95978	Adc95978 E. faeciu	230	6	7.5	213	9	AEA43741	Aea43741 Perhydrol
158	6	7.5	110	3	AY65677	Ay65677 C. elegan	231	6	7.5	213	9	AEA43753	Aea43753 Perhydrol
159	6	7.5	110	5	AAO15499	Aao15499 Porphyra	232	6	7.5	213	9	AEA43723	Aea43723 Perhydrol
160	6	7.5	111	9	ADX38815	Adx38815 Human can	233	6	7.5	213	9	AEA43168	Aea43168 Perhydrol
161	6	7.5	112	8	ADX92395	Adx92395 Plant ful	234	6	7.5	217	9	AEA40957	Aea40957 Novel hum
162	6	7.5	112	8	ADK76263	Adk76263 Plant ful	235	6	7.5	217	8	ADR15676	Adr15676 Kinase 63
163	6	7.5	113	4	ABG11212	Abg11212 Novel hum	236	6	7.5	221	4	AAE00187	Aae00187 Bacillus
164	6	7.5	113	6	ABM73551	Abm73551 Staphyloc	237	6	7.5	221	5	ABP27511	Abp27511 Streptoco
165	6	7.5	116	8	ABM81735	Abm81735 Tumour-as	238	6	7.5	221	8	ADV88430	Adv88430 Streptoco
166	6	7.5	118	6	ABU43101	Abu43101 Protein e	239	6	7.5	221	8	ADV79683	Adv79683 Streptoco
167	6	7.5	120	4	ABG07228	Abg07228 Novel hum	240	6	7.5	222	8	ADV81843	Adv81843 Streptoco
168	6	7.5	122	5	ABP39688	Abp39688 Staphyloc	241	6	7.5	222	2	AAH14159	Aah14159 Serine pr
169	6	7.5	122	6	ABP77038	Abp77038 N. gonorr	242	6	7.5	222	2	AAH26467	Aah26467 Sequence
170	6	7.5	122	8	ADS05804	Ads05804 Staphyloc	243	6	7.5	222	3	AAH43799	Aah43799 Human can

244	6	7.5	222	4	AAE00039	Bacillus	317	6	7.5	222	4	AAE00037	Bacillus
245	6	7.5	222	4	AAE00076	Bacillus	318	6	7.5	222	4	AAE00088	Bacillus
246	6	7.5	222	4	AAE00107	Bacillus	319	6	7.5	222	4	AAE00092	Bacillus
247	6	7.5	222	4	AAE00181	Bacillus	320	6	7.5	222	4	AAE00128	Bacillus
248	6	7.5	222	4	AAE00067	Bacillus	321	6	7.5	222	4	AAE00136	Bacillus
249	6	7.5	222	4	AAE00072	Bacillus	322	6	7.5	222	4	AAE00154	Bacillus
250	6	7.5	222	4	AAE00074	Bacillus	323	6	7.5	222	4	AAE00158	Bacillus
251	6	7.5	222	4	AAE00079	Bacillus	324	6	7.5	222	4	AAE00165	Bacillus
252	6	7.5	222	4	AAE00156	Bacillus	325	6	7.5	222	4	AAE00175	Bacillus
253	6	7.5	222	4	AAE00160	Bacillus	326	6	7.5	222	4	AAE00205	Bacillus
254	6	7.5	222	4	AAE00161	Bacillus	327	6	7.5	222	4	AAE00095	Bacillus
255	6	7.5	222	4	AAE00179	Bacillus	328	6	7.5	222	4	AAE00106	Bacillus
256	6	7.5	222	4	AAE00048	Bacillus	329	6	7.5	222	4	AAE00123	Bacillus
257	6	7.5	222	4	AAE00065	Bacillus	330	6	7.5	222	4	AAE00127	Bacillus
258	6	7.5	222	4	AAE00068	Bacillus	331	6	7.5	222	4	AAE00140	Bacillus
259	6	7.5	222	4	AAE00082	Bacillus	332	6	7.5	222	4	AAE00169	Bacillus
260	6	7.5	222	4	AAE00084	Bacillus	333	6	7.5	222	4	AAE00180	Bacillus
261	6	7.5	222	4	AAE00090	Bacillus	334	6	7.5	222	4	AAE00183	Bacillus
262	6	7.5	222	4	AAE00094	Bacillus	335	6	7.5	222	4	AAE00184	Bacillus
263	6	7.5	222	4	AAE00098	B. lichen	336	6	7.5	222	4	AAE00043	Bacillus
264	6	7.5	222	4	AAE00118	Bacillus	337	6	7.5	222	4	AAE00120	Bacillus
265	6	7.5	222	4	AAE00124	Bacillus	338	6	7.5	222	4	AAE00163	Bacillus
266	6	7.5	222	4	AAE00125	Bacillus	339	6	7.5	222	4	AAE00185	Bacillus
267	6	7.5	222	4	AAE00126	Bacillus	340	6	7.5	222	4	AAE00041	Bacillus
268	6	7.5	222	4	AAE00177	Bacillus	341	6	7.5	222	4	AAE00089	Bacillus
269	6	7.5	222	4	AAE00031	Bacillus	342	6	7.5	222	4	AAE00099	B. lichen
270	6	7.5	222	4	AAE00036	Bacillus	343	6	7.5	222	4	AAE00111	Bacillus
271	6	7.5	222	4	AAE00042	Bacillus	344	6	7.5	222	4	AAE00142	Bacillus
272	6	7.5	222	4	AAE00062	Bacillus	345	6	7.5	222	4	AAE00162	Bacillus
273	6	7.5	222	4	AAE00066	Bacillus	346	6	7.5	222	4	AAE00206	Bacillus
274	6	7.5	222	4	AAE00077	Bacillus	347	6	7.5	222	4	AAE00035	Bacillus
275	6	7.5	222	4	AAE00080	Bacillus	348	6	7.5	222	4	AAE00056	Bacillus
276	6	7.5	222	4	AAE00081	Bacillus	349	6	7.5	222	4	AAE00061	Bacillus
277	6	7.5	222	4	AAE00086	Bacillus	350	6	7.5	222	4	AAE00071	Bacillus
278	6	7.5	222	4	AAE00097	B. lichen	351	6	7.5	222	4	AAE00087	Bacillus
279	6	7.5	222	4	AAE00102	Bacillus	352	6	7.5	222	4	AAE00101	Bacillus
280	6	7.5	222	4	AAE00166	Bacillus	353	6	7.5	222	4	AAE00134	Bacillus
281	6	7.5	222	4	AAE00168	Bacillus	354	6	7.5	222	4	AAE00052	Bacillus
282	6	7.5	222	4	AAE00176	Bacillus	355	6	7.5	222	4	AAE00057	Bacillus
283	6	7.5	222	4	AAE00058	Bacillus	356	6	7.5	222	4	AAE00063	Bacillus
284	6	7.5	222	4	AAE00060	Bacillus	357	6	7.5	222	4	AAE00069	Bacillus
285	6	7.5	222	4	AAE00093	Bacillus	358	6	7.5	222	4	AAE00070	Bacillus
286	6	7.5	222	4	AAE00103	Bacillus	359	6	7.5	222	4	AAE00109	Bacillus
287	6	7.5	222	4	AAE00164	Bacillus	360	6	7.5	222	4	AAE00188	Bacillus
288	6	7.5	222	4	AAE00167	Bacillus	361	6	7.5	222	4	AAE00040	Bacillus
289	6	7.5	222	4	AAE00173	Bacillus	362	6	7.5	222	4	AAE00047	Bacillus
290	6	7.5	222	4	AAE00174	Bacillus	363	6	7.5	222	4	AAE00050	Bacillus
291	6	7.5	222	4	AAE000186	Bacillus	364	6	7.5	222	4	AAE00114	Bacillus
292	6	7.5	222	4	AAE000038	Bacillus	365	6	7.5	222	4	AAE00122	Bacillus
293	6	7.5	222	4	AAE000055	Bacillus	366	6	7.5	222	4	AAE00132	Bacillus
294	6	7.5	222	4	AAE000083	Bacillus	367	6	7.5	222	4	AAE00135	Bacillus
295	6	7.5	222	4	AAE000108	Bacillus	368	6	7.5	222	4	AAE00149	Bacillus
296	6	7.5	222	4	AAE000115	Bacillus	369	6	7.5	222	4	AAE00155	Bacillus
297	6	7.5	222	4	AAE000148	Bacillus	370	6	7.5	222	4	AAE00170	Bacillus
298	6	7.5	222	4	AAE000159	Bacillus	371	6	7.5	222	4	AAE00178	Bacillus
299	6	7.5	222	4	AAE000172	Bacillus	372	6	7.5	222	4	AAE00033	Bacillus
300	6	7.5	222	4	AAE000045	Bacillus	373	6	7.5	222	4	AAE00075	Bacillus
301	6	7.5	222	4	AAE000054	Bacillus	374	6	7.5	222	4	AAE00096	B. lichen
302	6	7.5	222	4	AAE000085	Bacillus	375	6	7.5	222	4	AAE00110	Bacillus
303	6	7.5	222	4	AAE000113	Bacillus	376	6	7.5	222	4	AAE00116	Bacillus
304	6	7.5	222	4	AAE000138	Bacillus	377	6	7.5	222	4	AAE00137	Bacillus
305	6	7.5	222	4	AAE000147	Bacillus	378	6	7.5	222	4	AAE00141	Bacillus
306	6	7.5	222	4	AAE000189	Bacillus	379	6	7.5	222	4	AAE00144	Bacillus
307	6	7.5	222	4	AAE000203	Bacillus	380	6	7.5	222	4	AAE00145	Bacillus
308	6	7.5	222	4	AAE000032	Bacillus	381	6	7.5	222	4	AAE00157	Bacillus
309	6	7.5	222	4	AAE000046	Bacillus	382	6	7.5	222	4	AAE00182	Bacillus
310	6	7.5	222	4	AAE000049	Bacillus	383	6	7.5	222	4	AAE00201	Bacillus
311	6	7.5	222	4	AAE000051	Bacillus	384	6	7.5	222	7	ADC99087	Human KPP
312	6	7.5	222	4	AAE000059	Bacillus	385	6	7.5	230	6	ABU33187	Protein e
313	6	7.5	222	4	AAE000119	Bacillus	386	6	7.5	230	9	ABE39502	L. pneumo
314	6	7.5	222	4	AAE000143	Bacillus	387	6	7.5	230	9	ABE36077	L. pneumo
315	6	7.5	222	4	AAE000146	Bacillus	388	6	7.5	235	6	ABU29765	Protein e
316	6	7.5	222	4	AAE000150	Bacillus	389	6	7.5	240	2	AAE22597	Foetal on

390	6	7.5	240	7	ADG73666	Adg73666	C. perfr	463	6	7.5	314	4	AAE00013	Aae00013	Bacillus
391	6	7.5	241	4	ABR71853	Abb71853	Drosophil	464	6	7.5	314	8	ADY08037	Ady08037	Plant ful
392	6	7.5	245	7	ABO77558	AbO77558	Pseudomon	465	6	7.5	316	2	AAZ23730	Aaz23730	Protease
393	6	7.5	247	6	ADB11458	AdB11458	Alloiooc	466	6	7.5	316	4	AAE00011	Aae00011	Bacillus
394	6	7.5	248	7	ABO76042	AbO76042	Pseudomo	467	6	7.5	316	8	ADG32274	AdG32274	Mutant B
395	6	7.5	248	9	ABE42645	Aeb42645	L. pneumo	468	6	7.5	318	4	AAE00015	Aae00015	Bacillus-
396	6	7.5	251	7	ADJ69728	AdJ69728	Human hea	469	6	7.5	319	3	AAE16397	Aab16397	Pinus rad
397	6	7.5	251	8	ADK16903	AdK16903	Nanoarcha	470	6	7.5	319	3	AAE16397	Aab16397	Pinus rad
398	6	7.5	252	7	ADJ71852	AdJ71852	Pseudomon	471	6	7.5	319	8	ADP90917	AdP90917	Isorflavon
399	6	7.5	255	7	ADJ70037	AdJ70037	Human hea	472	6	7.5	321	5	ABP29864	AbP29864	Streptoco
400	6	7.5	255	9	ADY70494	AdY70494	Human bet	473	6	7.5	322	6	AAE37822	Aae37822	Rat 3 alp
401	6	7.5	258	4	ABG75597	AbG75597	Human col	474	6	7.5	322	5	ADG55971	AdG55971	Rat prote
402	6	7.5	259	6	ABP78102	AbP78102	N. gonorr	475	6	7.5	324	7	ABG76658	AbG76658	Zebrafish
403	6	7.5	259	6	ADB06094	AdB06094	Alloiooc	476	6	7.5	325	8	ADS28687	AdS28687	Bacterial
404	6	7.5	261	2	AAW82855	Aaw82855	Ehrlichia	477	6	7.5	327	7	ADF05934	AdF05934	Bacterial
405	6	7.5	261	3	AAW78533	Aaw78533	Ehrlichia	478	6	7.5	332	3	AAE53447	AbE53447	Human col
406	6	7.5	261	5	ABG93430	AbG93430	Ehrlichia	479	6	7.5	332	4	ABG18841	AbG18841	Novel hum
407	6	7.5	261	5	AAU73327	Aau73327	Human gra	480	6	7.5	334	3	AAE51994	Aab51994	Human sec
408	6	7.5	265	3	AAV94451	Aav94451	Human inf	481	6	7.5	334	3	AAE51993	Aab51993	Gene 38 h
409	6	7.5	265	6	ABE74468	AbE74468	Human Ras	482	6	7.5	334	7	ABO78623	AbO78623	Pseudomon
410	6	7.5	265	7	AE38994	Aae38994	Human RAT	483	6	7.5	334	7	ABO78623	AbO78623	Pseudomon
411	6	7.5	265	7	ADC39998	AdC39998	Human Ras	484	6	7.5	336	8	ADY22408	AdY22408	Plant ful
412	6	7.5	265	7	ADG86497	AdG86497	Protein e	485	6	7.5	336	8	AAE79432	Aab79432	Corynebac
413	6	7.5	265	7	ABW01909	AbW01909	Human inf	486	6	7.5	343	8	ADJ64325	AdJ64325	Cartilage
414	6	7.5	265	8	ADO00801	AdO00801	Human RAP	487	6	7.5	344	7	ABO67971	AbO67971	Pseudomon
415	6	7.5	265	8	ADO00807	AdO00807	Mouset RAP	488	6	7.5	345	6	ABR39092	AbR39092	Cercopith
416	6	7.5	265	9	AEA26103	Aea26103	Human ren	489	6	7.5	345	6	ABR39093	AbR39093	Cercopith
417	6	7.5	273	6	ABU11546	AbU11546	Human MDD	490	6	7.5	345	7	ADE08054	AdE08054	Novel pro
418	6	7.5	273	8	ADP56325	AdP56325	Human PRO	491	6	7.5	345	9	ADU40424	AdU40424	Novel hum
419	6	7.5	274	8	ADP22698	AdP22698	Rice stre	492	6	7.5	346	8	ADR28819	AdR28819	Human tru
420	6	7.5	275	8	ADS30082	AdS30082	Bacterial	493	6	7.5	348	3	AAE24671	Aae24671	Arabidops
421	6	7.5	279	4	ABH86253	AbH86253	C. glutam	494	6	7.5	348	4	ABG05182	AbG05182	Novel hum
422	6	7.5	279	6	ABU44422	AbU44422	Protein e	495	6	7.5	349	4	AAE92143	Aae92143	C Glutam
423	6	7.5	280	6	ABU43599	AbU43599	Protein e	496	6	7.5	352	7	AAE38993	Aae38993	Human ant
424	6	7.5	281	8	ADG69516	AdG69516	Rice plan	497	6	7.5	353	6	ABO7962	AbO7962	Alloiooc
425	6	7.5	282	4	AAU34080	Aau34080	Staphyloc	498	6	7.5	356	4	ABE61320	AbE61320	Drosophil
426	6	7.5	288	2	AAW98949	Aaw98949	Streptoco	499	6	7.5	356	7	ADJ70253	AdJ70253	Human hea
427	6	7.5	288	6	ADB06062	AdB06062	Alloiooc	500	6	7.5	360	3	AAE24670	Aae24670	Arabidops
428	6	7.5	289	6	ABU25294	AbU25294	Protein e	501	6	7.5	362	7	ADK14197	AdK14197	Human strc
429	6	7.5	290	3	AAE58884	Aae58884	Breast an	502	6	7.5	362	7	ADK65829	AdK65829	Angiogene
430	6	7.5	292	4	AAU36847	Aau36847	Staphyloc	503	6	7.5	369	9	ADX38833	AdX38833	Human can
431	6	7.5	292	6	ABU16190	AbU16190	Protein e	504	6	7.5	369	3	ADG24669	Aag24669	Arabidops
432	6	7.5	292	5	ABW72449	AbW72449	Staphyloc	505	6	7.5	370	4	AAE93450	Aab93450	Human pro
433	6	7.5	293	5	ABE50136	AbE50136	Listeria	506	6	7.5	370	4	AAE47993	AdA47993	Pristanoy
434	6	7.5	293	6	ABU32844	AbU32844	Protein e	507	6	7.5	372	6	ADA34343	AdA34343	Acinetoba
435	6	7.5	296	3	AAE30066	Aae30066	Arabidops	508	6	7.5	372	7	ADM05595	AdM05595	Human pro
436	6	7.5	297	8	ADJ67238	AdJ67238	Lactobaci	509	6	7.5	375	7	ADE76397	AdE76397	Baker's y
437	6	7.5	299	8	ADP30102	AdP30102	Human sec	510	6	7.5	375	9	AEA25916	Aea25916	Caenorhab
438	6	7.5	300	6	ABW72865	AbW72865	Staphyloc	511	6	7.5	376	9	ABE10653	Aeb10653	SIVBK28 a
439	6	7.5	300	7	ADH87377	AdH87377	Enterococ	512	6	7.5	377	5	ABP28195	AbP28195	Streptoco
440	6	7.5	303	2	AAV59676	Aav59676	Secreted	513	6	7.5	378	6	ADB07964	AdB07964	Alloiooc
441	6	7.5	303	7	ADJ69038	AdJ69038	Human hea	514	6	7.5	379	8	ADN20362	AdN20362	Bacterial
442	6	7.5	303	7	ADJ69039	AdJ69039	Human hea	515	6	7.5	381	4	AAE09695	Aae09695	Human gen
443	6	7.5	303	7	ADM77826	AdM77826	Human pro	516	6	7.5	381	7	ADC22073	AdC22073	Human pro
444	6	7.5	303	8	ADL82985	AdL82985	Human PRO	517	6	7.5	382	6	ABU28948	AbU28948	Protein e
445	6	7.5	303	8	ADP19507	AdP19507	Human sec	518	6	7.5	384	4	AAU35149	Aau35149	Enterococ
446	6	7.5	303	8	ADP56144	AdP56144	Human PRO	519	6	7.5	384	4	ABE58862	AbE58862	Drosophil
447	6	7.5	303	8	ADR89538	AdR89538	Apoptosis	520	6	7.5	384	8	ADX93638	AdX93638	Plant ful
448	6	7.5	303	8	ADR89540	AdR89540	Apoptosis	521	6	7.5	386	2	AAW92507	Aaw92507	Yeast del
449	6	7.5	303	9	ADZ89286	AdZ89286	Secreted	522	6	7.5	387	5	ADE52958	Ade52958	Yeast rel
450	6	7.5	304	7	ADL22730	AdL22730	Human dis	523	6	7.5	387	9	ABE87185	Aeb87185	Yeast RAD
451	6	7.5	305	8	ADO63053	AdO63053	Transcrip	524	6	7.5	389	6	ABO06684	Abo06684	Novel hum
452	6	7.5	305	8	ADX73352	AdX73352	Plant ful	525	6	7.5	389	6	ADM77489	AdM77489	Human fib
453	6	7.5	305	9	AEA27129	Aea27129	Stress to	526	6	7.5	390	6	ABR43661	AbR43661	Human Max
454	6	7.5	306	8	ABU34158	AbU34158	Protein e	527	6	7.5	390	7	ADE54585	Ade54585	Human Pro
455	6	7.5	306	8	ADI67144	AdI67144	Lactobaci	528	6	7.5	390	8	ADM87228	AdM87228	Human pro
456	6	7.5	306	8	ADX71183	AdX71183	Plant ful	529	6	7.5	390	8	ADP12987	AdP12987	Protein e
457	6	7.5	307	7	ADH87945	AdH87945	Enterococ	530	6	7.5	390	9	AEA26101	Aea26101	Human ren
458	6	7.5	308	5	ABN97523	AbN97523	Novel hum	531	6	7.5	392	7	ADA66100	AdA66100	DNAP-rela
459	6	7.5	308	6	ABU41449	AbU41449	Protein e	532	6	7.5	394	7	ADM26772	AdM26772	Hyperther
460	6	7.5	311	4	AAE95509	Aae95509	Human pro	533	6	7.5	395	9	ADX38832	AdX38832	Human can
461	6	7.5	312	2	AAV07109	Aav07109	Colon can	534	6	7.5	397	8	ADN17608	AdN17608	Bacterial
462	6	7.5	312	7	ADC96592	AdC96592	E. faeciu	535	6	7.5	398	6	ABU19092	AbU19092	Protein e

536	6	7.5	399	6	AD54651	Ada54651 Human pro	609	6	7.5	440	9	AD259839	Ad259839 SIV CP-MA
537	6	7.5	399	8	ADN18018	Adn18018 Bacterial	610	6	7.5	440	9	AD259820	Ad259820 SIV NC-MA
538	6	7.5	399	2	AAW01114	Aaw01114 Brain-spe	611	6	7.5	440	9	AD259842	Ad259842 SIV CP-MA
539	6	7.5	400	2	AAW83429	Aaw83429 Human Doc	612	6	7.5	440	9	AD259819	Ad259819 SIV BK-28
540	6	7.5	400	7	AD259821	Ad259821 Human Pro	613	6	7.5	440	9	AD259827	Ad259827 SIV NC-MA
541	6	7.5	400	7	AD259821	Ad259821 Human Pro	614	6	7.5	440	9	AD259830	Ad259830 SIV CP-MA
542	6	7.5	400	9	AB40157	Ab40157 L. pneumo	615	6	7.5	440	9	AD259833	Ad259833 SIV CP-MA
543	6	7.5	402	5	AAE26853	Aae26853 Anabaena	616	6	7.5	440	9	AD259834	Ad259834 SIV CP-MA
544	6	7.5	403	7	ADB74355	Adb74355 Mycobacte	617	6	7.5	440	9	AD259840	Ad259840 SIV CP-MA
545	6	7.5	403	7	AD259840	Ad259840 Rat. Prote	618	6	7.5	440	9	AD259845	Ad259845 SIV CP-MA
546	6	7.5	403	8	ADN17541	Adn17541 Bacterial	619	6	7.5	440	9	AD259848	Ad259848 SIV CP-MA
547	6	7.5	403	8	AD259848	Ad259848 Bacterial	620	6	7.5	440	9	AD259831	Ad259831 SIV CP-MA
548	6	7.5	403	8	AD259831	Ad259831 Plant ful	621	6	7.5	440	9	AD259836	Ad259836 SIV CP-MA
549	6	7.5	403	9	AEA19980	Aea19980 Novel hum	622	6	7.5	440	9	AD259841	Ad259841 SIV CP-MA
550	6	7.5	405	2	AAV27275	Aav27275 Mouse Doc	623	6	7.5	440	9	AD259844	Ad259844 SIV CP-MA
551	6	7.5	405	6	ABU02242	Abu02242 S. pneumo	624	6	7.5	440	9	AD259849	Ad259849 SIV CP-MA
552	6	7.5	405	7	AD259849	Ad259849 Rat. Prote	625	6	7.5	442	8	AD259845	Ad259845 SIV CP-MA
553	6	7.5	406	3	AAV81562	Aav81562 Streptoco	626	6	7.5	442	8	AD259848	Ad259848 SIV CP-MA
554	6	7.5	406	6	ADA35277	Ada35277 Acinetoba	627	6	7.5	449	8	ADN19753	Adn19753 Bacterial
555	6	7.5	408	6	ABP80737	Abp80737 N. gonorr	628	6	7.5	451	8	AD259836	Ad259836 SIV CP-MA
556	6	7.5	409	7	AD259836	Ad259836 Novel hum	629	6	7.5	452	7	ABO66041	Ab066041 Klebsiell
557	6	7.5	409	8	ADF53516	Adf53516 Human hex	630	6	7.5	452	8	ADY10721	Ady10721 Plant ful
558	6	7.5	410	8	ADN17713	Adn17713 Bacterial	631	6	7.5	453	4	AB886601	Ab886601 Human hyd
559	6	7.5	411	6	ABU47023	Abu47023 Protein e	632	6	7.5	453	5	ABJ10916	Abj10916 Human sec
560	6	7.5	411	6	ABU47648	Abu47648 Protein e	633	6	7.5	453	5	AB494460	Ab494460 Listeria
561	6	7.5	411	6	ABU31631	Abu31631 Protein e	634	6	7.5	453	8	ADN19753	Adn19753 Bacterial
562	6	7.5	411	6	ABU31631	Abu31631 Protein e	635	6	7.5	453	8	ADN19753	Adn19753 Bacterial
563	6	7.5	411	6	ABU31631	Abu31631 Protein e	636	6	7.5	453	8	ADN19753	Adn19753 Bacterial
564	6	7.5	411	6	ADJ49805	Adj49805 Oil-assoc	637	6	7.5	455	5	ABP69701	Abp69701 Human pol
565	6	7.5	412	7	ADN97359	Adn97359 B. lichen	638	6	7.5	455	5	ABO84784	Ab084784 Human can
566	6	7.5	412	9	ABE36782	Abe36782 L. pneumo	639	6	7.5	456	5	ABO9697	Ab09697 Amino aci
567	6	7.5	413	2	AAW46822	Aaw46822 Amino aci	640	6	7.5	459	8	AD22711	Ad22711 Bacterial
568	6	7.5	413	2	AAW05724	Aaw05724 Ras bindi	641	6	7.5	460	2	AAV22924	Aav22924 Protein e
569	6	7.5	413	6	ABU49722	Abu49722 Protein e	642	6	7.5	462	3	AAV38287	Aav38287 Protein e
570	6	7.5	413	7	ADC40011	Adc40011 Mouse NOR	643	6	7.5	474	3	ABU38287	Abu38287 Protein e
571	6	7.5	413	7	ADC40011	Adc40011 Mouse NOR	644	6	7.5	475	4	ABG15897	Abg15897 Murine fe
572	6	7.5	413	7	ADC40011	Adc40011 Mouse NOR	645	6	7.5	475	4	ABG15897	Abg15897 Murine fe
573	6	7.5	413	8	ABA26109	Aba26109 Human ren	646	6	7.5	475	4	ABG15897	Abg15897 Murine fe
574	6	7.5	413	8	ABA26109	Aba26109 Human ren	647	6	7.5	475	4	ABG15897	Abg15897 Murine fe
575	6	7.5	414	2	AAV15484	Aav15484 Protein e	648	6	7.5	475	4	ABG15897	Abg15897 Murine fe
576	6	7.5	416	2	AAV37263	Aav37263 Chlamydia	649	6	7.5	475	4	ABG15897	Abg15897 Murine fe
577	6	7.5	416	2	ABO79650	Ab079650 Pseudomon	650	6	7.5	475	4	ABG15897	Abg15897 Murine fe
578	6	7.5	416	8	ADJ50949	Adj50949 Human nov	651	6	7.5	475	4	ABG15897	Abg15897 Murine fe
579	6	7.5	417	4	ABE64872	Abbe64872 Drosophil	652	6	7.5	478	8	AD26074	Ad26074 Bacterial
580	6	7.5	418	6	ABU15361	Abu15361 Protein e	653	6	7.5	480	8	AD26074	Ad26074 Bacterial
581	6	7.5	419	8	ADY22929	Ady22929 Plant ful	654	6	7.5	481	3	AAV38287	Aav38287 Protein e
582	6	7.5	420	4	ABG00313	Abg00313 Novel hum	655	6	7.5	481	3	AAV38287	Aav38287 Protein e
583	6	7.5	420	6	ABU21007	Abu21007 Protein e	656	6	7.5	481	3	AAV38287	Aav38287 Protein e
584	6	7.5	420	7	AD21639	Ad21639 Protein e	657	6	7.5	481	3	AAV38287	Aav38287 Protein e
585	6	7.5	422	5	AB847734	Ab847734 Listeria	658	6	7.5	481	3	AAV38287	Aav38287 Protein e
586	6	7.5	424	8	AD21026	Ad21026 Bacterial	659	6	7.5	482	3	AAV38287	Aav38287 Protein e
587	6	7.5	429	8	ADN1997	Adn1997 Bacterial	660	6	7.5	482	3	AAV38287	Aav38287 Protein e
588	6	7.5	430	4	AAV96652	Aav96652 Putative	661	6	7.5	482	3	AAV38287	Aav38287 Protein e
589	6	7.5	433	3	AAV19094	Aav19094 Protein e	662	6	7.5	482	3	AAV38287	Aav38287 Protein e
590	6	7.5	433	8	ADP87472	Adp87472 S. cerevis	663	6	7.5	482	3	AAV38287	Aav38287 Protein e
591	6	7.5	433	8	ADP87472	Adp87472 S. cerevis	664	6	7.5	482	3	AAV38287	Aav38287 Protein e
592	6	7.5	437	5	AAW47762	Aaw47762 RNA bindi	665	6	7.5	482	3	AAV38287	Aav38287 Protein e
593	6	7.5	438	7	ABO68045	Ab068045 Pseudomon	666	6	7.5	482	3	AAV38287	Aav38287 Protein e
594	6	7.5	439	7	AD242423	Ad242423 Human NOV	667	6	7.5	482	3	AAV38287	Aav38287 Protein e
595	6	7.5	439	9	AD259823	Ad259823 SIV NC-MA	668	6	7.5	482	3	AAV38287	Aav38287 Protein e
596	6	7.5	439	9	AD259823	Ad259823 SIV NC-MA	669	6	7.5	482	3	AAV38287	Aav38287 Protein e
597	6	7.5	440	9	AD259846	Ad259846 SIV CP-MA	670	6	7.5	482	3	AAV38287	Aav38287 Protein e
598	6	7.5	440	9	AD259846	Ad259846 SIV CP-MA	671	6	7.5	482	3	AAV38287	Aav38287 Protein e
599	6	7.5	440	9	AD259829	Ad259829 SIV NC-MA	672	6	7.5	482	3	AAV38287	Aav38287 Protein e
600	6	7.5	440	9	AD259832	Ad259832 SIV CP-MA	673	6	7.5	482	3	AAV38287	Aav38287 Protein e
601	6	7.5	440	9	AD259847	Ad259847 SIV CP-MA	674	6	7.5	482	3	AAV38287	Aav38287 Protein e
602	6	7.5	440	9	AD259847	Ad259847 SIV CP-MA	675	6	7.5	482	3	AAV38287	Aav38287 Protein e
603	6	7.5	440	9	AD259825	Ad259825 SIV NC-MA	676	6	7.5	482	3	AAV38287	Aav38287 Protein e
604	6	7.5	440	9	AD259825	Ad259825 SIV NC-MA	677	6	7.5	482	3	AAV38287	Aav38287 Protein e
605	6	7.5	440	9	AD259835	Ad259835 SIV CP-MA	678	6	7.5	482	3	AAV38287	Aav38287 Protein e
606	6	7.5	440	9	AD259843	Ad259843 SIV CP-MA	679	6	7.5	482	3	AAV38287	Aav38287 Protein e
607	6	7.5	440	9	AD259826	Ad259826 SIV NC-MA	680	6	7.5	482	3	AAV38287	Aav38287 Protein e
608	6	7.5	440	9	AD259838	Ad259838 SIV CP-MA	681	6	7.5	482	3	AAV38287	Aav38287 Protein e

682	6	7.5	501	6	ABR53864	Protein s	755	6	7.5	538	8	AD51817	Human sec
683	6	7.5	501	7	ADK64896	Disease t	756	6	7.5	538	8	AD537675	Human sec
684	6	7.5	501	8	ADS21678	Bacterial	757	6	7.5	538	8	AD537559	Human sec
685	6	7.5	502	3	AG30064	Arabidops	758	6	7.5	538	8	ADD95330	Human sec
686	6	7.5	503	2	ABR82837	SIVmac239	759	6	7.5	538	8	AD538030	Human PRO
687	6	7.5	505	2	AAR97731	Barley be	760	6	7.5	538	8	AD576119	Human PRO
688	6	7.5	506	6	ADA54661	Human pro	761	6	7.5	538	8	AD539442	Human PRO
689	6	7.5	507	4	AB655913	Drosophil	762	6	7.5	538	8	AD539442	Human PRO
690	6	7.5	507	5	AM48909	Zoysia te	763	6	7.5	538	8	AD504246	Human PRO
691	6	7.5	508	2	AW89793	Staphyloc	764	6	7.5	538	8	AD539843	Human PRO
692	6	7.5	509	7	ADH86922	Enterococ	765	6	7.5	538	8	AD519708	Human PRO
693	6	7.5	511	2	AAR57436	Human cal	766	6	7.5	538	8	AD577286	Human sec
694	6	7.5	511	8	AD543328	Rat PPP3C	767	6	7.5	538	8	AD565394	Human PRO
695	6	7.5	511	9	AD543328	Rat PPP3C	767	6	7.5	538	8	AD565394	Human PRO
696	6	7.5	511	9	AD543328	Rat PPP3C	767	6	7.5	538	8	AD565394	Human PRO
697	6	7.5	512	4	AM40648	Human pol	768	6	7.5	538	8	AD537914	Human PRO
698	6	7.5	520	7	ABO75051	Pseudomon	769	6	7.5	538	8	AD564524	Human PRO
699	6	7.5	521	4	AG67636	Amino aci	770	6	7.5	538	8	AD538859	Human PRO
700	6	7.5	521	4	AG67636	Amino aci	771	6	7.5	538	8	AD538859	Human PRO
701	6	7.5	521	5	AB09696	Amino aci	772	6	7.5	538	8	AD519333	Human sec
702	6	7.5	521	8	AD543226	Mouse PPP	773	6	7.5	538	8	AD5090964	Human sec
703	6	7.5	521	8	AD543226	Mouse PPP	774	6	7.5	538	8	AD538743	Human PRO
704	6	7.5	521	8	AD543226	Mouse PPP	774	6	7.5	538	8	AD538743	Human PRO
705	6	7.5	521	8	AD543226	Mouse PPP	774	6	7.5	538	8	AD538743	Human PRO
706	6	7.5	521	8	AD543226	Mouse PPP	774	6	7.5	538	8	AD538743	Human PRO
707	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
708	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
709	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
710	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
711	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
712	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
713	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
714	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
715	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
716	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
717	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
718	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
719	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
720	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
721	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
722	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
723	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
724	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
725	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
726	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
727	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
728	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
729	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
730	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
731	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
732	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
733	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
734	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
735	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
736	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
737	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
738	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
739	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
740	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
741	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
742	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
743	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
744	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
745	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
746	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
747	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
748	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
749	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
750	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
751	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
752	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
753	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO
754	6	7.5	522	9	ABE13006	Yeast pro	775	6	7.5	538	8	AD506260	Human PRO

828	6	7.5	558	8	ADR70103	Adr70103 Human atl	901	6	7.5	652	4	AAU69897	Aau69897 Human pro
829	6	7.5	558	2	ADY70455	Ady70455 Human bet	902	6	7.5	652	4	ABU71788	Abu71788 Prostate
830	6	7.5	560	9	AAW28505	Aaw28505 Mugwort g	903	6	7.5	652	5	ABB95357	Abb95357 Human p78
831	6	7.5	562	4	ABB60336	Abb60336 Drosophil	904	6	7.5	652	6	ABR54469	Abr54469 Prostate
832	6	7.5	565	9	ADW28506	Adw28506 Human klo	905	6	7.5	652	7	ADB14268	Adb14268 Human pro
833	6	7.5	567	8	ADR66342	Adr66342 Human pro	906	6	7.5	652	7	ABR39130	Abr39130 Human tra
834	6	7.5	567	8	ADR66684	Adr66684 Human pro	907	6	7.5	652	7	ABR39128	Abr39128 Human tra
835	6	7.5	567	9	ADW28508	Adw28508 Mouse klo	908	6	7.5	652	7	ADG26684	Adg26684 Human pro
836	6	7.5	569	4	ABM69913	Abm69913 Drosophil	909	6	7.5	654	9	ADX26333	Adx26333 Novel cel
837	6	7.5	569	7	ABM86636	Abm86636 Rice abio	910	6	7.5	654	9	ABO83196	Abos83196 Pseudomon
838	6	7.5	570	3	AAV49958	Aav49958 Human ves	911	6	7.5	670	7	ADC31780	Adc31780 Human nov
839	6	7.5	570	3	ABO3813	Abos3813 Human ves	912	6	7.5	674	6	ABJ19509	Abj19509 Ul15 DNA
840	6	7.5	570	4	AAW94478	Aaw94478 Human pro	913	6	7.5	674	6	ABJ19464	Abj19464 Ul15 DNA
841	6	7.5	570	5	ABE57217	Abes57217 Mouse isc	914	6	7.5	676	8	ADL24459	Adl24459 Rat trans
842	6	7.5	570	7	ADE61222	Ade61222 Rat Prote	915	6	7.5	676	8	ADL24459	Adl24459 Rat trans
843	6	7.5	570	7	ADBE61224	Adbe61224 Human Pro	916	6	7.5	676	9	ADY54162	Ady54162 Amino aci
844	6	7.5	570	8	ADP12603	Adp12603 Protein e	917	6	7.5	682	8	ADT60464	Adt60464 Plant pol
845	6	7.5	570	8	ADR99181	Adr99181 Vacuolar	918	6	7.5	682	8	AAW25719	Aaw25719 Human alp
846	6	7.5	571	5	ABP25425	Abp25425 Streptoco	919	6	7.5	686	2	AAW25719	Aaw25719 Human alp
847	6	7.5	571	8	ADJ48639	Adj48639 Oil-assoc	920	6	7.5	689	8	ADO09744	Ado09744 Human gen
848	6	7.5	571	8	ADV88216	Adv88216 Streptoco	921	6	7.5	691	7	ABO70760	Abos70760 Pseudomon
849	6	7.5	571	8	ADV79469	Adv79469 Streptoco	922	6	7.5	695	7	ADP30710	Adp30710 Rat angio
850	6	7.5	571	8	ADV81641	Adv81641 Streptoco	923	6	7.5	696	7	ADU42822	Adu42822 Protein e
851	6	7.5	572	7	ABO76340	Abos76340 Pseudomon	924	6	7.5	697	4	ABG11428	Abg11428 Novel hum
852	6	7.5	572	7	ABO76340	Abos76340 Pseudomon	925	6	7.5	697	4	ABG11428	Abg11428 Novel hum
853	6	7.5	572	9	ABE91419	Abes91419 Microbial	926	6	7.5	698	5	ABP38787	Abp38787 Staphyloc
854	6	7.5	574	8	ADJ48650	Adj48650 Oil-assoc	927	6	7.5	700	7	ABO79598	Abos79598 Pseudomon
855	6	7.5	578	4	ABG04478	Abg04478 Novel hum	928	6	7.5	704	2	AAV31754	Aav31754 Candida t
856	6	7.5	581	4	ABE58513	Abes58513 Drosophil	929	6	7.5	704	7	ADG42261	Adg42261 Fatty alc
857	6	7.5	581	7	ADN37921	Adn37921 D melanog	930	6	7.5	704	7	ADG42259	Adg42259 Fatty alc
858	6	7.5	582	8	ADN47488	Adn47488 Thermococ	931	6	7.5	704	7	ADG42265	Adg42265 Fatty alc
859	6	7.5	586	2	AAW07274	Aaw07274 Reverse t	932	6	7.5	705	4	ADG42267	Adg42267 Fatty alc
860	6	7.5	586	2	AAW11920	Aaw11920 Reverse t	933	6	7.5	715	4	AAU34857	Aau34857 E. coli c
861	6	7.5	586	3	AAW13935	Aaw13935 meDNA-Ec6	934	6	7.5	715	6	ABU47919	Abu47919 Protein e
862	6	7.5	586	3	AAW76811	Aaw76811 E. coli m	935	6	7.5	715	6	ABU15299	Abu15299 Protein e
863	6	7.5	586	5	AAW49402	Aaw49402 Escherich	936	6	7.5	715	8	ADU45230	Adu45230 Bacterial
864	6	7.5	588	4	ABG21171	Abg21171 Novel hum	937	6	7.5	719	3	AAW82644	Aaw82644 Ehrlichia
865	6	7.5	589	4	ABG21171	Abg21171 Novel hum	938	6	7.5	719	3	AAW82644	Aaw82644 Ehrlichia
866	6	7.5	594	4	ABG19168	Abg19168 Novel hum	939	6	7.5	719	5	ABG93417	Abg93417 Ehrlichia
867	6	7.5	598	8	ADW74760	Adw74760 Plant ful	940	6	7.5	723	4	ABE59070	Abes59070 Drosophil
868	6	7.5	599	5	ABE53321	Abes53321 Lactococc	941	6	7.5	728	8	ADJ67542	Adj67542 Human ova
869	6	7.5	599	8	ADS15133	Ads15133 Pseudomon	942	6	7.5	728	8	ADP81154	Adp81154 Protein o
870	6	7.5	600	7	ABO72957	Abos72957 Pseudomon	943	6	7.5	729	4	ABE60766	Abes60766 Drosophil
871	6	7.5	610	5	AAU12039	Aau12039 Clostridi	944	6	7.5	729	8	ADU44105	Adu44105 Bacterial
872	6	7.5	610	6	ABU25105	Abu25105 Protein e	945	6	7.5	730	2	ABM86046	Abm86046 Rice abio
873	6	7.5	610	7	ADD15932	Add15932 Aspergill	946	6	7.5	735	2	AAW41695	Aaw41695 Human PRO
874	6	7.5	610	7	ADD15932	Add15932 Aspergill	947	6	7.5	735	3	AAW44251	Aaw44251 Human PRO
875	6	7.5	610	7	ADD15930	Add15930 Wild-type	948	6	7.5	735	4	AAU29067	Aau29067 Human PRO
876	6	7.5	612	9	ADY30892	Ady30892 Campyloba	949	6	7.5	735	6	ABU58443	Abu58443 Human PRO
877	6	7.5	618	7	ABO73672	Abos73672 Pseudomon	950	6	7.5	735	6	ABU87991	Abu87991 Novel hum
878	6	7.5	624	8	ADY23706	Ady23706 Plant ful	951	6	7.5	735	6	ABU84306	Abu84306 Human sec
879	6	7.5	625	9	ADY30893	Ady30893 Campyloba	952	6	7.5	735	6	ABR66180	Abr66180 Human sec
880	6	7.5	630	9	ABM91886	Abm91886 M. xanthu	953	6	7.5	735	6	ABR66180	Abr66180 Human sec
881	6	7.5	631	9	ABO71672	Abos71672 Pseudomon	954	6	7.5	735	6	ABR65570	Abr65570 Human sec
882	6	7.5	631	9	ABO71672	Abos71672 Pseudomon	955	6	7.5	735	6	ABU99510	Abu99510 Human sec
883	6	7.5	632	3	AAW42782	Aaw42782 Human ORF	956	6	7.5	735	6	ABU82749	Abu82749 Human PRO
884	6	7.5	632	3	AAW26916	Aaw26916 Nitric ox	957	6	7.5	735	6	ABU89870	Abu89870 Novel hum
885	6	7.5	632	9	ADY62617	Ady62617 Pseudomon	958	6	7.5	735	6	ABR68119	Abr68119 Human sec
886	6	7.5	632	9	ADY62623	Ady62623 Novel cel	959	6	7.5	735	6	ABU96172	Abu96172 Novel hum
887	6	7.5	633	8	ADW74359	Adw74359 Plant ful	960	6	7.5	735	6	ABO02732	Abos02732 Human sec
888	6	7.5	634	5	AAE20287	Aae20287 Human Trp	961	6	7.5	735	6	ABO08680	Abos08680 Human sec
889	6	7.5	640	5	ABP92655	Abp92655 Herbicida	962	6	7.5	735	6	ABR74886	Abr74886 Human sec
890	6	7.5	642	7	ADG73672	Adg73672 Human acb	963	6	7.5	735	6	ABR94648	Abr94648 Human sec
891	6	7.5	643	4	ABE61390	Abes61390 Drosophil	964	6	7.5	735	6	ABO25197	Abos25197 Novel hum
892	6	7.5	645	4	AAW66531	Aaw66531 Human int	965	6	7.5	735	6	ABO25197	Abos25197 Novel hum
893	6	7.5	645	8	ADO19794	Ado19794 Human PRO	966	6	7.5	735	6	ABU98781	Abu98781 Novel hum
894	6	7.5	645	8	ABM80947	Abm80947 Tumour-as	967	6	7.5	735	6	ABU97996	Abu97996 Novel hum
895	6	7.5	645	9	ADP56088	Adp56088 Human PRO	968	6	7.5	735	6	ABU91702	Abu91702 Novel hum
896	6	7.5	645	9	AEA18850	Aea18850 Amino aci	969	6	7.5	735	6	ABU72203	Abu72203 Novel hum
897	6	7.5	646	4	AAU30243	Aau30243 Protein e	970	6	7.5	735	6	ABU89395	Abu89395 Human PRO
898	6	7.5	650	6	ABU20817	Abu20817 Protein e	971	6	7.5	735	6	ABU86236	Abu86236 Human sec
899	6	7.5	650	7	ABO83588	Abos83588 Pseudomon	972	6	7.5	735	6	ABU67449	Abu67449 Human sec
900	6	7.5	652	4	AAW01252	Aaw01252 P789P N-t	973	6	7.5	735	6	ABU80477	Abu80477 Human PRO

```
974 6 7.5 735 6 ABR99395
975 6 7.5 735 6 ABR98785
976 6 7.5 735 6 ABO16308
977 6 7.5 735 6 ABR92208
978 6 7.5 735 6 ABO18849
979 6 7.5 735 6 ABR78270
980 6 7.5 735 6 ABU85006
981 6 7.5 735 6 ABO00145
982 6 7.5 735 6 ABO11477
983 6 7.5 735 6 ABO02122
984 6 7.5 735 6 ABU88696
985 6 7.5 735 6 ABR83391
986 6 7.5 735 6 ABO06192
987 6 7.5 735 6 ABR59228
988 6 7.5 735 6 ABO09290
989 6 7.5 735 6 ABO19154
990 6 7.5 735 6 ABO11172
991 6 7.5 735 6 ABR66790
992 6 7.5 735 6 ABO16003
993 6 7.5 735 6 ABO13709
994 6 7.5 735 6 ABU84883
995 6 7.5 735 6 ABU65612
996 6 7.5 735 6 ABO07460
997 6 7.5 735 6 ABO03647
998 6 7.5 735 6 ABR67095
999 6 7.5 735 6 ABO15698
1000 6 7.5 735 6 ABU55979
```

ALIGNMENTS

```
RESULT 1
ID AAR86834 standard; protein; 227 AA.
XX
AC AAR86834;
XX
DT 12-JUL-1996 (first entry)
XX
DE Human CD9 sequence.
XX
KW CD9 antigen; stimulated T cell; antibody; ligand; proliferation;
KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;
KW immune response; cancer; infectious disease; growth factor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 51
FT Modified-site /note= "Potential N-linked glycosylation site"
FT Modified-site 52
FT Domain 111..194 /note= "Potential N-linked glycosylation site"
FT Domain 195..220 /note= "Extracellular domain"
FT Domain /note= "Transmembrane domain"
FT Domain 221..227 /note= "Cytoplasmic domain"
XX
PN WO9533823-A1.
XX
PD 14-DEC-1995.
XX
PF 01-DEC-1994; 94WO-US013782.
XX
PR 03-JUN-1994; 94US-00253751.
XX
PR 03-JUN-1994; 94US-00253964.
XX
PA (USNA ) US SEC OF NAVY.
PA (UNMI ) UNIV MICHIGAN.
PA (REPK ) REPLIGEN CORP.
PA (DAND ) DANA FARBER CANCER INST INC.
```

```
XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;
XX WPI; 1996-040230/04.
XX
DR Selectively inducing CD8 positive T cell proliferation - by activating
PT the T cells and stimulating CD9 cell surface ligand, useful for
PT immuno:therapy of, e.g. cancer.
XX
PS Example 10; Page 38-39; 79pp; English.
XX
CC This sequence represents CD9 from the surface of stimulated T cells. The
CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an
CC antibody or other ligand to stimulate the T cell population to
CC proliferate and expand leading to a 100- to 10000-fold increase in cell
CC number compared to the original population. The antigenic sequence fits
CC the generic sequence given in AAR86827. This epitope is recognised by the
CC monoclonal antibody (Mab) ES5.2D8. CD9 is a 27 kD accessory protein found
CC on activated T cells. The epitope was recognised by screening a phage
CC display library. Selective proliferation of an antigen-specific T cell
CC population is useful in cases where the immune response is to be up
CC regulated, e.g. in the treatment of cancer or infectious diseases. By
CC causing proliferation of the T cell population by stimulating T cell
CC epitope removes the need for exogenous growth factors or accessory cells
XX
SQ Sequence 227 AA;
XX
Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKVEQVFYKDTYNKLTKDDEPORETLLKAIHYALNCCGLAGGVQVFISDICPKKDV 60
DB 112 HKDEVIKVEQVFYKDTYNKLTKDDEPORETLLKAIHYALNCCGLAGGVQVFISDICPKKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191
XX
RESULT 2
ABR78366
ID ABR78366 standard; protein; 227 AA.
XX
AC ABR78366;
XX
DT 16-DEC-2002 (first entry)
XX
DE Amino acid sequence of CD9.
XX
KW T cell; T cell proliferation; infectious disease; cancer; immunotherapy;
KW immuno:therapy; CD9.
XX
OS Homo sapiens.
XX
PN US2002115214-A1.
XX
PD 22-AUG-2002.
XX
PF 26-JAN-1996; 96US-00592711.
XX
PR 23-NOV-1988; 88US-00275433.
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253964.
PR 10-MAR-1995; 95US-00403253.
PR 04-MAY-1995; 95US-00435816.
XX
PA (JUNE/) JUNE C H.
PA (THOM/) THOMPSON C B.
PA (NABE/) NABEL G J.
```

```

PA (GRAY/) GRAY G.S.
XX (RENN/) RENNERT P.D.
PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2002-712476/77.
XX
XX Inducing a population of T cells to proliferate, by activating population
PT of T cells and stimulating an accessory molecule on the surface of the T
PT cells with a ligand which binds the accessory molecule.
XX
XX Example 10; Page 25; 88pp; English.
XX
XX The specification describes method for inducing a population of T cells
CC to proliferate. The method involves activating population of T cells,
CC stimulating an accessory molecule on T cell surface with a ligand
CC protein) which binds the molecule, to induce proliferation of T cells,
CC monitoring proliferation of T cells in response to continuing exposure to
CC the ligand, and reactivating and restimulating T cells when rate of
CC proliferation has decreased to induce further proliferation of the cells.
CC The method is useful for inducing proliferation of T cells, for use in
CC treatment of infectious disease, cancer and immunotherapy. The method
CC allows for the expansion of a population of T cells in numbers sufficient
CC to reconstitute an individual's total CD4+ or CD8+ T cell population.
CC The resulting T cell population can be genetically transduced and used
CC for immunotherapy or can be used in methods of in vitro analyses of
CC infectious agents. A population of tumour-infiltrating lymphocytes can be
CC obtained from an individual afflicted with cancer and the T cells
CC stimulated to proliferate to sufficient numbers. The resulting T cell
CC population can be genetically transduced to express tumour necrosis
CC factor (TNF) or other factor and restored to the individual. CD4+ T cells
CC expanded by this method are useful in the treatment of HIV infection in
CC an individual. The present sequence represents CD9, an antigen present on
CC the surface of activated T cells
XX
XX Sequence 227 AA;
SQ
Query Match 100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVKEVQEFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPKDV 60
DB 112 HKDEVKEVQEFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191
RESULT 3
AAE14636
ID AAE14636 standard; protein; 227 AA.
XX
XX AAE14636;
AC
DT 16-JUL-2002 (first entry)
XX
DE Human CD9 antigen.
XX
KW T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;
KW human; CD9 antigen.
XX
OS Homo sapiens.
XX
PN US6352694-B1.
XX
XX 05-MAR-2002.
PD
PF 10-MAR-1995; 95US-00403253.
XX
XX 03-JUN-1994; 94US-00253964.
XX

```

```

XX (GEMY ) GENETICS INST INC.
PA (UNMI ) UNIV MICHIGAN.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2002-314696/35.
XX
XX Inducing T cell population to proliferate, useful in cancer therapy,
PT comprises activating T cells by contacting T cells in vitro with
PT immobilized anti-CD3 antibody and stimulating accessory molecule on T
PT cell surface.
XX
XX Example 10; Col 42; 71pp; English.
XX
XX The invention relates to a method of inducing T cell population to
CC proliferate for use in therapy comprising activating T cells by
CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
CC on solid phase surface, and stimulating accessory molecule on T cell
CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural
CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a
CC population of T cells to proliferate in sufficient numbers for use in
CC therapy e.g., for treating cancer or an infectious disease. The method
CC can be used to selectively expand the population of CD28+, CD4+, CD8+,
CC CD28RA+ or CD28RO+ T cells for immunotherapy. The T cell population
CC resulting by the method can be genetically transduced and used for
CC immunotherapy or can be used for in vitro analysis of infectious agents
CC such as human immunodeficiency virus (HIV). Proliferation of a population
CC of CD4+ T cells obtained from an individual infected with HIV can be
CC achieved and the cells rendered resistant to HIV infection. Following the
CC expansion of the T cells to sufficient numbers, the expanded T cells are
CC restored to the individual. Also CD4+ T cells expanded by the above
CC mentioned is useful for treating HIV infection in an individual. A
CC population of tumour-infiltrating lymphocytes can be obtained from an
CC individual afflicted with cancer and the T cells stimulated to
CC proliferate to sufficient numbers and restored to the individual. The
CC supernatants from cultures of T cells expanded from above mentioned
CC method are useful as a rich source of cytokines and can be used to
CC sustain T cells in vivo or ex vivo. Stimulating and expanding a
CC population of antigen specific T cells are useful in therapeutic
CC conditions where it is desirable to upregulate an immune response. The T
CC cell proliferation occurs in the absence of exogenous growth factors or
CC accessory cells. The present sequence is human CD9 antigen which is
CC expressed on surface of activated T cells
XX
XX Sequence 227 AA;
SQ
Query Match 100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVKEVQEFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPKDV 60
DB 112 HKDEVKEVQEFYKDTYNKLTQDEPQRTLKAIHYALNCCGLAGGVEQFISDIPKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191
RESULT 4
ABU05057
ID ABU05057 standard; protein; 227 AA.
XX
XX ABU05057;
AC
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1723.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW

```

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX Example 2; SEQ ID NO 1723; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 227 AA;

SQ Query Match 100.0%; Score 80; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKQVQEFYKDTYTKLTKDPEQRTLKAIHYALNCCGLAGGVQFISDICKKDV 60
DB 112 HKDEVKQVQEFYKDTYTKLTKDPEQRTLKAIHYALNCCGLAGGVQFISDICKKDV 171
QY 61 LETFTVKSCPDAIKEVFNK 80
DB 172 LETFTVKSCPDAIKEVFNK 191

RESULT 5

ABU05060

ID ABU05060 standard; protein; 227 AA.

XX ABU05060;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1726.

DE

XX

KW

KW

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PR

XX

PR

XX

PR

XX

PA

PI

XX

XX

DR

XX

XX

PT

PT

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

XX

KW

KW

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PR

XX

PR

XX

PR

XX

PA

PI

XX

XX

DR

XX

XX

PT

PT

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX Example 2; SEQ ID NO 1726; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 227 AA;

SQ Query Match 100.0%; Score 80; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKQVQEFYKDTYTKLTKDPEQRTLKAIHYALNCCGLAGGVQFISDICKKDV 60
DB 112 HKDEVKQVQEFYKDTYTKLTKDPEQRTLKAIHYALNCCGLAGGVQFISDICKKDV 171
QY 61 LETFTVKSCPDAIKEVFNK 80
DB 172 LETFTVKSCPDAIKEVFNK 191

RESULT 6

ABW00436

ID ABW00436 standard; protein; 227 AA.

XX ABW00436;

XX

AC

XX	15-JAN-2004	(first entry)	
DT	Human CD9 antigenic protein.		
XX	HIV infection; human immunodeficiency virus; therapy; antigen; human.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	Domain	111..194	
FT	Domain	/note= "Extracellular domain"	
FT	Domain	195..220	
FT	Domain	/note= "Transmembrane domain"	
FT	Domain	221..227	
FT	Domain	/note= "Cytoplasmic domain"	
XX	US2003099643-A1.		
PN	29-MAY-2003.		
XX	08-JUL-1999;	99US-00350202.	
XX	23-NOV-1988;	88US-00275433.	
PR	22-NOV-1989;	89WO-US005304.	
PR	07-APR-1992;	92US-00864805.	
PR	07-APR-1992;	92US-00864807.	
PR	07-APR-1992;	92US-00864866.	
PR	04-JUN-1993;	93US-00073223.	
PR	03-JUN-1994;	94US-00253694.	
PR	10-MAR-1995;	95US-00403253.	
XX	(JUNE/) JUNE C H.		
PA	(THOM/) THOMPSON C B.		
PA	(NABE/) NABEL G J.		
PA	(GRAY/) GRAY G S.		
PA	(RENN/) RENNERT P D.		
XX	June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;		
PI	WPI; 2003-801206/75.		
XX	Treating HIV infection in individual by isolating T cells from		
PT	leukocytes, contacting T cells with anti-CD3 antibody for T cell		
PT	proliferation, separating antibody from T cells, monitoring proliferation		
PT	of T cells.		
XX	Example 10; Page 23; Opp; English.		
XX	The present invention relates to a novel method of treating human		
CC	immunodeficiency virus (HIV) infection in an individual. The method		
CC	involves isolating population of CD4 T cells from leukocytes, contacting		
CC	population of CD4+ T cells with an anti-CD3 antibody for stimulating T		
CC	cell proliferation, separating antibody from T cells, monitoring		
CC	proliferation of T cells, restimulating T cells with antibody and		
CC	restoring T cells to individual. The present sequence is human CD9		
CC	antigenic protein. This sequence is used to illustrate the method of the		
CC	invention		
XX	Sequence 227 AA;		
XX	Query Match	100.0%; Score 80; DB 7; Length 227;	
XX	Best Local Similarity	100.0%; Pred. No. 1e-73;	
XX	Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 HKDEV1KEVQEFYKDYTNKLNKTDEPQRETLKAHYALNCCGLAGGVEQFISD1CPKKDV 60		
Db	112 HKDEV1KEVQEFYKDYTNKLNKTDEPQRETLKAHYALNCCGLAGGVEQFISD1CPKKDV 171		
QY	61 LETFTVKSCPD1KEVFDNK 80		
Db	172 LETFTVKSCPD1KEVFDNK 191		

RESULT 7
ADK69862
ID ADK69862 standard; protein; 227 AA.
XX AC ADK69862;
XX DT 06-MAY-2004 (first entry)
XX DE Human CD9 protein.
XX OS Homo sapiens.
XX KW CD28-associated signal; immunotherapy; infectious disease; cancer;
leukopheresis; human.
XX PN US6534055-B1.
XX PD 18-MAR-2003.
XX PF 04-MAY-1995; 95US-00435816.
XX PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253964.
PR 10-MAR-1995; 95US-00403253.
XX PA (GEMY) GENETICS INST INC.
XX PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2003-531074/50.
XX DR Expanding T cell populations, useful for preparing renewable sources of T
PT cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28-
PT -associated signal on the surface of the cells with an anti-CD28
PT antibody, B7-1 or B7-2.
PS Example 10; SEQ ID NO 6; 82pp; English.
XX CC The invention relates to a method for expanding a population of T cells
CC to about 100-100000-fold over the original T cell population, or to about
CC 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-
CC associated signal on the surface of the T cells with agent comprising an
CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a
CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T
CC cells) to proliferate. The method is particularly useful for preparing a
CC renewable source of CD4+ T cells. The expanded T cell population can be
CC genetically transduced, and used for immunotherapy to treat a variety of
CC human diseases (e.g. infectious diseases or cancer), or used in
CC diagnostic protocols. T cells were obtained from leukopheresis of a
CC normal donor, and purified with FICOLL density gradient centrifugation,
CC followed by magnetic immunobead sorting. The present sequence is CD9 used
CC in the exemplification of the invention.
XX SO Sequence 227 AA:
XX

```
AD119366
ID AD119366 standard; protein; 227 AA.
AC AD119366;
XX
DT 15-APR-2004 (first entry)
DE
XX
XX
DE Human CD9 protein.
XX
XX T cell; immunotherapy; therapy; HIV infection; cancer;
KW infectious disease; cytostatic; antimicrobial; human.
XX
XX Homo sapiens.
OS
XX
XX US2004001829-A1.
FN
XX
PD 01-JAN-2004.
XX
XX 17-MAR-2003; 2003US-00390330.
XX
XX 23-NOV-1988; 88US-00275433.
PR 22-NOV-1989; 89WO-US005304.
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253964.
PR 10-MAR-1995; 95US-00403253.
PR 04-MAY-1995; 95US-00435816.
XX
XX (JUNE//) JUNE C H.
PA (THOM//) THOMPSON C B.
PA (NABEL//) NABEL G J.
PA (GRAY//) GRAY G S.
PA (RENN//) RENNERT P D.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2004-061648/06.
XX
XX Inducing a population of T cells to proliferate, for immunotherapy or
PT treating HIV infection, cancer or infectious disease, comprises
PT activating a population of T cells and stimulating an accessory molecule
PT on the surface of the T cells.
XX
XX Example 10; SEQ ID NO 6; 80pp; English.
XX
XX The invention relates to a method for inducing a population of T cells to
CC proliferate. The method comprising activating a population of T cells,
CC and stimulating an accessory molecule on the surface of the T cells with
CC a ligand that binds the accessory molecule. The invention is useful for
CC immunotherapy, for treating HIV infection, cancer or infectious disease,
CC or in diagnostic applications. The present sequence is human CD9 protein.
XX
XX Sequence 227 AA;
XX
XX Query Match 100.0%; Score 80; DB 8; Length 227;
XX Best Local Similarity 100.0%; Pred. No. 1e-73;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 HKDEVKEVQEFYKDTYNNKLTKEPQRETILKAIHYALNCCGLAGGVQFISDICKPKDV 60
DB 112 HKDEVKEVQEFYKDTYNNKLTKEPQRETILKAIHYALNCCGLAGGVQFISDICKPKDV 171
XX
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191
XX
XX
XX
XX 25-MAR-2003 (revised)
DT 05-MAR-1993 (first entry)
XX
XX Metastasis controlling peptide.
XX
XX M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;
KW
```

```
AC AEA89005;
XX
DT 25-AUG-2005 (first entry)
DE
XX
XX Human CD9 antigenic protein, SEQ ID NO: 6.
XX
XX Cell therapy; immune stimulation; immunotherapy; diagnosis;
KW infectious disease; antimicrobial; infection; cancer; cytostatic;
KW neoplasm; CD9; antigen.
XX
XX Homo sapiens.
OS
XX
XX US6905681-B1.
PN
XX
PD 14-JUN-2005.
XX
XX 08-JUL-1999; 99US-00349915.
XX
XX 03-JUN-1994; 94US-00253964.
PR 10-MAR-1995; 95US-00403253.
XX
XX (GEMY ) GENETICS INST INC.
PA (UNMI ) UNIV MICHIGAN.
PA (USNA ) US SEC OF NAVY.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
PI WPI; 2005-464777/47.
XX
XX Ex vivo proliferation of T cell population for use in therapy, involves
PT contacting population of T cells with surface having anti-CD3 antibody
PT and anti-CD28 antibody for activating T cells and stimulating activated T
PT cells, respectively.
XX
XX Example 10; SEQ ID NO 6; 76pp; English.
XX
XX The present invention relates to a method of including ex vivo
CC proliferation of a population of T cells to sufficient numbers for use in
CC therapy. The method involves contacting population of T cells with
CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T
CC cells and stimulating activated T cells, respectively. The invention is
CC useful for treating cancer and infectious disease and also useful in cell
CC therapy. The present sequence is the human CD9 antigenic protein. This
CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used
CC to stimulate a CD8+ T cell population.
XX
XX Sequence 227 AA;
XX
XX Query Match 100.0%; Score 80; DB 9; Length 227;
XX Best Local Similarity 100.0%; Pred. No. 1e-73;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 HKDEVKEVQEFYKDTYNNKLTKEPQRETILKAIHYALNCCGLAGGVQFISDICKPKDV 60
DB 112 HKDEVKEVQEFYKDTYNNKLTKEPQRETILKAIHYALNCCGLAGGVQFISDICKPKDV 171
XX
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 172 LETFTVKSCPDAIKEVFDNK 191
XX
XX
XX
XX AEA89005 standard; protein; 228 AA.
ID AEA89005
XX
XX AEA89005;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-MAR-1993 (first entry)
XX
XX Metastasis controlling peptide.
XX
XX M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;
KW
```

KW lung; glioblastoma.
XX Homo sapiens.
XX EP508417-A2.
XX 14-OCT-1992.
XX 09-APR-1992; 92EP-00106093.
XX 12-APR-1991; 91JP-00079996.
XX 17-APR-1991; 91JP-00085396.
XX 07-FEB-1992; 92JP-00022321.
XX (TAKE) TAKEDA CHEM IND LTD.
PA (MIYA/) MIYAKE M.
XX Ikeyama S, Koyama M, Senoo M, Miyake M;
XX WPI; 1992-341723/42.
XX N-PSDB; AAQ29182.
XX New monoclonal antibody M31-15 specific for metastasis-controlling
PT peptide - useful for treating and preventing cancer and metastasis.
XX Claim 7; Fig 4; 34pp; English.
XX The sequence is that of a cancer cell surface protein which is capable of
CC suppressing the motility of cancer cells. It is specifically recognised
CC by the monoclonal (Mab) antibody M31-15 which is useful for suppressing
CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in
CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and
CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 80; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVKEVQEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60
DB 113 HKDEVKEVQEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 11
ABB44581
ID ABB44581 standard; protein; 228 AA.
XX ABB44581;
XX 25-JAN-2002 (first entry)
DE Human wound healing related polypeptide SEQ ID NO 38.
XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW Gene therapy.
XX Homo sapiens.
XX CA2325226-A1.
XX 17-MAY-2001.
XX 16-NOV-2000; 2000CA-02325226.
XX 17-NOV-1999; 99DE-01055349.
XX 17-DEC-1999; 99US-0172511P.
XX 20-JUN-2000; 2000DE-01030149.

XX (SWIT-) SWITCH BIOTECH AG.
XX Regenbogen J, Wolf E, Coppelt A, Werner S, Halle J;
XX WPI; 2001-433142/47.
XX Use of novel polypeptide or its variant or nucleic acid encoding the
PT polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances.
XX Disclosure; Page 193-194; 265pp; English.
XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-
CC ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological
CC activity for the diagnosis, prevention and treatment of skin disorders
CC and treatment in wound healing or for the identification of
CC pharmacologically active substances. The nucleic acids are useful in gene
CC therapy. Note: The printed sequence listing for this specification was
CC incomplete, terminating part way through SEQ ID NO 106. The remaining
CC data was obtained from EPO data for an equivalent patent (SP1114862)
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 80; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVKEVQEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 60
DB 113 HKDEVKEVQEFYKDTYKLTQKDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 12
ABU05059
ID ABU05059 standard; protein; 228 AA.
XX ABU05059;
XX 29-JAN-2003 (first entry)
DE Human expressed protein tag (EPT) #1725.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
PI

```
XX WPI; 2003-040607/03.
DR
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1725; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKDV 60
DB 113 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 13
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX
XX ABU05052;
AC
XX
XX 29-JAN-2003 (first entry)
DE Human expressed protein tag (EPT) #1718.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
FN
XX 10-OCT-2002.
PD
XX
XX 28-MAR-2002; 2002WO-US009671.
PF
XX
XX 28-MAR-2001; 2001US-0279495P.
PR
XX 21-MAY-2001; 2001US-0292544P.
PR
XX 08-AUG-2001; 2001US-0310801P.
PR
XX 01-OCT-2001; 2001US-0326370P.
PR
XX 04-DEC-2001; 2001US-0336780P.
PR
XX 20-FEB-2002; 2002US-0358985P.
PR
```

```
XX (ZYCO-) ZYCOS INC.
PA
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1718; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKDV 60
DB 113 HKDEVIKEVQEFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDIPCKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 14
ABU05048
ID ABU05048 standard; protein; 228 AA.
XX
XX ABU05048;
AC
XX
XX 29-JAN-2003 (first entry)
DE Human expressed protein tag (EPT) #1714.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
FN
XX 10-OCT-2002.
PD
XX
XX 28-MAR-2002; 2002WO-US009671.
PF
XX
XX 28-MAR-2001; 2001US-0279495P.
PR
XX 21-MAY-2001; 2001US-0292544P.
PR
XX 08-AUG-2001; 2001US-0310801P.
PR
XX 01-OCT-2001; 2001US-0326370P.
PR
XX 04-DEC-2001; 2001US-0336780P.
PR
XX 20-FEB-2002; 2002US-0358985P.
PR
```

```
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1714; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 60
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 15
ABU05056
ID ABU05056 standard; protein; 228 AA.
AC
ABU05056;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1722.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
```

```
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1722; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 60
Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDICKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192
Search completed: January 20, 2006, 17:42:25
Job time : 141.923 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:21:43 ; Search time 94.7654 Seconds
(without alignments)
176.187 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207
Sequence: 1 KDEPQRETLKAIHYALNCCGLAGVQVFISDICPKKDV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	38	ADJ57561	Human CD9
2	128	61.8	30	ABU05051	Human exp
3	60	29.0	22	ADJ57564	Human CD9
4	44	21.3	33	AAY45292	Human sec
5	44	21.3	44	ABG99705	Conus sp
6	43	20.8	23	AAR26006	Influenza
7	43	20.8	23	AAB70092	Cationic
8	43	20.8	23	AAB34271	Synthetic
9	43	20.8	26	AAR26004	Influenza
10	43	20.8	26	AAB70090	Cationic
11	43	20.8	26	AAB34269	Synthetic
12	43	20.8	44	ABM95674	M. xanthu
13	42.5	20.5	50	AAB20282	Human nov
14	41.5	20.0	32	ABG99385	Conus sp
15	41.5	20.0	49	AAV55679	E. coli y
16	41	19.8	32	AAR13376	Adult t-c
17	41	19.8	44	AAV16377	Peptide #
18	41	19.8	44	AAV74910	Human col
19	41	19.8	44	ABB35365	Peptide #
20	41	19.8	44	AAV28874	Peptide #
21	41	19.8	44	ABB30202	Peptide #
22	41	19.8	44	ABB20807	Protein #
23	41	19.8	44	AAV68569	Human bon
24	41	19.8	44	AAV56196	Human bra

25	41	19.8	44	4	ABG50232	Human liv
26	41	19.8	44	4	AAV04113	Peptide #
27	41	19.8	44	5	ABG38147	Human pep
28	41	19.8	46	2	AAV31910	Spider ve
29	41	19.8	49	3	AAV55680	H. influe
30	40.5	19.6	32	5	ABG99768	Conus sp
31	40.5	19.6	32	5	ABG99387	Conus sp
32	40	19.3	25	2	AAV47052	HIV-1 V3
33	40	19.3	44	4	AAV84731	Human imm
34	40	19.3	45	3	AAV55688	M. genita
35	40	19.3	47	4	ABV41557	Peptide #
36	40	19.3	47	4	AAV35348	Peptide #
37	40	19.3	47	4	AAV75236	Human bon
38	40	19.3	47	4	AAV62428	Human bra
39	40	19.3	47	4	ABG56998	Human liv
40	40	19.3	47	5	ABG44889	Human pep
41	39.5	19.1	32	5	ABG99769	Conus sp
42	39.5	19.1	40	3	AAV21587	Cone snai
43	39	18.8	17	9	ADV66592	Integrin
44	39	18.8	20	3	AAV66841	T cell an
45	39	18.8	28	5	AAV18036	Human ion
46	39	18.8	29	4	AAV85963	Human imm
47	39	18.8	41	4	ABV16717	Human ner
48	39	18.8	45	3	AAV66046	Transcrip
49	39	18.8	45	4	AAV19061	Peptide #
50	39	18.8	45	4	ABV38268	Peptide #

ALIGNMENTS

RESULT 1
ADJ57561
ID ADJ57561 standard; protein; 38 AA.
XX
AC ADJ57561;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human CD9 fibronectin-binding domain polypeptide fragment.

XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
KW haemostatic; antiangiogenic; cytostatic.
XX Homo sapiens.
XX WO2004007685-A2.
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-US022050.
XX
PR 12-JUL-2002; 2002US-0395864P.
XX
PA (UYTE-) UNIV TENNESSEE RES FOUND.
XX
PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;
PI Crossno JT, Lu Y;
XX WPI; 2004-122924/12.
PT Interfering with CD9 binding to fibronectin by binding a fibronectin-
PT binding domain of the CD9 protein or polypeptide, useful in treating
PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
PT and cancers.
XX Claim 7; SEQ ID NO 4; 126pp; English.
XX
CC The present sequence is that of a polypeptide fragment from the
CC fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an
CC antibody that binds to it, is used in claimed methods for: interfering
CC with CD9 binding to fibronectin; modifying adhesion, motility or
CC spreading of a CD9-expressing cell on fibronectin; inhibiting

CC proliferation or survival of CD9-expressing cells; modifying pericellular
 CC fibronectin matrix assembly; modifying invasiveness of a cell through a
 CC collagen and/or laminin matrix; and modifying cell-to-cell interaction.
 CC The methods are based on the finding that increased CD9 expression is
 CC implicated in (i) decreased adhesiveness of cells to extracellular matrix
 CC (via alpha5-beta1 integrin) and/or decreased cell invasiveness and/or
 CC decreased pericellular fibronectin matrix assembly, and/or (ii) increased
 CC cell motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.

XX SQ Sequence 38 AA;

Query Match 100.0%; Score 207; DB 8; Length 38;
 Best Local Similarity 100.0%; Pred. No. 5,1e-22;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKKDV 38
 |||||
 Db 1 KDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKKDV 38

RESULT 2

ABU05051
 ID ABU05051 standard; protein; 30 AA.

AC ABU05051;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1717.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US0095671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chiciz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX Example 2; SEQ ID NO 1717; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 30 AA;

Query Match 61.8%; Score 128; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 8.7e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LNCCGLAGGVQFTSDICPKKDV 38
 |||||
 Db 1 LNCCGLAGGVQFTSDICPKKDV 23

RESULT 3

ADJ57564

ID ADJ57564 standard; peptide; 22 AA.

AC ADJ57564;

DT 06-MAY-2004 (first entry)

DE Human CD9 fibronectin-binding domain peptide fragment.

KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
 KW haemostatic; antiangiogenic; cytostatic.

OS Homo sapiens.

PN WO2004007685-A2.

PD 22-JAN-2004.

PF 14-JUL-2003; 2003WO-US022050.

PR 12-JUL-2002; 2002US-0395864P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
 XX Crossno JT, Lu Y;

XX WPI; 2004-122924/12.

XX Interfering with CD9 binding to fibronectin by binding a fibronectin-
 PT binding domain of the CD9 protein or polypeptide, useful in treating
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
 PT and cancers.

XX Example 1; SEQ ID NO 7; 126pp; English.

XX The present sequence is that of a peptide fragment from the extracellular
 CC domain (amino acids 125-146) of human CD9 ADJ57558. The peptide was used
 CC in an example from the invention to investigate the interaction between
 CC CD9 and fibronectin. Peptide fragments ADJ57560-ADJ57563 of human CD9 are
 CC used in claimed methods for: interfering with CD9 binding to fibronectin;
 CC modifying adhesion, motility or spreading of a CD9-expressing cell on
 CC fibronectin; inhibiting proliferation or survival of CD9-expressing cells
 CC ; modifying pericellular fibronectin matrix assembly; modifying
 CC invasiveness of a cell through a collagen and/or laminin matrix; and
 CC modifying cell-to-cell interaction. The methods are based on the finding

CC that increased CD9 expression is implicated in (i) decreased adhesiveness
 CC of cells to extracellular matrix (via alpha5-beta1 integrin) and/or
 CC decreased cell invasiveness and/or decreased pericellular fibronectin
 CC matrix assembly, and/or (ii) increased cell motility, spreading,
 CC proliferation, cell survival against apoptosis, and/or cell-to-cell
 CC contacts. Conditions or disease states involving proliferation or
 CC survival of CD9-expressing cells can be treated, e.g. thrombosis,
 CC atherosclerosis, vein graft failure, restenosis, transplant arteriopathy,
 CC bleeding disorders, angiogenesis, and primary and metastatic cancers
 CC including breast cancer, prostate cancer, colon cancer, melanoma, ovarian
 CC cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 22 AA;

Query Match 29.0%; Score 60; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDEPQRETLKAI 12
 |||||
 Db 11 KDEPQRETLKAI 22

RESULT 4
 AAY45292
 ID AAY45292 standard; protein; 33 AA.

AC AAY45292;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE Human secreted protein fragment encoded from gene 4.
 XX
 KW Secreted protein; human; gene therapy; diagnosis; treatment; cancer;
 KW protein therapy; tumor; neurodegenerative disorder; blood disorder; AIDS;
 KW developmental abnormality; leukemia; immune system; autoimmune disease;
 KW hepatic disease; renal disease; inflammation; allergy; schizophrenia;
 KW Alzheimer's disease; cognitive disorder; arthritis; infection; psoriasis;
 KW transplant rejection; diabetes; asthma; sepsis; acne; metabolic disorder;
 KW cardiovascular disorder; food additive; preservative.
 XX
 OS Homo sapiens.
 XX
 PN WO9946289-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-US005721.
 XX
 PR 12-MAR-1998; 98US-0077686P.
 PR 12-MAR-1998; 98US-0077687P.
 PR 12-MAR-1998; 98US-0077696P.
 PR 12-MAR-1998; 98US-0077714P.
 XX
 (HUMA-) HUMAN GENOME SCI INC.

XX
 XX Ruben SM, Ferrie AM, Rosen CA, Florence C, Young PE, Yu G, Ni J;
 XX WPI; 1999-551363/46.
 XX N-PSDB; AA27236.
 XX
 XX New isolated human genes, useful for diagnosis and treatment of, e.g.
 XX cancers.
 XX
 XX Disclosure; 195; 306pp; English.

XX This invention describes novel human genes and the secreted proteins they
 CC encode. The polynucleotides and their corresponding secreted polypeptides
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the polynucleotides of the

CC invention, based on which tissues they are most highly expressed in, and
 CC include developing products for the diagnosis or treatment of cancer,
 CC tumors, neurodegenerative disorders, developmental abnormalities, blood
 CC disorders, leukemias, diseases of the immune system, autoimmune diseases,
 CC hepatic and renal disease, inflammation, allergies, Alzheimer's and
 CC cognitive disorders, schizophrenia, arthritis, infections, AIDS,
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,
 CC cardiovascular disorders, and metabolic disorders. The polypeptides or
 CC polynucleotides can also be used as food additives or preservatives. The
 CC polypeptides are also useful for identifying their binding partners.
 CC AAY45290-Y45389 represent human secreted protein fragments described in
 XX the method of the invention
 XX
 SQ Sequence 33 AA;

Query Match 21.3%; Score 44; DB 2; Length 33;
 Best Local Similarity 42.9%; Pred. No. 1.1e+02;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 10 KAIHYALNCCGLAG 23
 | : | | | : |
 Db 16 KVVXFLACCGVSG 29

RESULT 5
 ABG99705
 ID ABG99705 standard; peptide; 44 AA.

AC ABG99705;
 XX
 DT 17-JAN-2003 (first entry)
 XX
 DE Conus sp conotoxin-associated peptide SEQ ID 490.
 XX
 KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.
 XX
 OS Conus radiatus.
 XX
 PN WO200264740-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 11-FEB-2002; 2002WO-US003887.
 XX
 PR 09-FEB-2001; 2001US-0267408P.

XX (COGN-) COGNETIX INC.
 XX (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 XX Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX WPI; 2002-706921/76.

XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX
 XX Claim 1; Page 281; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterizing a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the

CC above-mentioned channels or receptors, which are monoamine transporters,
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention
XX
SQ Sequence 44 AA;

Query Match 21.3%; Score 44; DB 5; Length 44;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 12; Indels 2; Gaps 1;
QY 14 YALNCCGLAGGVEQFISDI--CPK 35
| | | | | : | | | |
Db 1 YGLGAGTCGSSSNCVRDYDCPK 24
| | | | | : | | | |

RESULT 6

AAR26006

ID AAR26006 standard; peptide; 23 AA.

XX

AC AAR26006;

XX

DT 25-MAR-2003 (revised)

DD 26-JAN-1993 (first entry)

XX

DE Influenza fusion peptide #3.

XX

KW Haemagglutinin; cysteine; liposome.

XX

OS Synthetic.

XX

PN EP497997-A1.

XX

PD 12-AUG-1992.

XX

PF 02-FEB-1991; 91EP-00101414.

XX

PR 02-FEB-1991; 91EP-00101414.

XX

PA (NIPP) NIPPON INST BIOLOGICAL SCIENCE.

XX

PI Glueck R, Herrmann P, Klein P;

XX

WPI; 1992-270078/33.

XX

PT Drug-contg. phospholipid bi:layer vesicle with cell-specific markers on
PT membrane - where markers have at least 90 per cent biological activity,
PT used as pharmaceuticals against e.g. cancer and AIDS.

XX

PS Disclosure; Fig 2; 13pp; English.

XX

CC The sequences given in AAR26004-19 are Influenza fusion peptides, derived
CC from the Influenza virus haemagglutinin gene which were used for the
CC preparation of synthetic membrane vesicles. The arrangement of at least
CC one, pref. three cysteine residues at one end of these peptides has been
CC found useful for the fusion activity, for the fusion of the liposome to
CC the target cell membrane. The liposomes produced using these peptides can
CC contain at least one active drug and can be used to target cells infected
CC with cancer or AIDS. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.)

SQ Sequence 23 AA;

Query Match 20.8%; Score 43; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 CCGLAGGVEQFISD 31

| | | | | : | | | |

Db 2 CCGLFAGTAGFIEN 15

| | | | | : | | | |

RESULT 7

Virosome; vesicle; cationic lipid bilayer; viral fusion peptide;

AAB70092

ID AAB70092 standard; peptide; 23 AA.

XX

AC AAB70092;

XX

DT 14-MAY-2001 (first entry)

XX

DE Cationic virosome crosslinker #3 for polypeptide binding.

XX

KW Cationic virosome; cytostatic; gene therapy; lipid bilayer vesicle;
KW viral haemagglutinin; drug delivery; cancer; leukaemia; viral infection;
KW crosslinker.

XX

OS Unidentified.

XX

PN NZ504444-A.

XX

PD 24-NOV-2000.

XX

PF 10-MAY-2000; 200NZ-00504444.

XX

PR 08-MAY-1996; 96EP-00107282.

XX

PR 04-MAY-1997; 97NZ-00332666.

XX

PA (NIKA-) NIKA HEALTH PROD LTD.

XX

PI Walti ER, Gluck R, Klein P;

XX

WPI; 1997-558673/51.

XX

PT Vesicle with cationic lipid bilayer that includes viral fusion peptide -

XX

PT used for delivery of genetic material to cells, especially for gene

XX

PT therapy of cancer, leukaemia and viral infections.

XX

PS Disclosure; Page 14; 41pp; English.

XX

CC The present sequence is a crosslinker which is capable of linking to the
CC surface of a novel cationic virosome and is capable of binding
CC polypeptides. The cationic virosome is a lipid bilayer vesicle comprising
CC a membrane with a net positive charge and contains 5-30 weight % based on
CC total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermyl)-propyl-amide
CC (DOSPER), together with other lipids and at least one active fusogenic
CC peptide. The fusogenic peptide is a viral haemagglutinin that causes the
CC vesicle to be internalised by target cells through phagocytosis or
CC endocytosis. The virosome is useful for delivering a desired drug or
CC substance, preferably a nucleic acid, to target cells (resting or
CC proliferating mammalian cells) such as cancer cells, leukaemic cells or
CC virally infected cells in vitro, in diagnostic or medical applications
CC and for the manufacture of medicament for carrying out non-infectious
CC gene therapy

SQ Sequence 23 AA;

Query Match 20.8%; Score 43; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 CCGLAGGVEQFISD 31

| | | | | : | | | |

Db 2 CCGLFAGTAGFIEN 15

| | | | | : | | | |

RESULT 8

AAW34271

ID AAW34271 standard; peptide; 23 AA.

XX

AC AAW34271;

XX

DT 14-MAY-1998 (first entry)

XX

DE Synthetic lipid vesicle fusion peptide 3.

XX

KW Virosome; vesicle; cationic lipid bilayer; viral fusion peptide;

KW drug delivery system; membrane; gene therapy; diagnosis; treatment;
 KW cancer; leukaemia; viral infection.
 OS Synthetic.
 XX WO9741834-A1.
 PN
 PD 13-NOV-1997.
 XX
 XX 04-MAY-1997; 97WO-EP002268.
 XX
 XX 08-MAY-1996; 96EP-00107282.
 PR
 XX (NIKA-) NIKA HEALTH PROD LTD.
 XX
 XX Waelti ER, Glueck R, Klein P;
 PI
 XX WPI; 1997-558673/51.
 DR
 XX
 XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -
 PT used for delivery of genetic material to cells, especially for gene
 PT therapy of cancer, leukaemia and viral infections.
 XX
 XX Disclosure; Page 10; 52pp; English.
 XX
 CC Peptides AAW34269-W34284 represent novel lipid vesicles with positively
 CC charged lipid bilayer membranes composed of a cationic and/or
 CC polycationic lipid and at least one natural or synthetic viral fusion
 CC peptide integrated in, or covalently linked to, the membrane. Such
 CC peptides are used as drug delivery systems, preferably for (non-)specific
 CC delivery of genetic material to target cells or tissues, particularly for
 CC diagnosis, treatment (especially antisense treatment) of cancer,
 CC leukaemia and viral infections in humans or animals. Genetic material is
 CC delivered, without infection, to resting or proliferating cells, in vitro
 CC or in vivo. When the genetic material is an antisense molecule, it is
 CC targeted to mRNA encoding a (proto)oncogene. The continuous lipid layer
 CC does not leak. The peptides do not need to fuse with, or destabilise,
 CC plasma membranes in order to enter the cytoplasm, since the fusion
 CC peptide ensures cell penetration by endocytosis (after which fusion of
 CC the vesicle and endosomal membrane occurs). The genetic material thus has
 CC a greater chance of reaching the nucleus before it is degraded or
 CC expelled. Transfer of the material is 1000-20000 times more efficient
 CC than when using liposomes or conventional virosomes, so smaller doses can
 CC be used, avoiding possible toxicity associated with the genetic material
 XX
 SQ Sequence 23 AA;
 Query Match 20.8%; Score 43; DB 2; Length 23;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 18 CCGLAGGVQVFISD 31
 Db ||||| : || :
 2 CCGLFGAAGFIEN 15
 RESULT 9
 AAR26004
 ID AAR26004 standard; peptide; 26 AA.
 AC
 XX
 XX AAR26004;
 XX
 XX 25-MAR-2003 (revised)
 DT 26-JAN-1993 (first entry)
 DT
 XX Influenza fusion peptide #1.
 DE
 XX Haemagglutinin; cysteine; liposome.
 KW
 XX
 XX Synthetic.
 OS
 XX EP497997-A1.
 PN
 XX

PD 12-AUG-1992.
 XX
 XX 02-FEB-1991; 91EP-00101414.
 XX
 PR 02-FEB-1991; 91EP-00101414.
 XX
 XX (NIPP) NIPPON INST BIOLOGICAL SCIENCE.
 PA
 XX Glueck R, Herrmann P, Klein P;
 PI
 XX WPI; 1992-270078/33.
 DR
 XX Drug-contg. phospholipid bi-layer vesicle with cell-specific markers on
 PT membrane - where markers have at least 90 per cent biological activity,
 PT used as pharmaceuticals against e.g. cancer and AIDS.
 XX
 XX Disclosure; Fig 2; 13pp; English.
 XX
 CC The sequences given in AAR26004-19 are influenza fusion peptides, derived
 CC from the influenza virus haemagglutinin gene which were used for the
 CC preparation of synthetic membrane vesicles. The arrangement of at least
 CC one, pref. three cysteine residues at one end of these peptides has been
 CC found useful for the fusion activity, for the fusion of the liposome to
 CC the target cell membrane. The liposomes produced using these peptides can
 CC contain at least one active drug and can be used to target cells infected
 CC with cancer or AIDS. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 26 AA;
 Query Match 20.8%; Score 43; DB 2; Length 26;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 18 CCGLAGGVQVFISD 31
 Db ||||| : || :
 2 CCGLFGAAGFIEN 15
 RESULT 10
 AAB70090
 ID AAB70090 standard; peptide; 26 AA.
 XX
 XX AAB70090;
 XX
 XX 14-MAY-2001 (first entry)
 DT
 XX
 XX Cationic virosome crosslinker #1 for polypeptide binding.
 DE
 XX Cationic virosome; cytostatic; gene therapy; lipid bilayer vesicle;
 KW viral haemagglutinin; drug delivery; cancer; leukaemia; viral infection;
 KW crosslinker.
 XX
 XX Unidentified.
 OS
 XX NZ504444-A.
 PN
 XX 24-NOV-2000.
 PD
 XX 10-MAY-2000; 2000NZ-00504444.
 PF
 XX 08-MAY-1996; 96EP-00107282.
 PR
 XX 04-MAY-1997; 97NZ-00332666.
 PR
 XX (NIKA-) NIKA HEALTH PROD LTD.
 PA
 XX Waelti ER, Glueck R, Klein P;
 PI
 XX WPI; 1997-558673/51.
 DR
 XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -
 PT used for delivery of genetic material to cells, especially for gene
 PT

PT therapy of cancer, leukaemia and viral infections.
XX Disclosure; Page 14; 41pp; English.
XX The present sequence is a crosslinker which is capable of linking to the
CC surface of a novel cationic virosome and is capable of binding
CC polypeptides. The cationic virosome is a lipid bilayer vesicle comprising
CC a membrane with a net positive charge and contains 5-30 weight % based on
CC total lipids, 1,3-dioleoyloxy-2-(6-carboxy-spermyl)-propyl-amide
CC (DOSPER), together with other lipids and at least one active fusogenic
CC peptide. The fusogenic peptide is a viral haemagglutinin that causes the
CC vesicle to be internalised by target cells through phagocytosis or
CC endocytosis. The virosome is useful for delivering a desired drug or
CC substance, preferably a nucleic acid, to target cells (resting or
CC proliferating mammalian cells) such as cancer cells, leukaemic cells or
CC virally infected cells in vitro, in diagnostic or medical applications
CC and for the manufacture of medicament for carrying out non-infectious
CC gene therapy
XX
SQ Sequence 26 AA;
Query Match 20.8%; Score 43; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 18 CCGLAGGVQEFISD 31
Db ||||| : ||| :
2 CCGLFGAIGAFIEN 15
RESULT 11
AAW34269
ID AAW34269 standard; peptide; 26 AA.
XX
AC AAW34269;
XX
XX 14-MAY-1998 (first entry)
XX
DE Synthetic lipid vesicle fusion peptide 1.
XX
XX Virosome; vesicle; cationic lipid bilayer; viral fusion peptide;
KW drug delivery system; membrane; gene therapy; diagnosis; treatment;
KW cancer; leukaemia; viral infection.
XX
OS Synthetic.
XX
XX WO9741834-A1.
XX
XX 13-NOV-1997.
XX
XX 04-MAY-1997; 97WO-EP002268.
XX
XX 08-MAY-1996; 96EP-00107282.
XX
XX (NIKA-) NIKA HEALTH PROD LTD.
XX
XX Waelti ER, Glueck R, Klein P;
XX
XX WPI; 1997-558673/51.
XX
XX Vesicle with cationic lipid bilayer that includes viral fusion peptide -
PT used for delivery of genetic material to cells, especially for gene
PT therapy of cancer, leukaemia and viral infections.
XX
PS Disclosure; Page 10; 52pp; English.
XX
XX Peptides AAW34269-W34284 represent novel lipid vesicles with positively
CC charged lipid bilayer membranes composed of a cationic and/or
CC polycationic lipid and at least one natural or synthetic viral fusion
CC peptide integrated in, or covalently linked to, the membrane. Such
CC peptides are used as drug delivery systems, preferably for (non-)specific
CC delivery of genetic material to target cells or tissues, particularly for
CC diagnosis, treatment (especially antisense treatment) of cancer,
XX
CC leukaemia and viral infections in humans or animals. Genetic material is
CC delivered, without infection, to resting or proliferating cells, in vitro
CC or in vivo. When the genetic material is an antisense molecule, it is
CC targeted to mRNA encoding a (proto)oncogene. The continuous lipid layer
CC does not leak. The peptides do not need to fuse with, or destabilise,
CC plasma membranes in order to enter the cytoplasm, since the fusion of
CC peptide ensures cell penetration by endocytosis (after which fusion of
CC the vesicle and endosomal membrane occurs). The genetic material thus has
CC a greater chance of reaching the nucleus before it is degraded or
CC expelled. Transfer of the material is 1000-20000 times more efficient
CC than when using liposomes or conventional virosomes, so smaller doses can
CC be used, avoiding possible toxicity associated with the genetic material
XX
SQ Sequence 26 AA;
Query Match 20.8%; Score 43; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 18 CCGLAGGVQEFISD 31
Db ||||| : ||| :
2 CCGLFGAIGAFIEN 15
RESULT 12
ABW95674
ID ABW95674 standard; protein; 44 AA.
XX
AC ABW95674;
XX
XX 02-JUN-2005 (first entry)
XX
XX M. xanthus protein sequence, seq id 14873.
DE
XX
XX Transgenic plant; DNA replication; gene regulation; gene expression.
KW
XX Myxococcus xanthus.
OS
XX US6833447-B1.
XX
XX 21-DEC-2004.
XX
XX 10-JUL-2001; 2001US-00902540.
XX
XX 10-JUL-2000; 2000US-0217883P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
XX WPI; 2005-028716/03.
XX
XX New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
XX Example 2; SEQ ID NO 14873; 25pp; English.
PS
XX The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
XX
SQ Sequence 44 AA;
Query Match 20.8%; Score 43; DB 9; Length 44;
PS

PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-457726/49.
DR N-PSDB; AAS32385.
XX
PT Isolated polypeptide for treating, preventing and prognosing disorders
PT related to the endocrine system including endocrine disorders,
PT reproductive disorders, and gastrointestinal disorders and also for
PT testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 339; 559pp; English.
XX
XX The invention relates to cDNAs encoding novel human endocrine antigens or
CC a fragment having biological activity, a domain, an epitope, full length
CC protein, variant, allelic variant or a species homologue of the
CC cDNA/antigen. The DNAs and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition when administered (e.g. by
CC gene therapy or antisense-therapy). Identifying mutations in the genes
CC coding for the antigens is useful for diagnosing a pathological condition
CC or a susceptibility to a pathological condition. The DNAs, antigens and
CC antibodies raised against the antigens useful for treating, preventing
CC and/or prognosing disorders related to the endocrine system or hormone
CC imbalance or reproductive disorders, cancers of endocrine tissues,
CC disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands
CC (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples
CC of diseases and disorders are given in the specification. The present
CC sequence represents an endocrine antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 50 AA;
Query Match 20.5%; Score 42.5; DB 4; Length 50;
Best Local Similarity 42.3%; Pred. No. 3e+02; Indels 5; Gaps 1;
Matches 11; Conservative 2; Mismatches 8;
QY 6 RETLKAIHYALNCCGLAGVEQFISD 31
|:|:|
Db 17 RKTIVA----QCCGLKGFENNAISD 37
|:|:|
RESULT 14
AAG99385
ID AAG99385 standard; peptide; 32 AA.
XX

AC AAG99385;
XX 17-JAN-2003 (first entry)
XX
XX Conus sp conotoxin-associated peptide SEQ ID 39.
XX
XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
KW ligand-gated ion channel modulator; pain-relief.
XX
XX Conus arenatus.
XX WO200264740-A2.
XX
XX 22-AUG-2002.
XX
XX 11-FEB-2002; 2002WO-US003887.
XX
XX 09-FEB-2001; 2001US-0267408P.
XX (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX WPI; 2002-706921/76.
XX
XX New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
XX Claim 1; Page 122; 305pp; English.
XX
XX This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders, ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC AAG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention
XX
SQ Sequence 32 AA;
Query Match 20.0%; Score 41.5; DB 5; Length 32;
Best Local Similarity 43.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
QY 18 CCGLAGGVEQFISDIC 33
|:|:|:|:|:|:|
Db 17 CCGLXNG-QXFCAXVC 31
|:|:|:|:|:|:|
RESULT 15
AAY55679
ID AAY55679 standard; protein; 49 AA.
XX
XX AAY55679;
XX
XX 07-FEB-2000 (first entry)
XX
XX E. coli ycfB peptide motif 3.
XX
XX ycfB polypeptide; gram negative bacteria; gram positive bacteria;
KW antibacterial; bacterial infection; bacterial viability; antibiotic.
XX

OS Escherichia coli.
 PN WO9544462-A2.
 XX
 PD 28-OCT-1999.
 XX
 XX 20-APR-1999; 99WO-EP002638.
 PF
 XX 22-APR-1998; 98GB-00008350.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Arigoni F, Edgerton MD, Lofrer H, Peitsch MC;
 PI
 XX WPI; 2000-013249/01.
 DR
 XX Novel bacterial polypeptides used to identify broad spectrum antibiotics.
 PT
 XX
 PS Claim 3; Fig 2C; 56pp; English.
 XX
 CC The invention discloses a novel family of polypeptides, designated the
 CC ycfB family, required for the growth of both gram negative and gram
 CC positive bacteria. The novel polypeptide of ycfB family is defined by:
 CC (a) a HSP score of greater than or equal to 100 when compared with one of
 CC the amino acid sequences of the ycfB family members given in the
 CC specification, when the BLAST algorithm is used with a BLOSUM62 scoring
 CC matrix; (b) containing a set of amino acid sequences which are positively
 CC identified when position dependent scoring matrices according to tables 1
 CC -4 (given in the specification) are used to yield a p-value of less than
 CC 110-60; or (c) comprising any one of the sequences shown in AAY55710-
 CC 711. The ycfB polypeptides and polynucleotides can be used in method to
 CC identify antagonists and antibacterial compounds. These antagonists and
 CC compounds can be used to treat bacterial infections. The polypeptides of
 CC the invention are essential proteins for bacterial viability, and
 CC represent new targets for antibiotics. Sequences AAY5647-709 represent
 CC different motifs of the ycfB family polypeptides of various bacterial
 CC species
 CC
 XX Sequence 49 AA;
 SQ
 Query Match 20.0%; Score 41.5; DB 3; Length 49;
 Best Local Similarity 32.1%; Pred. No. 4e+02;
 Matches 9; Conservative 6; Mismatches 8; Indels 5; Gaps 1;
 QY 3 EPORETLKAIHYALNCCGLAGGVEQFIS 30
 DB 3 DPMSETAKV-----IVGMSGGVDSVS 25
 RESULT 16
 AAR13376
 ID AAR13376 standard; protein; 32 AA.
 XX
 AC AAR13376;
 XX
 XX 25-MAR-2003 (revised)
 DT 24-OCT-1991 (first entry)
 XX
 DE Adult T-cell leukaemia antigen detecting peptide (7).
 XX
 KW ATLA; antibodies; detection; immobilisation.
 XX
 OS Synthetic.
 XX
 XX JP03161499-A.
 PN
 XX 11-JUL-1991.
 PD
 XX 20-NOV-1989; 89JP-00302699.
 PF
 XX 20-NOV-1989; 89JP-00302699.
 PR
 XX (KURS) KURARAY CO LTD.
 PA

PA (NISE-) NIHON SEKI JIJISHA.
 XX
 DR WPI; 1991-248729/34.
 XX
 XX Peptide for detecting adult T-cell leukaemia antigen - based on units of
 PT proline, serine, threonine, aspartic acid, glutamine, isoleucine,
 PT tyrosine, valine, glycine, alanine, leucine etc.
 XX
 PS Example 7; Page 9; 25pp; Japanese.
 XX
 CC The peptide is an example of a generic formula. The peptide is capable of
 CC specifically binding to an adult T-cell leukaemia-related antigen (ATLA)-
 CC specific antibody. ATLA can be successfully detected and anti-ATLA
 CC antibodies can be removed from a patients body using an agent contg. the
 CC peptide and an adsorbent for the antibody, formed by immobilising the
 CC peptide on a support. See also AAR13370-78 and AAR13437. (Updated on 25-
 CC MAR-2003 to correct PA field.)
 XX
 SQ Sequence 32 AA;

Query Match 19.8%; Score 41; DB 2; Length 32;
 Best Local Similarity 40.0%; Pred. No. 3e+02;
 Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 QY 14 YALNCCGLAGGVEQFISDIC 33
 DB 5 YSPSCCTLTIGVSSYHSKPC 24
 RESULT 17
 AAM16377
 ID AAM16377 standard; protein; 44 AA.
 XX
 AC AAM16377;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Peptide #2811 encoded by probe for measuring cervical gene expression.
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-488901/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 PT
 XX Claim 27; SEQ ID NO 21203; 487pp; English.
 PS
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs; see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for

CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 44 AA;
Query Match 19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 47.4%; Pred. No. 4.2e+02;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 KDEPQRETLKAIHYALNCC 19
||| :|||
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 18
AAG74910
ID AAG74910 standard; protein; 44 AA.
XX AC AAG74910;
XX DT 03-SEP-2001 (first entry)
XX DE Human colon cancer antigen protein SEQ ID NO:5674.
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma; chromosome 19.
XX OS Homo sapiens.
XX PN WO200122920-A2.
XX PD 05-APR-2001.
XX PF 28-SEP-2000; 2000WO-US026524.
XX PR 29-SEP-1999; 99US-0157137P.
XX PR 03-NOV-1999; 99US-0163280P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
XX DR N-PSDB; AAH34315.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX Claim 11; Page 7216; 9803pp; English.
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patients own production of P. Additionally, N may be used
XX to produce the colon cancer-associated P, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P
XX can be used in the prevention, diagnosis and treatment of colorectal
XX carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
XX sequences used in the exemplification of the present invention. N.B.
XX Pages 666 to 682 and page 7053 of the sequence listing were missing at
XX time of publication, meaning no sequences are present for SEQ ID NO:1027
XX to 1052, 7921 and 7922

SQ Sequence 44 AA;
Query Match 19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 35.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
QY 17 NCCGLAGGVEQFISDICKK 36
||| :|||
Db 3 NCITVTNEILSLLSICKK 22
RESULT 19
ABB35365
ID ABB35365 standard; peptide; 44 AA.
XX AC ABB35365;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #2871 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX PS Claim 27; SEQ ID NO 28000; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 44 AA;
Query Match 19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 47.4%; Pred. No. 4.2e+02;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 KDEPQRETLKAIHYALNCC 19
||| :|||
Db 10 KDRASQTLQKIYCGNGC 28
RESULT 20
AAM28874
ID AAM28874 standard; protein; 44 AA.


```

XX AC AAM28874;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #2911 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234587P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-496933/54.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234587P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-496933/54.
XX PF New spatially-addressable set of single exon nucleic acid probes, useful
XX PT for measuring gene expression in sample derived from human breast,
XX PT comprises number of single exon nucleic acid probes.
XX PS Claim 27; SEQ ID NO 13170; 327pp + Sequence Listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting the
XX CC probes with a collection of detectably labelled nucleic acids derived
XX CC from mRNA of human breast, and then measuring the label bound to each
XX CC probe of the microarray. The probes are useful for verifying the
XX CC expression of regions of genomic DNA predicted to encode proteins. They
XX CC are useful for gene discovery, and for determining predisposition and/or
XX CC prognosing breast disease. Gene expression analysis is useful for
XX CC assessing the toxicity of chemical agents on cells. The microarray of
XX CC this invention presents a far greater diversity of probes for measuring
XX CC gene expression, with far less bias than expressed sequence tag
XX CC microarrays. The method is suitable for rapid production of functional
XX CC information from genomic sequence. The present sequence is a peptide
XX CC encoded by a single exon nucleic acid probe of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 44 AA;
XX Query Match 19.8%; Score 41; DB 4; Length 44;
XX Best Local Similarity 47.4%; Pred. No. 4.2e+02;
XX Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
XX QY 1 KDEPQRETILKAHYALNCC 19
XX DB |||:|:|:|:|
XX 10 KDRASQSTLQKIYCGNGC 28
XX RESULT 21
XX ABB30202
XX ID ABB30202 standard; peptide; 44 AA.
XX AC ABB30202;
XX DT 01-FEB-2002 (first entry)
XX DE Peptide #2853 encoded by breast cell single exon nucleic acid probe.
XX KW Human; microarray; single exon probe; gene expression; breast; disease;
XX KW cancer.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234587P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-488997/53.
XX PF Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PS Claim 27; SEQ ID NO 29143; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders
XX SQ Sequence 44 AA;
XX Query Match 19.8%; Score 41; DB 4; Length 44;
XX Best Local Similarity 47.4%; Pred. No. 4.2e+02;
XX Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
XX QY 1 KDEPQRETILKAHYALNCC 19
XX DB |||:|:|:|:|
XX 10 KDRASQSTLQKIYCGNGC 28
XX RESULT 22
XX ABB20807
XX ID ABB20807 standard; protein; 44 AA.
XX AC ABB20807;
XX DT 23-JAN-2002 (first entry)
XX DE Protein #2806 encoded by probe for measuring heart cell gene expression.
XX KW Human; gene expression; heart; microarray; vascular system;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.

```

PF 30-JAN-2001; 2001WO-US000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-48899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX
 PS Claim 15; SEQ ID NO 22577; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting, the
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 44 AA;

 Query Match 19.8%; Score 41; DB 4; Length 44;
 Best Local Similarity 47.4%; Pred. No. 4.2e+02;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

 QY 1 KDEPQRETLKAIHYALNCC 19
 |||:|:|:|:|
 Db 10 KDRASQTLQKIYCGNGC 28

 RESULT 23
 AAM68569
 ID AAM68569 standard; protein; 44 AA.
 XX
 AC AAM68569;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28875.
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28875.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PI WPI; 2001-488900/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 PT
 XX Example 4; SEQ ID NO 28875; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 SQ Sequence 44 AA;

 Query Match 19.8%; Score 41; DB 4; Length 44;
 Best Local Similarity 47.4%; Pred. No. 4.2e+02;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

 QY 1 KDEPQRETLKAIHYALNCC 19
 |||:|:|:|:|
 Db 10 KDRASQTLQKIYCGNGC 28

 RESULT 24
 AAM56196
 ID AAM56196 standard; protein; 44 AA.
 XX
 AC AAM56196;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28301.
 XX
 DE Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX
 PS Example 4; SEQ ID NO 28301; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention

XX SQ Sequence 44 AA;

Query Match 19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 47.4%; Pred. No. 4.2e+02;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCC 19
|||:|:|
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 25

ABG50232
ID ABG50232 standard; peptide; 44 AA.

XX AC ABG50232;

DT 25-FEB-2003 (first entry)

XX DE Human liver peptide, SEQ ID No 28880.

XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000664.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.

XX PS Claim 27; SEQ ID NO 28880; 658pp; English.

XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 44 AA;

Query Match 19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 47.4%; Pred. No. 4.2e+02;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCC 19
|||:|:|
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 26

AA04113
ID AA04113 standard; protein; 44 AA.

XX AC AA04113;

XX DT 09-OCT-2001 (first entry)

XX DE Peptide #2795 encoded by probe for measuring breast gene expression.

XX KW Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX OS Homo sapiens.

XX PN WO200157270-A2.

XX PD 09-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US000661.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX PT Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.

XX PS Claim 27; SEQ ID NO 12853; 322pp; English.

XX CC The present invention relates to novel single exon nucleic acid probes
XX (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for measuring human gene expression in
XX a human breast sample, where the probe hybridises at high stringency to a
XX nucleic acid expressed in the human breast. The probes are useful for
XX predicting, diagnosing, grading, staging, monitoring and prognosing
XX diseases of the human breast, particularly those diseases with polygenic
XX aetiology. The diseases include: breast cancer, disorders of development,
XX inflammatory diseases of the breast, fibrocystic changes, proliferative
XX breast disease and non-carcinoma tumours. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 44 AA;

Query Match 19.8%; Score 41; DB 4; Length 44;
Best Local Similarity 47.4%; Pred. No. 4.2e+02;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCC 19
|||:|:|
Db 10 KDRASQTLQKIYCGNGC 28

RESULT 27
 ABG38147
 ID ABG38147 standard; peptide; 44 AA.
 XX
 AC ABG38147;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 27812.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID NO 27812; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 44 AA;
 Query Match 19.8%; Score 41; DB 5; Length 44;
 Best Local Similarity 47.4%; Pred. No. 4.2e+02;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 KDEPQRETLLKAIHYALNCC 19
 |||:|:|
 Db 10 KDRASQTLQKIYCGNC 28
 RESULT 28
 AAY31910
 ID AAY31910 standard; protein; 46 AA.
 XX
 AC AAY31910;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Spider venom insecticidal toxin.
 XX
 KW Spider venom; toxin; insecticide; pesticide; transgenic plant;
 KW biological control; crop protection.
 XX
 OS Segestria florentina.
 XX
 PN WO9949035-A2.
 XX
 PD 30-SEP-1999.
 XX
 PF 23-MAR-1999; 99WO-GB000907.
 XX
 PR 26-MAR-1998; 98RU-00105686.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Windass JD, Blake AN, Grishin EV, Nosyreva ED, Koslov SA;
 PI Lipkin AV;
 XX
 DR WPI; 1999-591091/50.
 DR N-PSDB; AAZ20006.
 XX
 PT Segestria florentina derived insecticidal agents and related
 PT polynucleotides.
 XX
 PS Claim 8; Page 17; 40pp; English.
 XX
 CC The present sequence comprises the sequence of a F5.5/F5.6/F5.7 family
 CC toxin of Segestria florentina spider venom. The sequence was deduced from
 CC cDNA (see AAZ20006) produced by PCR amplification of S. florentina venom
 CC gland cDNA. Claimed insecticidal agents include the partial and extended
 CC peptides given in AAY31905-17. These peptides can be isolated from S.
 CC florentina spider venom and/or are encoded by S. florentina venom gland
 CC mRNA. Nucleic acid sequences (see AAZ20001-11) encoding these toxins may
 CC be incorporated into insect viruses such as baculoviruses for use in
 CC biological control of insect pests, or into recombinant plants for crop
 CC protection
 XX
 SQ Sequence 46 AA;

Query Match 19.8%; Score 41; DB 2; Length 46;
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 ETLKAIHYALNCCG 20
 ||: || ||||
 Db 7 ETVCYIHNNCCG 20

RESULT 29

AAV55680
 ID AAY55680 standard; protein; 49 AA.

AC AAY55680;

XX 07-FEB-2000 (first entry)

DE H. influenza ycfB peptide motif 3.

XX ycfB polypeptide; gram negative bacteria; gram positive bacteria;
 KW antibacterial; bacterial infection; bacterial viability; antibiotic.

XX Haemophilus influenzae.

XX WO9954462-A2.

XX 28-OCT-1999.

XX 20-APR-1999; 99WO-EP002638.

XX 22-APR-1998; 98GB-00008350.

XX (GLAX) GLAXO GROUP LTD.

PI Arigoni F, Edgerton MD, Loferer H, Peitsch MC;

XX WPI; 2000-013249/01.

XX Novel bacterial polypeptides used to identify broad spectrum antibiotics.

PS Claim 3; Fig 2C; 56pp; English.

XX The invention discloses a novel family of polypeptides, designated the
 CC ycfB family, required for the growth of both gram negative and gram
 CC positive bacteria. The novel polypeptide of ycfB family is defined by:
 CC (a) a HSP score of greater than or equal to 100 when compared with one of
 CC the amino acid sequences of the ycfB family members given in the
 CC specification, when the BLAST algorithm is used with a BLOSUM62 scoring
 CC matrix; (b) containing a set of amino acid sequences which are positively
 CC identified when position dependent scoring matrices according to tables 1
 CC -4 (given in the specification) are used to yield a p-value of less than
 CC 110-60; or (c) comprising any one of the sequences shown in AAY55710-
 CC 711. The ycfB polypeptides and polynucleotides can be used in method to
 CC identify antagonists and antibacterial compounds. These antagonists and
 CC compounds can be used to treat bacterial infections. The polypeptides of
 CC the invention are essential proteins for bacterial viability, and
 CC represent new targets for antibiotics. Sequences AAY55647-709 represent
 CC different motifs of the ycfB family polypeptides of various bacterial
 CC species

XX Sequence 49 AA;

Query Match 19.8%; Score 41; DB 3; Length 49;
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 19 CGLAGGVQFIS 30

||: ||||: :||
 Db 14 CGMSGGVDSVS 25

RESULT 30

ABG99768

ID ABG99768 standard; peptide; 32 AA.

XX AC ABG99768;

XX 17-JAN-2003 (first entry)

XX Conus sp conotoxin-associated peptide SEQ ID 553.

XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.

XX Conus sp.

XX WO200264740-A2.

XX 22-AUG-2002.

XX 11-FEB-2002; 2002WO-US003887.

XX 09-FEB-2001; 2001US-0267408P.

XX (COGN-) COGNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 PI Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

XX WPI; 2002-706921/76.

XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.

PS Claim 1; Page 289; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterizing a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention

XX Sequence 32 AA;

Query Match 19.6%; Score 40.5; DB 5; Length 32;
 Best Local Similarity 43.8%; Pred. No. 3.5e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGLAGGVQFISDTC 33

||||: ||: ||
 Db 17 CCGLENG-QPFCAPVC 31

RESULT 31

ABG99387

ID ABG99387 standard; peptide; 32 AA.

XX AC ABG99387;

XX 17-JAN-2003 (first entry)

XX Conus sp conotoxin-associated peptide SEQ ID 42.

KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.
 XX
 OS Conus arenatus.
 XX
 PN WO200264740-A2.
 XX
 PD 22-AUG-2002.
 XX
 XX 11-FEB-2002; 2002WO-US003887.
 PF
 XX 09-FEB-2001; 2001US-0267408P.
 PR
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 PI Grilleley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 PI
 DR WPI; 2002-706921/76.
 XX
 XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX
 XX Claim 1; Page 123; 305pp; English.
 XX
 CC This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG9360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 19.6%; Score 40.5; DB 5; Length 32;
 Best Local Similarity 41.2%; Pred. No. 3.5e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 QY 17 NCGLAGGVQPTSDIC 33
 :||||| :|:|:
 Db 16 HCCGLXNG-QXFCALC 31
 RESULT 32
 AA47052
 ID AA47052 standard; peptide; 25 AA.
 XX
 AC AA47052;
 XX
 XX 15-MAY-1998 (first entry)
 DT
 XX HIV-1 V3 loop peptide sequence 4 (strain SC.B).
 DE
 XX Human rhinovirus; HRV 14; influenza virus; HIV-1; V3 loop; chimeric;
 KW immunogenic epitope; immunisation; immune response; vaccine; pathogen;
 KW tumour; Human immunodeficiency virus type 1.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 PN US5714374-A.
 XX

PD 03-FEB-1998.
 XX
 PF 17-MAR-1995; 95US-00406347.
 XX
 PR 12-SEP-1990; 90US-00582335.
 PR 01-APR-1993; 93US-00041790.
 PR 12-SEP-1994; 94US-00304635.
 XX
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA
 XX Arnold EV, Arnold GF;
 PI
 XX WPI; 1998-129862/12.
 DR
 XX Chimeric human rhino-viruses expressing heterologous antigens for use in
 PT vaccines, etc. - is constructed by inserting heterologous nucleotide
 PT sequence encoding chimeric region into the nucleotide sequence of human
 PT rhinovirus encoding part of a neutralising immunogenic site.
 XX
 XX Example 3; Col 23; 27pp; English.
 XX
 CC This peptide sequence is from the human immunodeficiency virus (HIV-1) V3
 CC loop sequence library. A library of chimeric human rhinovirus 14 (HRV 14)
 CC displaying many HIV-1 V3 loop sequences in a vast array of conformations
 CC can be constructed. A recombinant chimeric HRV can be constructed by
 CC inserting a heterologous nucleotide sequence encoding a chimeric region
 CC into the nucleotide sequence of a HRV encoding part of a neutralising
 CC immunogenic site. The chimeric region is expressed on the surface of the
 CC chimeric virus and is capable of participating in an immune reaction. The
 CC rhinovirus is an HRV serotype that binds to ICAM-1. The chimeric region
 CC is presented in neutralising immunogenic site Nim-II of viral protein
 CC VP2. The virus is a retrovirus, preferably HIV-1 or HIV-2. The virus can
 CC also be an orthomyxovirus, preferably an influenza virus for other
 CC chimeric constructs. The chimeric region is from the haemagglutinin
 CC antigen of the influenza virus, the region comprising amino acids 128-136
 CC of the haemagglutinin antigen. In other chimeric constructs, a HRV 14
 CC chimeric region can also be presented in neutralising immunogenic site
 CC Nim-IA of viral protein VP1. The virus can be a picorna virus, preferably
 CC poliovirus, where the chimeric region is from the N-Agi site of the polio
 CC virus and comprises amino acids 93-100 of the N-Agi site and the
 CC poliovirus is of type 3. When the chimeric region is of nonviral origin,
 CC it is derived from a neoplasm, parasite or bacterium. Multiple
 CC neutralising sites of the chimeric rhinovirus contain a chimeric region
 CC which at each neutralising site is different. The rhinoviruses are used
 CC in vaccines against the pathogen or tumour from which the heterologous
 CC sequence is derived. It can be used for generating antibodies for passive
 CC immunisation and immunodiagnostic testing and for research into
 CC antigenicity and immunogenicity. Chimeric human rhinoviruses are only
 CC mildly pathogenic and have numerous potential serotypes and can elicit
 CC significant mucosal and serum immunological responses
 XX
 XX Sequence 25 AA;
 SQ
 Query Match 19.3%; Score 40; DB 2; Length 25;
 Best Local Similarity 58.3%; Pred. No. 3.1e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 FQRETLKAIHYA 15
 :|:|:|:
 Db 10 PNNNTTKSIHYA 21
 RESULT 33
 AA47052
 ID AA47052 standard; protein; 44 AA.
 XX
 AC AA47052;
 XX
 XX 07-NOV-2001 (first entry)
 DT
 XX Human immune/haematopoietic antigen SEQ ID NO:12324.
 DE
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW

KW cytostatic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

XX WO200157182-A2.

PN

XX

PD

XX

PF 17-JAN-2001; 2001WO-US001354.

XX

31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184564P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225271P.

PR 14-AUG-2000; 2000US-0225275P.

PR 14-AUG-2000; 2000US-0225278P.

PR 18-AUG-2000; 2000US-0225279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 13-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 17-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249264P.

PR 17-NOV-2000; 2000US-0249265P.

PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.

PR 17-NOV-2000; 2000US-0249300P.

PR 01-DEC-2000; 2000US-0250160P.

PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.

PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.

PR 11-DEC-2000; 2000US-0254097P.

PR 05-JAN-2001; 2001US-02559678P.

```
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI; 2001-483426/52.
XX DR N-PSDB; AAK57512.
XX CC Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX CC Claim 11; SEQ ID NO 12324; 3071pp + Sequence Listing; English.
XX PS
XX CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX CC activity, and can be used in gene therapy and vaccine production. (I)
XX CC proteins and polynucleotides may be used in the prevention, diagnosis and
XX CC treatment of diseases associated with inappropriate (I) expression. For
XX CC example, they may be used to treat disorders associated with decreased
XX CC expression by rectifying mutations or deletions in a patient's genome
XX CC that affect the activity of (I) by expressing inactive proteins or to
XX CC supplement the patients own production of (I). Additionally, (I)
XX CC polynucleotides may be used to produce the secreted (I), by inserting the
XX CC nucleic acids into a host cell and culturing the cell to express the
XX CC protein. (I) proteins and polynucleotides may be used to prevent,
XX CC diagnose and treat immune/haematopoietic-related diseases, especially
XX CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX CC to AAK87694 represent human immune/haematopoietic antigen genomic
XX CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX CC represent sequences used in the exemplification of the present invention
XX CC
XX CC Sequence 44 AA;
XX CC
XX CC Query Match 19.3%; Score 40; DB 4; Length 44;
XX CC Best Local Similarity 36.7%; Pred. No. 5.9e+02;
XX CC Matches 11; Conservative 6; Mismatches 11; Indels 2; Gaps 1;
XX CC
XX CC QY 2 DEPQRETLKAHYNCCGLAGVQFISD 31
XX CC | | | | | : | | | | | : | | | | | : | | | | | : | |
XX CC 10 DTYQXETGKKNY--QGIGSGGVQITAN 37
XX CC
XX CC RESULT 34
XX CC AAY55688
XX CC ID AAY55688 standard; protein; 45 AA.
XX CC AC
XX CC AAY55688;
XX CC DT 07-FEB-2000 (first entry)
XX CC DE
XX CC M. genitalium ycfB peptide motif 3.
XX CC ycfB polypeptide; gram negative bacteria; gram positive bacteria;
XX CC antibacterial; bacterial infection; bacterial viability; antibiotic.
XX CC Mycoplasma genitalium.
XX CC OS
XX CC WO9954462-A2.
XX CC PN
XX CC 28-OCT-1999.
XX CC PD
XX CC 20-APR-1999; 99WO-BF002638.
XX CC PF
XX CC 22-APR-1998; 98GB-00008350.
XX CC PR
XX CC (GLAX ) GLAXO GROUP LTD.
XX CC PA
XX CC Arigoni F, Edgerton MD, Loferer H, Peitsch MC;
XX CC WPI; 2000-013249/01.
XX CC DR
XX CC Novel bacterial polypeptides used to identify broad spectrum antibiotics.
XX CC
XX PS Claim 3; Fig 2C; 56pp; English.
XX CC The invention discloses a novel family of polypeptides, designated the
XX CC ycfB family, required for the growth of both gram negative and gram
XX CC positive bacteria. The novel polypeptide of ycfB family is defined by:
XX CC (a) a HSP score of greater than or equal to 100 when compared with one of
XX CC the amino acid sequences of the ycfB family members given in the
XX CC specification, when the BLAST algorithm is used with a BLOSUM62 scoring
XX CC matrix; (b) containing a set of amino acid sequences which are positively
XX CC identified when position dependent scoring matrices according to tables 1
XX CC -4 (given in the specification) are used to yield a p-value of less than
XX CC 110-60; or (c) comprising any one of the sequences shown in AAY55710-
XX CC 711. The ycfB polypeptides and polynucleotides can be used in method to
XX CC identify antagonists and antibacterial compounds. These antagonists and
XX CC compounds can be used to treat bacterial infections. The polypeptides of
XX CC the invention are essential proteins for bacterial viability, and
XX CC represent new targets for antibiotics. Sequences AAY55647-709 represent
XX CC different motifs of the ycfB family polypeptides of various bacterial
XX CC species
XX CC Sequence 45 AA;
XX CC
XX CC Query Match 19.3%; Score 40; DB 3; Length 45;
XX CC Best Local Similarity 47.1%; Pred. No. 6e+02;
XX CC Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX CC
XX CC QY 20 GLAGVGEQFISDIPCK 36
XX CC | | | | | : | | | | | : | |
XX CC 11 GLSGGVDVSAVALLLK 27
XX CC DB
XX CC
XX CC RESULT 35
XX CC ABB41557
XX CC ID ABB41557 standard; peptide; 47 AA.
XX CC AC ABB41557;
XX CC XX
XX CC DT 04-FEB-2002 (first entry)
XX CC DE
XX CC Peptide #9063 encoded by human foetal liver single exon probe.
XX CC Human; foetal liver; gene expression; single exon nucleic acid probe.
XX CC OS
XX CC Homo sapiens.
XX CC PN
XX CC WO200157277-A2.
XX CC XX
XX CC PD 09-AUG-2001.
XX CC PF
XX CC 30-JAN-2001; 2001WO-US000669.
XX CC PR
XX CC 04-FEB-2000; 2000US-0180312P.
XX CC PR
XX CC 26-MAY-2000; 2000US-0207456P.
XX CC PR
XX CC 30-JUN-2000; 2000US-00608408.
XX CC PR
XX CC 03-AUG-2000; 2000US-00632366.
XX CC PR
XX CC 21-SEP-2000; 2000US-0234687P.
XX CC PR
XX CC 27-SEP-2000; 2000US-0236359P.
XX CC PR
XX CC 04-OCT-2000; 2000GB-00024263.
XX CC XX
XX CC (MOLE-) MOLECULAR DYNAMICS INC.
XX CC XX
XX CC Penn SG, Hanzel DK, Chen W, Rank DR;
XX CC WPI; 2001-483447/52.
XX CC DR
XX CC Human genome-derived single exon nucleic acid probes useful for analyzing
XX CC gene expression in human fetal liver.
XX CC PS
XX CC Claim 27; SEQ ID NO 34192; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
```


CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;
 Best Local Similarity 50.0%; Pred. No. 6.3e+02;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 25 VEQFISDICKVDV 38
 DB 11 VETISTDVCKVDV 24

RESULT 36

AAW35348
 ID AAW35348 standard; protein; 47 AA.

XX AC AAW35348;

XX DT 17-OCT-2001 (first entry)

XX DE Peptide #9385 encoded by probe for measuring placental gene expression.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;

XX KW genetic disorder.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PF WI; 2001-48897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.

XX PS Claim 27; SEQ ID NO 35617; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders

XX Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;
 Best Local Similarity 50.0%; Pred. No. 6.3e+02;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 25 VEQFISDICKVDV 38
 DB 11 VETISTDVCKVDV 24

RESULT 37

AAW75236
 ID AAW75236 standard; protein; 47 AA.

XX AC AAW75236;

XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35542.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PF WI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 35542; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention

XX Sequence 47 AA;

Query Match 19.3%; Score 40; DB 4; Length 47;
 Best Local Similarity 50.0%; Pred. No. 6.3e+02;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 25 VEQFISDICKVDV 38

DB 11 VETISTDVCKVDV 24

RESULT 38

AAW62428

ID AAW62428 standard; protein; 47 AA.

XX AC AAW62428;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34533.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

```
OS Homo sapiens.
XX WO200157275-A2.
PN
XX
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 34533; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 47 AA;
XX
XX Query Match 19.3%; Score 40; DB 4; Length 47;
XX Best Local Similarity 50.0%; Pred. No. 6.3e+02;
XX Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 25 VEQFISDICPKKDV 38
XX || :||: |||
XX 11 VETISTDVCKRKDV 24
XX
XX
XX RESULT 39
XX ABG56998
XX ID ABG56998 standard; peptide; 47 AA.
XX
XX AC ABG56998;
XX
XX DT 25-FEB-2003 (first entry)
XX
XX DE Human liver peptide, SEQ ID No 35646.
XX
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200157273-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000664.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
```

```
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 35646; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 47 AA;
XX
XX Query Match 19.3%; Score 40; DB 4; Length 47;
XX Best Local Similarity 50.0%; Pred. No. 6.3e+02;
XX Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 25 VEQFISDICPKKDV 38
XX || :||: |||
XX 11 VETISTDVCKRKDV 24
XX
XX
XX RESULT 40
XX ABG44889
XX ID ABG44889 standard; peptide; 47 AA.
XX
XX AC ABG44889;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 34554.
XX
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200186003-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000665.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
```

PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 34554; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 47 AA;

Query Match 19.3%; Score 40; DB 5; Length 47;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 25 VEQFISDICKQDV 38
||| :||| :|||
Db 11 VETISTDVCKRQDV 24

Search completed: January 20, 2006, 17:30:38
Job time : 96.7654 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:26:44 ; Search time 26.2716 Seconds
(without alignments)
119.584 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207
Sequence: 1 KQEPQETLKAHYALNCCLAGGVQFISDICPKDV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	75.8	29	1 US-08-254-493-5	Sequence 5, Appli
2	157	75.8	29	1 US-08-408-222B-5	Sequence 5, Appli
3	50	24.2	29	1 US-08-254-493-6	Sequence 6, Appli
4	50	24.2	29	1 US-08-408-222B-6	Sequence 6, Appli
5	47	22.7	30	1 US-08-254-493-4	Sequence 4, Appli
6	47	22.7	30	1 US-08-408-222B-4	Sequence 4, Appli
7	43	20.8	23	2 US-07-930-593-3	Sequence 3, Appli
8	43	20.8	23	2 US-09-414-872-3	Sequence 3, Appli
9	43	20.8	26	2 US-07-930-593-1	Sequence 1, Appli
10	43	20.8	26	2 US-09-414-872-1	Sequence 1, Appli
11	43	20.8	44	2 US-09-902-540-14873	Sequence 14873, A
12	42	20.3	37	2 US-08-900-230-54	Sequence 54, Appl
13	41.5	20.0	50	2 US-09-004-406C-26	Sequence 26, Appl
14	41	19.8	30	1 US-07-596-081A-33	Sequence 33, Appl
15	41	19.8	32	1 US-07-596-081A-12	Sequence 12, Appl
16	40	19.3	25	1 US-08-406-347A-12	Sequence 12, Appl
17	39.5	19.1	40	2 US-09-493-795B-302	Sequence 302, App
18	39	18.8	45	2 US-09-674-973A-363	Sequence 363, App
19	39	18.8	46	2 US-09-674-973A-364	Sequence 364, App
20	38.5	18.6	26	2 US-09-201-227A-26	Sequence 26, Appl
21	38.5	18.6	26	2 US-09-084-303B-222	Sequence 222, App
22	38.5	18.6	44	1 US-08-747-915-1	Sequence 1, Appli
23	38.5	18.6	44	2 US-09-285-783-1	Sequence 1, Appli
24	38.5	18.6	44	2 US-09-670-537A-1	Sequence 1, Appli
25	38.5	18.6	47	2 US-09-860-503-2	Sequence 2, Appli
26	38.5	18.6	48	2 US-09-219-019-22	Sequence 22, Appl
27	38.5	18.6	49	1 US-08-747-915-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-254-493-5
; Sequence 5, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOTAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:

Sequence 5, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 23, Appli
Sequence 22, Appli
Sequence 52, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 179, App
Sequence 5, Appli
Sequence 6, Appli
Sequence 1244, Ap
Sequence 6, Appli
Sequence 307, App
Sequence 308, App
Sequence 309, App
Sequence 310, App
Sequence 311, App
Sequence 307, App
Sequence 308, App
Sequence 309, App

; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-254-493-5

Query Match 75.8%; Score 157; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33
Db 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 2

US-08-408-222B-5
; Sequence 5, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 22-MAR-1995
; APPLICATION NUMBER: US/08/408,222B
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-408-222B-5

Query Match 75.8%; Score 157; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33
Db 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 3

US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-254-493-6

Query Match 24.2%; Score 50; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 SDICPKDV 38

Db 1 SDICPKDV 9

RESULT 4
US-08-408-222B-6
; Sequence 6, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-408-222B-6

Query Match 24.2%; Score 50; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 SDICPKDV 38
Db 1 SDICPKDV 9

RESULT 5
US-08-254-493-4
; Sequence 4, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI

; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-4

Query Match 22.7%; Score 47; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOEPQRETL 9
Db 22 KOEPQRETL 30

RESULT 6
US-08-408-222B-4
; Sequence 4, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman

STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,222B
FILING DATE: 22-MAR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,493
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-085396-1991
FILING DATE: 14-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-022321-1992
FILING DATE: 07-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41777-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-408-222B-4

Query Match 22.7% Score 47; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETL 9
||| |||||
Db 22 KDEPQRETL 30

RESULT 7
US-07-930-593-3
Sequence 3, Application US/07930593
Patent No. 6040167
GENERAL INFORMATION:
APPLICANT: Gluck, Reinhard
APPLICANT: Klein, Peter
TITLE OF INVENTION: SYNTHETIC MEMBRANE VESICLES CONTAINING
TITLE OF INVENTION: FUNCTIONALLY ACTIVE FUSION PEPTIDES AS DRUG DELIVERY
TITLE OF INVENTION: SYSTEMS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,593
FILING DATE: 02-NOV-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP92/00089
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91101414.0
FILING DATE: 02-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: FA-1423 PCT (167-74)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: myxovirus, paramyxovirus, rhabdovirus
US-07-930-593-3

Query Match 20.8% Score 43; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 CCGLAGGVEQFISD 31
||| ||| :
Db 2 CCGLFGAIGFIEN 15

RESULT 8
US-09-414-872-3
Sequence 3, Application US/09414872
Patent No. 6210708
GENERAL INFORMATION:
APPLICANT: Witi, Ernst Rudolf
APPLICANT: Gluck, Reinhard
APPLICANT: Klein, Peter
TITLE OF INVENTION: Cationic virosones as transfer system for genetic
TITLE OF INVENTION: material
FILE REFERENCE: 101909.01
CURRENT APPLICATION NUMBER: US/09/414,872
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: US 09/171,882
EARLIER FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: PCT/EP97/02268
EARLIER FILING DATE: 1997-05-04
EARLIER APPLICATION NUMBER: EP 96107282.4
EARLIER FILING DATE: 1996-05-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: hemagglutinin-type fusogenic peptide
US-09-414-872-3

Query Match 20.8% Score 43; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 CCGLAGGVEQFISD 31


```
Db      ||||| : || :
        2 CCGLFGAIGFIEN 15

RESULT 9
US-07-930-593-1
; Sequence 1, Application US/07930593
; Patent No. 6040167
; GENERAL INFORMATION:
; APPLICANT: Gluck, Reinhard
; APPLICANT: Klein, Peter
; APPLICANT: Herrmann, Peter
; TITLE OF INVENTION: SYNTHETIC MEMBRANE VESICLES CONTAINING
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE FUSION PEPTIDES AS DRUG DELIVERY
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07930,593
; APPLICATION NUMBER: US/07930,593
; FILING DATE: 02-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP92/00089
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91101414.0
; FILING DATE: 02-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: FA-1423 PCT (167-74)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: myxovirus, paramyxovirus, rhabdovirus
;
US-07-930-593-1
Query Match      20.8%; Score 43; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 17;
Matches      7; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

QY      18 CCGLAGGVEQFISD 31
Db      ||||| : || :
        2 CCGLFGAIGFIEN 15

RESULT 10
US-09-414-872-1
; Sequence 1, Application US/09414872
; Patent No. 6210708
; GENERAL INFORMATION:
; APPLICANT: Witi, Ernst Rudolf
; APPLICANT: Gluck, Reinhard
; APPLICANT: Klein, Peter

; TITLE OF INVENTION: Cationic virosones as transfer system for genetic
; TITLE OF INVENTION: material
; FILE REFERENCE: 101909.01
; CURRENT APPLICATION NUMBER: US/09/414,872
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: US 09/171,882
; EARLIER FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: PCT/EP97/02268
; EARLIER FILING DATE: 1997-05-04
; EARLIER APPLICATION NUMBER: EP 96107282.4
; EARLIER FILING DATE: 1996-05-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: hemagglutinin-type fusogenic peptide
;
US-09-414-872-1
Query Match      20.8%; Score 43; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 17;
Matches      7; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

QY      18 CCGLAGGVEQFISD 31
Db      ||||| : || :
        2 CCGLFGAIGFIEN 15

RESULT 11
US-09-902-540-14873
; Sequence 14873, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14873
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
;
US-09-902-540-14873
Query Match      20.8%; Score 43; DB 2; Length 44;
Best Local Similarity 53.3%; Pred. No. 32;
Matches      8; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

QY      17 NCCGLAGGVEQFISD 31
Db      :||| : || :
        29 DCCGAAGRPVKFILD 43

RESULT 12
US-08-900-230-54
; Sequence 54, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
```

STREET: 1185 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/900,230
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-900-230-54

Query Match 20.3%; Score 42; DB 2; Length 37;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ALNCCGLAGG 24
DB 21 ACTCCGAAGG 30

RESULT 13

US-09-004-406C-26
Sequence 26, Application US/09004406C
Patent No. 6174706

GENERAL INFORMATION:

APPLICANT: Vinci, Victor A.
APPLICANT: Conder, Michael J.
APPLICANT: McAda, Phyllis C.
APPLICANT: Reeves, Christopher D.
APPLICANT: Rambosek, John
APPLICANT: Davis, Charles Ray
APPLICANT: Hendrickson, Lee E.

TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE

FILE REFERENCE: 19076PPA
CURRENT APPLICATION NUMBER: US/09/004,406C
CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 08/637,640
PRIOR FILING DATE: 1996-08-23
PRIOR APPLICATION NUMBER: 08/148,132
PRIOR FILING DATE: 1993-11-02

NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 50
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-004-406C-26

Query Match 20.0%; Score 41.5; DB 2; Length 50;
Best Local Similarity 32.3%; Pred. No. 62;
Matches 10; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 3 BPQRETLKAIHYALNCCGLAG-GVBOQFISDI 32
DB 4 EAQRDLVKAVAHILGIRDLAGINLDSLADL 34

RESULT 14

US-07-596-081A-33
Sequence 33, Application US/07596081A
Patent No. 5194586
GENERAL INFORMATION:
APPLICANT: Maeda, Yoshiaki
APPLICANT: Shiraki, Hiroshi
APPLICANT: Washitani, Yukiko
APPLICANT: Kuroda, Naotaka
APPLICANT: Yamada, Kyoko
APPLICANT: Oka, Kiichiro
APPLICANT: Namba, Toshihiro
TITLE OF INVENTION: Peptides and Use Thereof
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eric S. Spector
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/596,081A
FILING DATE: 19901011
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 266983/1989
FILING DATE: 13-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: Spector, Eric S.
REGISTRATION NUMBER: 22495
REFERENCE/DOCKET NUMBER: 513904
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-596-081A-33

Query Match 19.8%; Score 41; DB 1; Length 30;
Best Local Similarity 40.0%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 14 YALNCCGLAGGVBOQFISDIC 33
DB 3 YSPSCCTLTIGVSSVHSKPC 22

RESULT 15

US-07-596-081A-12
Sequence 12, Application US/07596081A
Patent No. 5194586

GENERAL INFORMATION:

APPLICANT: Maeda, Yoshiaki
APPLICANT: Shiraki, Hiroshi
APPLICANT: Washitani, Yukiko
APPLICANT: Kuroda, Naotaka
APPLICANT: Yamada, Kyoko
APPLICANT: Oka, Kiichiro

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/041,790
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/583,335
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 1984/46203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 12 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-347A-12

Query Match 19.3%; Score 40;
Best Local Similarity 58.3%; Pred. No.
Matches 7; Conservative 1; Mismatch

QY 4 PORETLKAIHYA 15
DB 10 PNNTTKSIHYA 21

RESULT 17
US-09-493-795B-302
; Sequence 302, Application US/09493795B
; Patent No. 6797808
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Pept.
; FILE REFERENCE: 2314-179-A
; CURRENT APPLICATION NUMBER: US/09/493,795
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 302
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus arenatus
US-09-493-795B-302

Query Match 19.1%; Score 39.5
Best Local Similarity 40.0%; Pred. No.
Matches 8; Conservative 3; Mismatch

QY 16 LNCCLAGVGEQFTSDICPK 35
DB 20 LNCISPGCWNEY-KDRCSK 38

RESULT 18
US-09-674-973A-363
; Sequence 363, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 363
; LENGTH: 45
; TYPE: PRT
; ORGANISM: H
US-09-674-973A-

```

Query Match 18.8%; Score 39; DB 2; Length 45;
Best Local Similarity 38.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 19 CGLA--GGVEQFISDICKKD 37
| | | | | : : : : :
Dd 1 CSLAKDGSTEDTVSSLGGEED 21

```

RESULT 19
US-09-674-973A-364
; Sequence 364, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 364
;   LENGTH: 46
;   TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-973A-364

```

Query Match 18.8%; Score 39; DB 2; Length 46;
Best Local Similarity 38.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

```

QY      19  CGLA--GGVEQFISDICKPKD 37
          |||  |  |  |  |  |  |  |
Db      2  CSLAKDGSTEDTVSSLCGEED 22

```

```

RESULT 20
US-09-201-227A-26
; Sequence 26, Application US/09201227A
; Patent No. 6468770
; GENERAL INFORMATION:
; APPLICANT: Keyes, Linda N.
; APPLICANT: Doberstein, Stephen K.
; APPLICANT: Buchman, Andrew R.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOCASTER INSULIN-LIKE
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 7326-066
; CURRENT APPLICATION NUMBER: US/09/201,227A
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-227A-26

```

```
Query Match      18.6%; Score 38.5; DB 2; Length 26;
Best Local Similarity 37.5%; Pred. No. 81;
Matches 9: Conservative 5; Mismatches 9; Indels 1; Gaps 1;
```

QY	11	ATHYALNCCGLAGGVEQFISD	34
		: : : : : :	
Db	3	ATNPARHCC-LSGCTRQDLTL	25
		: : : : : :	

RESULT 21

US-09-084-303B-222
; Sequence 222, Application US/09084303B
; Patent No. 6627746
; GENERAL INFORMATION:

APPLICANT: Doberstein, Stephen
APPLICANT: Reddy, Bindu
APPLICANT: Platt, Darren
APPLICANT: Ferguson, Kimberly
TITLE OF INVENTION: NUCLEIC ACIDS AND PROT
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 7326-069-999
CURRENT APPLICATION NUMBER: US/09/084,303B
CURRENT FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patent in version 3.1

Query Match	18.6%	Score 38.5;	DB 2;	Length 26;
Best Local Similarity	37.5%	Pred. No. 81;		
Matches	9;	Conservative	5;	Mismatches 9;
				Indels 1;
				Gaps 1;

Qy	11	AIHYALNCCGLAGGVEQFISD	34
		: : : : : :	
Dd	3	ATNPARHCC-LSGCTRODLLTL	25

```

RESULT 22
US-08-747-915-1
; Sequence 1, Application US/08747915
; Patent No. 5942492
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,915
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 32904-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNFORSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-747-915-1

```

```

; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-537A-1

Query Match      18.6%; Score 38.5; DB 2; Length 44;
Best Local Similarity 40.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY      17 NCCGLAGGV---EQFTSDI----CPKK 36
        ||| |||| :| | :| |||
Db       10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 25
US-09-880-503-2
; Sequence 2, Application US/0980503
; Patent No. 6833357
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-2

Query Match      18.6%; Score 38.5; DB 2; Length 47;
Best Local Similarity 40.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY      17 NCCGLAGGV---EQFTSDI----CPKK 36
        ||| |||| :| | :| |||
Db       10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 26
US-09-219-019-22
; Sequence 22, Application US/09219019
; Patent No. 6268341
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, STEVEN
; APPLICANT: STRATTON-THOMAS, JENNIFER R.
; TITLE OF INVENTION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
; TITLE OF INVENTION: INHIBITORS
; FILE REFERENCE: 23533-0005
; CURRENT APPLICATION NUMBER: US/09/219,019
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 08/438,263
; PRIOR FILING DATE: 1995-05-10
; PRIOR APPLICATION NUMBER: 08/280,288
; PRIOR FILING DATE: 1994-07-26
; PRIOR APPLICATION NUMBER: 08/070,153
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-09-219-019-22

Query Match 18.6%; Score 38.5; DB 2; Length 48;
Best Local Similarity 40.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCLAGGV---EQFISDI-----CPKK 36
||| ||| :|:| |||
Db 10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 27

US-08-747-915-5
; Sequence 5, Application US/08747915
; Patent No. 5942492
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,915
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 32904-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: group(11..19, 13..31, 33..42)
US-08-747-915-5

Query Match 18.6%; Score 38.5; DB 1; Length 49;
Best Local Similarity 40.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCLAGGV---EQFISDI-----CPKK 36
||| ||| :|:| |||
Db 10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 28

US-09-285-783-5
; Sequence 5, Application US/09285783
; Patent No. 6514710
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.

Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RADER, FISHMAN & GRAUER
; STREET: 1233 20TH STREET NW, SUITE 501
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,783
; FILING DATE: 05-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 955-8787
; TELEFAX: (202) 955-3751
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: group(11..19, 13..31, 33..42)
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-285-783-5

Query Match 18.6%; Score 38.5; DB 2; Length 49;
Best Local Similarity 40.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

QY 17 NCCLAGGV---EQFISDI-----CPKK 36
||| ||| :|:| |||
Db 10 NCDCLNGGTCVSNKYFSNIHWCNCPKK 36

RESULT 29

PCT-US96-08811-2
; Sequence 2, Application PC/TUS9608811
; GENERAL INFORMATION:
; APPLICANT: VERNON, Leo P., RAEI, Eppie D. and
; APPLICANT: GASANOV, Sardar E.
; TITLE OF INVENTION: Pyruvate thionin containing
; immunotoxins and immunotoxin-like compounds
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MADSON & METCALF
; STREET: 950 First Interstate Building, 170 South
; STREET: Main Street
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08811
; FILING DATE:


```

; ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; ;
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/849,248
; ; FILING DATE: 27 Aug 1997
; ; INFORMATION FOR SEQ ID NO: 1:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 47 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: peptide
; ; US-08-849-248-1

```

Query Match 17.9%; Score 37; DB 1; Length 47;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 7; Indels

QY	16	LNCCGLAGGVEQFISD	31
Db	8	LICVNNGGCEQYCS	23

RESULT 36

US-08-849-248-3
Sequence 3, Application US/08849248
Patent No. 5948759
GENERAL INFORMATION:
APPLICANT: Huebryn, Mette
APPLICANT: Fischer, Peter
APPLICANT: Orling, Lars
TITLE OF INVENTION: Factor VII Fragment 82-128 and its use
in blood clotting disorders
TITLE OF INVENTION: in blood clotting disorders
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon and Thomas
STREET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,248

```

;      OTHER INFORMATION: /product= "46"
;      OTHER INFORMATION: /note= "Xaa represents Abu"
US-08-849-248-3

```

Query Match 17.9%; Score 37; DB 1; Length 47;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY	16	L	N	C	C	L	A	G	G	V	E	Q	F	S	D	31	
Db	8	L	I	C	V	N	E	N	G	G	X	E	Q	Y	C	S	23

RESULT 37

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```
Query Match      17.4%; Score 36; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

Qy	18	CCGLAGGVEQFISD 31
	:	
Db	1	CVNENGGC EOYCSD 14

RESULT 38

US-09-493-795B-179
; Sequence 179, Application US/09493795B
; Patent No. 6797808
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hayward, David R.
; APPLICANT: McIlntosh, J. Michael

```
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-179.A
; CURRENT APPLICATION NUMBER: US/09/493,795B
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 179
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus arenatus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)..(13)
; OTHER INFORMATION: Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at
; OTHER INFORMATION: residue 10 is Trp (D or L) or halo-Trp; Xaa at
; OTHER INFORMATION: residue 12 is Glu or gamma-carboxy-Glu; Xaa at
; OTHER INFORMATION: residue 13 is Tyr, nor-Tyr, mono-halo-Tyr,
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)..(19)
; OTHER INFORMATION: di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
; OTHER INFORMATION: nitro-Tyr; Xaa at residues 14 and 19 is Lys,
; OTHER INFORMATION: N-methyl-Lys, N,N-dimethyl-Lys or
; OTHER INFORMATION: N,N,N-trimethyl-Lys.
US-09-493-795B-179

Query Match 17.4%; Score 36; DB 2; Length 21;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 16 LNCCLAG 23
DB 1 LNCCLAG 8

RESULT 39
PCT-US96-01720-5
; Sequence 5, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01720-5

Query Match 17.4%; Score 36; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCGLAGG 24
DB 8 CCGGAGG 14

Search completed: January 20, 2006, 17:35:32
Job time : 27.2716 secs
```

```
QY 18 CCGLAGG 24
DB 8 CCGGAGG 14

RESULT 40
PCT-US96-01720-6
; Sequence 6, Application PC/TUS9601720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,055
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-5PC
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01720-6

Query Match 17.4%; Score 36; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCGLAGG 24
DB 8 CCGGAGG 14

Search completed: January 20, 2006, 17:35:32
Job time : 27.2716 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:27:09 ; Search time 72.716 Seconds
(without alignments)
218.350 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207
Sequence: 1 KDBPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	4	US-10-619-323-4
2	128	61.8	30	5	US-10-473-127-1717
3	60	29.0	22	4	US-10-619-323-7
4	45	21.7	32	6	US-11-111-953-658
5	44	21.3	33	3	US-09-798-889-81
6	44	21.3	33	4	US-10-633-680-81
7	44	21.3	44	4	US-10-072-602B-490
8	44	21.3	44	6	US-11-097-315-490
9	42.5	20.5	57	4	US-10-425-115-188223
10	42.5	20.5	50	4	US-10-074-024-339
11	42	20.3	37	2	US-08-900-230-54
12	42	20.3	40	4	US-10-424-599-232491
13	42	20.3	42	4	US-10-424-599-165084
14	41.5	20.0	32	4	US-10-072-602B-39
15	41.5	20.0	32	6	US-11-097-315-39
16	41	19.8	40	4	US-10-425-115-259736
17	41	19.8	44	3	US-09-864-761-36105
18	41	19.8	44	4	US-10-106-698-5684
19	41	19.8	44	4	US-10-425-115-206370
20	41	19.8	46	4	US-10-424-599-233026
21	41	19.8	49	4	US-10-425-115-200533
22	40.5	19.6	32	4	US-10-072-602B-42
23	40.5	19.6	32	4	US-10-072-602B-553
24	40.5	19.6	32	6	US-11-097-315-42
25	40.5	19.6	32	6	US-11-097-315-553
26	40	19.3	44	4	US-10-424-599-283568
27	40	19.3	47	3	US-09-864-761-45041

28	40	19.3	47	4	US-10-425-115-220604	Sequence 220604,
29	40	19.3	49	4	US-10-424-599-234805	Sequence 234805,
30	39.5	19.1	22	4	US-10-072-602B-554	Sequence 554, App
31	39.5	19.1	32	6	US-11-097-315-554	Sequence 554, App
32	39.5	19.1	40	5	US-10-895-372-302	Sequence 302, App
33	39.5	19.1	43	4	US-10-425-115-355346	Sequence 355346,
34	39	18.8	28	3	US-09-866-066-31	Sequence 31, Appl
35	39	18.8	28	5	US-10-969-677-31	Sequence 31, Appl
36	39	18.8	45	3	US-09-864-761-38744	Sequence 38744, A
37	39	18.8	45	5	US-10-776-224-363	Sequence 363, App
38	39	18.8	46	4	US-10-424-599-216516	Sequence 216516,
39	39	18.8	46	5	US-10-425-115-300697	Sequence 300697,
40	39	18.8	46	5	US-10-776-224-364	Sequence 364, App
41	39	18.8	47	4	US-10-424-599-191877	Sequence 191877,
42	39	18.8	49	4	US-10-425-115-266792	Sequence 266792,
43	39	18.8	50	4	US-10-425-115-202414	Sequence 202414,
44	39	18.8	50	4	US-10-425-115-248925	Sequence 248925,
45	38.5	18.6	26	4	US-10-339-740-222	Sequence 222, App
46	38.5	18.6	27	4	US-10-196-394-54	Sequence 54, Appl
47	38.5	18.6	37	4	US-10-425-115-256841	Sequence 256841,
48	38.5	18.6	40	4	US-10-437-963-152437	Sequence 152437,
49	38.5	18.6	44	4	US-10-349-543-1	Sequence 1, Appli
50	38.5	18.6	44	4	US-10-744-927-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-619-323-4
; Sequence 4, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide

US-10-619-323-4
Query Match 100.0%; Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDBPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 38
Db 1 KDBPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 38

RESULT 2

US-10-473-127-1717
; Sequence 1717, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING


```

RESULT 7
US-10-072-602B-490
; Sequence 490, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Mcintosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig

```

RESULT 9
US-10-425-115-188223
; Sequence 188223, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

RESULT 15
US-11-097-315-39
; Sequence 39, Application US/11097315
; Publication No. US20050214213A1

Qy 14 YALNCCGLAGVEQFISD 31
Dy 9 YAKCCRLVGSIPHATDD 26

Query Match 19.8%; Score 41; DB 3; Length 44;
 Best Local Similarity 47.4%; Pred. No. 3.2e+02;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KDEPQRETLKAIHYALNCC 19
 Db 10 KDRASQOTLQIIYCGNGC 28

RESULT 18
 US-10-106-698-5684
 ; Sequence 5684, Application US/101066598
 ; Publication No. US20030109690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
 ; FILE REFERENCE: PA005P1
 ; CURRENT APPLICATION NUMBER: US/10/106,698
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/26524
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US 60/157,137
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: US 60/163,280
 ; PRIOR FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 8564
 ; SOFTWARE: PatentIn Ver. 3.0
 ; SEQ ID NO 5684
 ; LENGTH: 44
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (34)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (38)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-106-698-5684

Query Match 19.8%; Score 41; DB 4; Length 44;
 Best Local Similarity 35.0%; Pred. No. 3.2e+02;
 Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 17 NCCGLAGGVEQFISDICKPK 36
 Db 3 NCITVTNEILSLLSICKPK 22

RESULT 19
 US-10-425-115-206370
 ; Sequence 206370, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 206370
 ; LENGTH: 44
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MGT4577_119792C.1.pep
 US-10-425-115-206370

Query Match 19.8%; Score 41; DB 4; Length 44;

US-10-072-602B-553

Query Match 19.6%; Score 40.5; DB 4; Length 32;
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGLAGGVQPFISDIC 33
||||| : : : :
DB 17 CCGLENG-QPFCAPVC 31

RESULT 24

US-11-097-315-42
; Sequence 42, Application US/11097315
; Publication No. US20050214213A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-293
; CURRENT APPLICATION NUMBER: US/11/097,315
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 10/072,602
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus arenatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(31)
; OTHER INFORMATION: Xaa at residues 7, 8, 11, 13, 14 and 21 is Glu or gamma-carboxy-
; OTHER INFORMATION: Glu; Xaa at residue 25 is Pro or hydroxy-Pro
US-11-097-315-42

Query Match 19.6%; Score 40.5; DB 6; Length 32;
Best Local Similarity 41.2%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGGVQPFISDIC 33
||||| : : : :
DB 16 HCCGLXNG-QXFCARLC 31

RESULT 25

US-11-097-315-553
; Sequence 553, Application US/11097315
; Publication No. US20050214213A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-293
; CURRENT APPLICATION NUMBER: US/11/097,315
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 10/072,602
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 553
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus arenatus
US-11-097-315-553

Query Match 19.6%; Score 40.5; DB 6; Length 32;
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 18 CCGLAGGVQPFISDIC 33
||||| : : : :
DB 17 CCGLENG-QPFCAPVC 31

RESULT 26

US-10-424-599-283568
; Sequence 283568, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283568
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98084C.1.pep
US-10-424-599-283568

Query Match 19.3%; Score 40; DB 4; Length 44;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LKAIHYALNCC 19
||| : |||||
DB 29 LKIVHVALNSC 39

RESULT 27

US-09-864-761-45041
; Sequence 45041, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeo mica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

```

Query Match      19.3%; Score 40; DB 3; Length 47;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      25  VEQFSDICPKKDV 38
      ||| :||: |||
Db       11  VETISTDVCKRQDV 24

RESULT 28
US-10-425-115-220604
; Sequence 220604, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 554
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus arenatus
US-10-072-602B-554

Query Match      19.1%; Score 39.5; DB 4; Length 32;
Best Local Similarity 41.2%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGGVQFISDIC 33
      ||||| : : : :
Db 16 HCCGLENG-QPFCARLC 31

RESULT 31
US-11-097-315-554
; Sequence 554, Application US/11097315
; Publication No. US20050214213A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-293
; CURRENT APPLICATION NUMBER: US/11/097,315
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 10/072,602
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 554
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus arenatus
US-11-097-315-554

Query Match      19.1%; Score 39.5; DB 6; Length 32;
Best Local Similarity 41.2%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 17 NCCGLAGGVQFISDIC 33
      ||||| : : : :
Db 16 HCCGLENG-QPFCARLC 31

RESULT 32
US-10-895-372-302
; Sequence 302, Application US/10895372
; Publication No. US20050032705A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-286
; CURRENT APPLICATION NUMBER: US/10/895,372
; CURRENT FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: US 09/493,795
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 302
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus arenatus
US-10-895-372-302

Query Match      19.1%; Score 39.5; DB 5; Length 40;
Best Local Similarity 40.0%; Pred. No. 4.8e+02;
Matches 8; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 16 LNCCLAGGVQFISDICPK 35
      ||||| : : : :
Db 20 LNCSSIPGCWNEY-KDRCSK 38

RESULT 33
US-10-425-115-355346
; Sequence 355346, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 355346
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87242C.1.pep
US-10-425-115-355346

Query Match      19.1%; Score 39.5; DB 4; Length 43;
Best Local Similarity 38.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 2 DEPORETLKAIHYALNCCGLAGGVEQ 27
      | : | : | | | | |
Db 18 DQAGRDRCEYTRH-CLNCTSLGPGYQ 42

RESULT 34
US-09-866-066-31
; Sequence 31, Application US/09866066
; Publication No. US20030113888A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Christopher
; APPLICANT: Roberts, Steve
; APPLICANT: Ruble, Cara
; APPLICANT: Gotow, Lisa
; APPLICANT: Karnovsky, Alla
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00229.US1
; CURRENT APPLICATION NUMBER: US/09/866,066
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,152
; PRIOR FILING DATE: 2000-05-26
```

; PRIOR APPLICATION NUMBER: 60/207,257
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,119
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-066-31

Query Match 18.8%; Score 39; DB 3; Length 28;
Best Local Similarity 35.7%; Pred. No. 3.8e+02;
Matches 10; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

Qy 1 KDEPQRETLKAIHYALNCCGLAGGVEQF 28
Db 3 KNSQQHIKKLIHY--NQVFGMDWDF 28

RESULT 35

US-10-969-677-31
; Sequence 31, Application US/10969677
; Publication No. US20050176098A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Christopher
; APPLICANT: Roberds, Steve
; APPLICANT: Ruble, Cara
; APPLICANT: Gotow, Lisa
; APPLICANT: Karnovsky, Alla
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00229 US1
; CURRENT APPLICATION NUMBER: US/10/969,677
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: US/09/866,066
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,152
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,257
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,119
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-969-677-31

Query Match 18.8%; Score 39; DB 5; Length 28;
Best Local Similarity 35.7%; Pred. No. 3.8e+02;
Matches 10; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

Qy 1 KDEPQRETLKAIHYALNCCGLAGGVEQF 28
Db 3 KNSQQHIKKLIHY--NQVFGMDWDF 28

RESULT 36

US-09-864-761-38744
; Sequence 38744, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38744
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z98884.11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: O70361, EVALU6 6.00e-13
US-09-864-761-38744

Query Match 18.8%; Score 39; DB 3; Length 45;
Best Local Similarity 63.8%; Pred. No. 6.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TLKAIHYALNC 18
Db 20 TLDALNYALRC 30

RESULT 37

US-10-776-224-363
; Sequence 363, Application US/10776224
; Publication No. US20050074849A1
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Erickson, Jon Amund
; APPLICANT: Moller, Mona
; APPLICANT: Gjertsen, Marianne Klemp
; APPLICANT: Saeterdal, Ingvil

```
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 01702.4015LO
; CURRENT APPLICATION NUMBER: US/10/776,224
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US 09/674,973
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 363
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-224-363

Query Match      18.8%; Score 39; DB 5; Length 45;
Best Local Similarity 38.1%; Pred. No. 6.4e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 19 CGLA--GGVEQFISDICPKD 37
Db 1 CSLAKDGTEDTVSSLGSED 21

RESULT 38
US-10-424-599-216516
; Sequence 216516, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216516
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37542C.1.pep
US-10-424-599-216516

Query Match      18.8%; Score 39; DB 4; Length 46;
Best Local Similarity 36.4%; Pred. No. 6.6e+02;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 DEPORETLKAIHYALNCCGLAG 23
Db 23 EECYKAALIAVTLSPCCSILG 44

RESULT 39
US-10-425-115-300697
; Sequence 300697, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 300697
; LENGTH: 46
; TYPE: PRT
```

```
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_37305C.1.pep
US-10-425-115-300697

Query Match      18.8%; Score 39; DB 4; Length 46;
Best Local Similarity 29.4%; Pred. No. 6.6e+02;
Matches 10; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 4 PQRETLKAIHYALNCCGLAGVEQFISDICPKD 37
Db 10 PQSYILGYINYCLVLCQLI--IKPCVNDLGRSN 41

RESULT 40
US-10-776-224-364
; Sequence 364, Application US/10776224
; Publication No. US20050074849A1
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Ericksen, Jon Amund
; APPLICANT: Moller, Mona
; APPLICANT: Gjertsen, Marianne Klemp
; APPLICANT: Saeterdal, Ingvil
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 01702.4015LO
; CURRENT APPLICATION NUMBER: US/10/776,224
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US 09/674,973
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 364
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-224-364

Query Match      18.8%; Score 39; DB 5; Length 46;
Best Local Similarity 38.1%; Pred. No. 6.6e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 19 CGLA--GGVEQFISDICPKD 37
Db 2 CSLAKDGTEDTVSSLGSED 22

Search completed: January 20, 2006, 17:38:18
Job time : 73.716 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw_model

Run on: January 20, 2006, 17:30:50 ; Search time 6.5679 Seconds
(without alignments)
58.632 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207
Sequence: 1 KDBPQRETLKAIHYALNCCGLAGVGFISDIPCKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 1013881 residues

Total number of hits satisfying chosen parameters: 41278

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	18.1	44	6	US-10-957-887B-193
2	37.5	18.1	44	6	US-10-729-121-52
3	36.5	17.6	45	6	US-10-957-887B-243
4	35	17.4	47	7	US-11-123-896-372
5	35.5	17.1	30	6	US-10-467-657-3382
6	35	16.9	31	7	US-11-145-035-45
7	34	16.4	47	7	US-11-038-501-4
8	34	16.4	47	7	US-11-059-633-7
9	32.5	15.7	20	7	US-11-106-415-285
10	32	15.5	46	7	US-11-068-783-111
11	31	15.0	15	7	US-11-045-024-13448
12	31	15.0	21	6	US-10-939-890-535
13	31	15.0	24	7	US-11-198-847-180
14	31	15.0	24	7	US-11-198-847-282
15	31	15.0	31	7	US-11-033-039-631
16	31	15.0	36	6	US-10-957-351-184
17	30.5	14.7	21	6	US-10-939-890-537
18	30.5	14.7	49	6	US-10-467-657-2116
19	30	14.5	15	7	US-11-045-024-13229
20	30	14.5	15	7	US-11-045-024-13251
21	30	14.5	20	7	US-11-106-415-284
22	30	14.5	21	7	US-11-198-847-323
23	30	14.5	25	7	US-11-198-847-177
24	30	14.5	25	7	US-11-198-847-281
25	30	14.5	35	6	US-10-467-657-5682

26	30	14.5	35	6	US-10-467-657-7098	Sequence 7098, Ap
27	30	14.5	35	6	US-10-467-657-8030	Sequence 8030, Ap
28	30	14.5	35	6	US-10-957-351-20	Sequence 10, Appl
29	30	14.5	40	6	US-10-979-871-10	Sequence 12, Appl
30	30	14.5	40	6	US-10-979-871-12	Sequence 393, App
31	30	14.5	47	7	US-11-123-896-393	Sequence 43, Appl
32	30	14.5	31	7	US-11-043-590-43	Sequence 6618, Ap
33	29.5	14.3	36	6	US-10-467-657-6618	Sequence 628, App
34	29.5	14.3	10	6	US-10-859-843-628	Sequence 628, App
35	29	14.0	10	7	US-11-097-864-628	Sequence 628, App
36	29	14.0	10	7	US-11-097-912-628	Sequence 2377, Ap
37	29	14.0	11	7	US-11-045-024-2377	Sequence 4816, Ap
38	29	14.0	11	7	US-11-045-024-4816	Sequence 86, Appl
39	29	14.0	11	6	US-10-939-890-86	Sequence 13207, A
40	29	14.0	15	7	US-11-045-024-13207	Sequence 3, Appli
41	29	14.0	20	7	US-11-133-465A-6	Sequence 3, Appli
42	29	14.0	26	7	US-11-114-813-3	Sequence 3, Appli
43	29	14.0	26	7	US-11-115-003-3	Sequence 299, App
44	29	14.0	27	7	US-11-110-274-299	Sequence 12, Appl
45	29	14.0	34	7	US-11-121-301-12	Sequence 14, Appl
46	29	14.0	34	7	US-11-121-301-14	Sequence 89, Appl
47	29	14.0	38	6	US-10-957-351-89	Sequence 66, Appl
48	29	14.0	39	6	US-10-632-150-66	Sequence 3, Appli
49	29	14.0	39	7	US-11-027-111-3	
50	29	14.0	39	7	US-11-027-111-3	

ALIGNMENTS

RESULT 1

US-10-957-887B-193
; Sequence 193, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre

; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-957-887B-193

Query Match 18.1%; Score 37.5; DB 6; Length 44;
Best Local Similarity 44.1%; Pred. No. 27;
Matches 15; Conservative 3; Mismatches 11; Indels 5; Gaps 3;

Qy 1 KDBPQRETLKAIHYALN-CCGLAG--GVRFQFISD 31
||| : ||| ||| ||| : ||| |||
Db 1 KDIQEGDTLNAI--ALQYCCCTVADIKRVNLLISD 32

RESULT 2

US-10-729-121-52
; Sequence 52, Application US/10729121
; Publication No. US20040144397A1
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark
; TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
; TITLE OF INVENTION: LEVELS IN TOBACCO
; FILE REFERENCE: VTOB.033C1
; CURRENT APPLICATION NUMBER: US/10/729,121

```
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/297,154
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: PCTUS02/18040
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-729-121-52

Query Match      18.1%; Score 37.5; DB 6; Length 44;
Best Local Similarity 36.8%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 13 HYALNCCGLAGGVQFISD 31
   ||| :||| :||| :||| :|||
Db 11 HFLLE-CGLNDNLEEYLCD 28

RESULT 3
US-10-957-887B-243
; Sequence 243, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 243
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-957-887B-243

Query Match      17.6%; Score 36.5; DB 6; Length 45;
Best Local Similarity 41.2%; Pred. No. 40;
Matches 14; Conservative 4; Mismatches 11; Indels 5; Gaps 3;

QY 1 KDEPQRETLKAIHYALN-CCGLAG--GVQFISD 31
   ||| :||| :||| :||| :|||
Db 2 KDIQEGDTLNAV--ALQVCCTVADIKRVNLIISD 33

RESULT 4
US-11-123-896-372
; Sequence 372, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06

; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Vernonia mespilifolia
US-11-123-896-372

Query Match      17.4%; Score 36; DB 7; Length 47;
Best Local Similarity 35.5%; Pred. No. 50;
Matches 11; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

QY 3 EPORETLKAIHYALNCCGLAGGVQFISDIC 33
   ||| :||| :||| :||| :|||
Db 4 ESQSHGFKGRCMNNNCGLVCRNEGPAAGIC 34

RESULT 5
US-10-467-657-3382
; Sequence 3382, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3382
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3382

Query Match      17.1%; Score 35.5; DB 6; Length 30;
Best Local Similarity 39.1%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 4; Indels 9; Gaps 1;

QY 12 IHYALNCCGLAGGVQFISDIP 34
   ||| :||| :||| :||| :|||
Db 3 IHYSLN-----NFIQDFIP 16

RESULT 6
US-11-145-035-45
; Sequence 45, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 31
; TYPE: PRT
```


; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-145-035-45

Query Match 16.9%; Score 35; DB 7; Length 31;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;

QY 1 KDEPQRETLK 10
||||| :
Db 1 KDEPQRSAR 10

RESULT 7

US-11-038-501-4
; Sequence 4, Application US/11038501
; Publication No. US2005024419A1

; GENERAL INFORMATION:

; APPLICANT: Tosi, Pierre-Francois

; APPLICANT: Madoulet, Claudine

; APPLICANT: Nicolau, Claude Yves

; APPLICANT: Hickman, David T.

; TITLE OF INVENTION: THERAPEUTIC VACCINE TARGETED AGAINST P-GLYCOPROTEIN 170 FOR INHIBITION OF MULTIDRUG RESISTANCE IN THE TREATMENT OF CANCERS

; FILE REFERENCE: 3024-104B

; CURRENT FILING DATE: 2005-01-21

; PRIOR FILING DATE: 2003-07-25

; PRIOR APPLICATION NUMBER: PCT/EP2004/008330

; PRIOR FILING DATE: 2004-07-25

; PRIOR APPLICATION NUMBER: US 10/038,501

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 4

; LENGTH: 47

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-038-501-4

Query Match

Best Local Similarity 16.4%; Score 34; DB 7; Length 47;
Best Local Similarity 35.3%; Pred. No. 99;
Matches 6; Conservative 5; Mismatches 0; Gaps 0;

QY 22 AGGVEQFISDICKPKOV 38
||:|:|:|:|:
Db 10 AGNLEDLMSNITRSDI 26

RESULT 8

US-11-059-633-7

; Sequence 7, Application US/11059633

; Publication No. US20050255561A1

; GENERAL INFORMATION:

; APPLICANT: University of Reims

; APPLICANT: AC Immune S.A.

; TITLE OF INVENTION: THERAPEUTIC VACCINE TARGETED AGAINST P-GLYCOPROTEIN 170 FOR INHIBITION OF MULTIDRUG RESISTANCE IN THE TREATMENT OF CANCERS

; FILE REFERENCE: 3024-104A

; CURRENT FILING DATE: 2005-02-16

; PRIOR FILING DATE: 2003-07-25

; PRIOR APPLICATION NUMBER: PCT/EP2004/008330

; PRIOR FILING DATE: 2004-07-25

; PRIOR APPLICATION NUMBER: 10/902,276

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 7

; LENGTH: 47

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-633-7

Query Match 16.4%; Score 34; DB 7; Length 47;
Best Local Similarity 35.3%; Pred. No. 99;
Matches 6; Conservative 5; Mismatches 0; Gaps 0;

QY 22 AGGVEQFISDICKPKOV 38
||:|:|:|:|:
Db 10 AGNLEDLMSNITRSDI 26

RESULT 9

US-11-106-415-285

; Sequence 285, Application US/11106415

; Publication No. US20050287153A1

; GENERAL INFORMATION:

; APPLICANT: MARK S. DENNIS

; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting

; FILE REFERENCE: P1774R1P2

; CURRENT APPLICATION NUMBER: US/11/106,415

; CURRENT FILING DATE: 2005-04-13

; PRIOR APPLICATION NUMBER: US 10/186,229

; PRIOR FILING DATE: 2002-06-28

; NUMBER OF SEQ ID NOS: 425

; SEQ ID NO 285

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

US-11-106-415-285

Query Match

Best Local Similarity 15.7%; Score 32.5; DB 7; Length 20;
Best Local Similarity 63.6%; Pred. No. 64;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 26 EQFISDICKPK 35
||:|:|:|:|:
Db 1 EQWLHDLCLPK 11

RESULT 10

US-11-068-783-111

; Sequence 111, Application US/11068783

; Publication No. US20050260715A1

; GENERAL INFORMATION:

; APPLICANT: Burian, Jan

; APPLICANT: Bartfeld, Daniel

; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS

; FILE REFERENCE: 660081.411

; CURRENT APPLICATION NUMBER: US/11/068,783

; CURRENT FILING DATE: 2005-02-28

; PRIOR APPLICATION NUMBER: US/09/444,281

; PRIOR FILING DATE: 1999-11-19

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 111

; LENGTH: 46

; TYPE: PRT

; ORGANISM: Hordeum vulgare

US-11-068-783-111

Query Match 15.5%; Score 32; DB 7; Length 46;
Best Local Similarity 32.1%; Pred. No. 1.9e+02;
Matches 9; Conservative 3; Mismatches 14; Indels 2; Gaps 1;

QY 6 RETLKAIHYALNCCGLAGVEQFISDICK 33
:|:|:|:|:|:|:
Db 5 KDTLARNY--NTRCPAGGSRPVCAGAC 30

```
RESULT 11
US-11-045-024-13448
; Sequence 13448, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: Virus-1 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13448
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13448
Query Match 15.0%; Score 31; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 78;
Matches 5; Conservative 4; Mismatches 4; Indels 4; Gaps 0;

QY 26 EQFISDICKQDV 38
:|:|:|:|:|
Db 2 DQILIEGKKAI 14

RESULT 12
US-10-939-890-535
; Sequence 535, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
```

```
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 535
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-535
Query Match 15.0%; Score 31; DB 6; Length 21;
Best Local Similarity 41.7%; Pred. No. 11e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 15 ALNCCGLAGGVE 26
:|:|:|:|:|
Db 2 SFNACGFEEGLE 13

RESULT 13
US-11-198-847-180
; Sequence 180, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 180
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Conus parius
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(24)
; OTHER INFORMATION: Xaa at residues 1, 2, 15, 16 and 20 may be Pro or hydroxy-Pro; X
; OTHER INFORMATION: a at residue 24 may be Glu or Gla
US-11-198-847-180
Query Match 15.0%; Score 31; DB 7; Length 24;
```

```
; NAME/KEY: MOD RES
; LOCATION: (5)---(5)
; OTHER INFORMATION: Ava
US-11-033-039-631

Query Match      15.0%; Score 31; DB 7; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ETLKAIHYALNCCG 20
Db 11 ETLLEINGSVTCFG 24

RESULT 16
US-10-957-351-184
; Sequence 184, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 184
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-184

Query Match      15.0%; Score 31; DB 6; Length 36;
Best Local Similarity 39.1%; Pred. No. 2.1e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 6; Gaps 2;

Qy 19 CGLAGGV---EQFISDI--CPK 35
Db 7 CGVAPGLCLTPEQLCDGIPDCPQ 29

RESULT 17
US-10-939-890-537
; Sequence 537, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjeppan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
```

```
; NAME/KEY: MOD RES
; LOCATION: (5)---(5)
; OTHER INFORMATION: Ava
US-11-033-039-631

Query Match      15.0%; Score 31; DB 7; Length 24;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 17 MCCGLAGG 24
Db 4 SCAGLRGG 11

RESULT 14
US-11-198-847-282
; Sequence 282, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 282
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Conus parius
; OTHER INFORMATION:
US-11-198-847-282

Query Match      15.0%; Score 31; DB 7; Length 24;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 17 MCCGLAGG 24
Db 4 SCAGLRGG 11

RESULT 15
US-11-033-039-631
; Sequence 631, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 631
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
```

```
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 537
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
;
US-10-939-890-537

Query Match      14.7%   Score 30.5; DB 6; Length 21;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY      16  LNCCLAGGVEQFISDIC 33
      :|||  |||  :|
Db       4  MNC-----GAEQGLSIC 16
      :|||  |||  :|

RESULT 18
US-10-467-657-2116
; Sequence 2116, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2116
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
;
US-10-467-657-2116

Query Match      14.7%   Score 30.5; DB 6; Length 49;
Best Local Similarity 47.1%; Pred. No. 3.5e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY      3  EPORETIKATH-YALNC 18
      :|||  |||  |||
Db       26  QARRNFLKSITKTVANN 42
      :|||  |||  |||

RESULT 19
US-11-045-024-13229
; Sequence 13229, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Greenwood, Scott
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
```

```
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13229
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
;
US-11-045-024-13229

Query Match      14.5%   Score 30; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      26  EGFISDICPKK 36
      :|||  :|||  |||
Db       5  DQILIEICGK 15
      :|||  :|||  |||

RESULT 20
US-11-045-024-13251
; Sequence 13251, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
```

; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13251
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13251

Query Match 14.5%; Score 30; DB 7; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LKAIHYALNCCG 20
|:|:|:|:|
Db 4 LQAIHLALQDSG 15

RESULT 21
US-11-106-415-284
; Sequence 284, Application US/11106415
; Publication No. US20050287153A1
; GENERAL INFORMATION:
; APPLICANT: MARK S. DENNIS
; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
; FILE REFERENCE: P1774R1P2
; CURRENT APPLICATION NUMBER: US/11/106,415
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: US 10/186,229
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SEQ ID NO 284
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-415-284

Query Match 14.5%; Score 30; DB 7; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 26 EQFISDIC 33
|:|:|:|
Db 1 EGFLGDIC 8

RESULT 22
US-11-198-847-323
; Sequence 323, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James B.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053

; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 323
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(21)
; OTHER INFORMATION: Xaa may be Trp (D or L)
US-11-198-847-323

Query Match 14.5%; Score 30; DB 7; Length 21;
Best Local Similarity 38.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 22 AGGVEQFISDICP 34
|:|:|:|:|
Db 2 SNGVEICMKKVC 14

RESULT 23
US-11-198-847-177
; Sequence 177, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James B.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 177
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Conus parius
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(25)
; OTHER INFORMATION: Xaa at residues 1, 3, 15, 16 and 20 may be Pro or hydroxy-Pro
US-11-198-847-177

Query Match 14.5%; Score 30; DB 7; Length 25;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 17 NCCGLAGG 24
|:|:|:|:|
Db 4 SCSGLRGG 11

RESULT 24
US-11-198-847-281
; Sequence 281, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.

```
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Conus parius
; US-11-198-847-281

Query Match      14.5%; Score 30; DB 7; Length 25;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 17 NCCGLAGG 24
   :|||:
Db 4 SCGSLRG 11

RESULT 25
US-10-467-657-5682
; Sequence 5682, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5682
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-5682

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 33.3%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 5 QRETLKAHVAlNCCGLA 22
   :|||:
Db 5 RREVRKALSDMVSCKIA 22

RESULT 26
US-10-467-657-7098
; Sequence 7098, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8030
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-8030

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 18 CCGLAGGVQFISD 31
   :|||:
Db 14 CRSLDGDFDAGVSD 27

RESULT 27
US-10-467-657-8030
; Sequence 8030, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8030
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-8030

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 18 CCGLAGGVQFISD 31
   :|||:
Db 14 CRSLDGDFDAGVSD 27

RESULT 28
US-10-957-351-20
; Sequence 20, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: C-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-00140005
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-20

Query Match      14.5%; Score 30; DB 6; Length 35;
Best Local Similarity 46.2%; Pred. No. 2.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      8 TLKAIHYALNCCG 20
Db      10 TGKCLNYSLVCDG 22

RESULT 29
US-10-979-871-10
; Sequence 10, Application US/10979871
; Publication No. US20050267071A1
; GENERAL INFORMATION:
; APPLICANT: Freire, Ernesto
; APPLICANT: Bacha, Usman
; APPLICANT: Barrila, Jennifer
; APPLICANT: Leavitt, Stephanie A.
; APPLICANT: Vellazquez-Campoy, Adrian
; APPLICANT: Xiao, Yingxin
; APPLICANT: Ottenbrite, Raphael
; TITLE OF INVENTION: INHIBITORS OF CORONAVIRUS PROTEASE AND METHODS OF USE THEREOF
; FILE REFERENCE: 03173/1200093-US1
; CURRENT APPLICATION NUMBER: US/10/979,871
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,008
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: BCV Quebec
US-10-979-871-10

Query Match      14.5%; Score 30; DB 6; Length 40;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      19 CGLAGGVEQFISDICK 35
Db      23 CGSCGSGVYVIMGDCVK 39

RESULT 30
US-10-979-871-12
; Sequence 12, Application US/10979871
; Publication No. US20050267071A1
; GENERAL INFORMATION:
; APPLICANT: Freire, Ernesto
; APPLICANT: Bacha, Usman
; APPLICANT: Barrila, Jennifer
; APPLICANT: Leavitt, Stephanie A.
; APPLICANT: Vellazquez-Campoy, Adrian
; APPLICANT: Xiao, Yingxin
; APPLICANT: Ottenbrite, Raphael
; TITLE OF INVENTION: INHIBITORS OF CORONAVIRUS PROTEASE AND METHODS OF USE THEREOF
; FILE REFERENCE: 03173/1200093-US1
; CURRENT APPLICATION NUMBER: US/10/979,871
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,008
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: BCV Mebus
US-10-979-871-12

Query Match      14.5%; Score 30; DB 6; Length 40;
Best Local Similarity 41.2%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      19 CGLAGGVEQFISDICK 35
Db      23 CGSCGSGVYVIMGDCVK 39

RESULT 31
US-11-123-896-390
; Sequence 390, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Licania michauxii
US-11-123-896-390

Query Match      14.5%; Score 30; DB 7; Length 47;
Best Local Similarity 29.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy      3 EPORETAKAIHYALNCCGLAGGVEQFISDICK 33
Db      4 ESQSHGFGKMCVRDHNCAWVCRVEGFGGIC 34

RESULT 32
US-11-123-896-393
; Sequence 393, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
```

```
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Chrysobalanus icaco
US-11-123-896-393

Query Match      14.5%; Score 30; DB 7; Length 47;
Best Local Similarity 29.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 3 EPQRETLKAIHYALNCCGLAGGYEQFISDTC 33
   ||| | | | | | | | | | | | | | | |
Db 4 ESQSHGFKGCMRDHNCAMVCRVEGFGGIC 34

RESULT 33
US-11-043-590-43
; Sequence 43, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 43
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-043-590-43

Query Match      14.3%; Score 29.5; DB 7; Length 31;
Best Local Similarity 30.0%; Pred. No. 3e+02;
Matches 6; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 20 GLAGVE---QFISDTCPKK 36
   | : | | : : : | | | :
Db 5 GSSGGLDSSNERNVLTCCPKR 24

RESULT 34
US-10-467-657-6618
; Sequence 6618, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6618
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6618

Query Match      14.3%; Score 29.5; DB 6; Length 36;

; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Chrysobalanus icaco
US-11-123-896-393

Query Match      14.5%; Score 30; DB 7; Length 47;
Best Local Similarity 29.0%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 3 EPQRETLKAIHYALNCCGLAGGYEQFISDTC 33
   ||| | | | | | | | | | | | | | | |
Db 4 ESQSHGFKGCMRDHNCAMVCRVEGFGGIC 34

RESULT 33
US-11-043-590-43
; Sequence 43, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 43
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-043-590-43

Query Match      14.3%; Score 29.5; DB 7; Length 31;
Best Local Similarity 30.0%; Pred. No. 3e+02;
Matches 6; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 20 GLAGVE---QFISDTCPKK 36
   | : | | : : : | | | :
Db 5 GSSGGLDSSNERNVLTCCPKR 24

RESULT 34
US-10-467-657-6618
; Sequence 6618, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6618
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6618

Query Match      14.3%; Score 29.5; DB 6; Length 36;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 7; Gaps 1;

QY 24 GVEQFISD-----ICPKK 36
   | : | | | | | | | | | |
Db 9 GCKDFIEDVGHVVFRICPKK 28

RESULT 35
US-10-859-643-628
; Sequence 628, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-628

Query Match      14.0%; Score 29; DB 6; Length 10;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 KAIHYALN 17
   | : | | |
Db 3 KRLHYAKN 10

RESULT 36
US-11-097-864-628
; Sequence 628, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-628

Query Match      14.0%; Score 29; DB 7; Length 10;
```



```
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KAIHYALN 17
Db 3 KRLHYAKN 10

RESULT 37
US-11-097-912-628
; Sequence 628, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158206204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-628

Query Match 14.0%; Score 29; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KAIHYALN 17
Db 3 KRLHYAKN 10

RESULT 38
US-11-045-024-2377
; Sequence 2377, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4816
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4816

Query Match 14.0%; Score 29; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2377
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2377

Query Match 14.0%; Score 29; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 11 AIHYALNCCGL 21
Db 1 AIHLAQDSGL 11

RESULT 39
US-11-045-024-4816
; Sequence 4816, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4816
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4816

Query Match 14.0%; Score 29; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

QY 11 AIHYALNCCGL 21
Db 1 AIHLALQDSGL 11

RESULT 40

US-10-939-890-86
; Sequence 86, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ledner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617, 70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-86

Query Match 14.0%; Score 29; DB 6; Length 14;
Best Local Similarity 57.1%; Pred.No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IHYALNC 18
Db 5 MHYGLGC 11

Search completed: January 20, 2006, 17:38:43
Job time : 7.5679 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:23:49 ; Search time 14.0741 Seconds
(without alignments)
259.785 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCLAGGVEQFISDICPKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	19.3	33	2 I46600	myosin - pig (frag
2	39.5	19.1	48	2 AD2809	hypothetical prote
3	39	18.8	38	2 S33484	hypothetical prote
4	38	18.4	12	2 PH1481	T-cell receptor be
5	38	18.4	47	1 A24074	pyruvate thionin
6	38	18.4	50	2 A82772	hypothetical prote
7	37.5	18.1	48	2 S29216	neurotoxin Tx2 - s
8	36.5	17.6	33	2 T22565	R-phycoerythrin ga
9	36	17.4	33	1 S66586	hypothetical prote
10	35.5	17.1	33	2 A05136	neurotoxin IX - sc
11	35.5	17.1	48	2 T16032	hypothetical prote
12	35	16.9	20	2 I46940	6-phosphofructo-2-
13	34	16.4	34	2 JQ1620	hypothetical 4.3K
14	33.5	16.2	33	2 C82390	hypothetical prote
15	33.5	16.2	44	2 B85569	hypothetical prote
16	33	15.9	16	4 I79565	hypothetical TGL3/
17	33	15.9	40	2 T64014	hypothetical prote
18	33	15.9	41	2 T18202	hypothetical prote
19	33	15.9	46	2 B81717	hypothetical prote
20	32.5	15.7	37	2 A59487	parabutoxin 2 - Pa
21	32.5	15.7	48	2 JY0019	hypothetical prote
22	32	15.4	41	2 B24910	probable tyrosine
23	32	15.5	42	2 T01991	hypothetical prote
24	32	15.5	42	2 T07324	hypothetical prote
25	32	15.5	48	2 I50819	MHC class I protei
26	32	15.5	48	2 AC1046	entericidin B prec
27	32	15.5	48	2 H86110	hypothetical prote
28	31.5	15.2	36	2 A59486	parabutoxin 10 - p
29	31.5	15.2	46	2 H71262	hypothetical prote

30	31.5	15.2	47	2 C26534	hypothetical prote
31	31.5	15.2	49	2 T37008	hypothetical prote
32	31.5	15.2	50	2 B60718	phospholipase A2 h
33	31	15.0	34	2 S77646	hypothetical prote
34	31	15.0	35	2 JX0200	gummarin - Gymnema
35	31	15.0	36	2 PH1751	Ig heavy chain v r
36	31	15.0	36	2 S04184	fixC protein - Bra
37	31	15.0	37	2 A49591	spike protein - po
38	31	15.0	37	2 PS0131	H-2 class I histoc
39	31	15.0	39	2 C37264	E2 glycoprotein -
40	31	15.0	45	2 S77773	probable thymidine
41	31	15.0	46	2 B45174	eye cell developme
42	31	15.0	48	2 D82817	hypothetical prote
43	31	15.0	50	2 T08019	hypothetical prote
44	30.5	14.7	30	2 B81346	hypothetical prote
45	30.5	14.7	37	2 C60580	growth hormone-rel
46	30.5	14.7	44	2 T21578	hypothetical prote
47	30.5	14.7	47	2 B58319	gamma-zeathionin 2
48	30	14.5	30	2 G71359	hypothetical prote
49	30	14.5	33	2 I46601	myosin - pig (frag
50	30	14.5	36	2 S70092	hypothetical prote

ALIGNMENTS

RESULT 1

I46600

myosin - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I46600

R/Bement, W.M.; Haason, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.

Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994

A/Title: Identification and overlapping expression of multiple unconventional myosin ge

A/Reference number: A55758; MUID:94294418; PMID:8022818

A/Accession: I46600

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-33 <BEM>

A/Cross-references: UNIPROT:Q29066; UNIPARC:UPI0000087769; GB:L29135; NID:9457345; PIDN

C/Superfamily: myosin heavy chain 95F; myosin motor domain homology

Query Match 19.3%; Score 40; DB 2; Length 33;
Best Local Similarity 55.0%; Pred.No. 1.1e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 12 IHV--ALNCCGLAGGVEQFI 29

Db 7 IHULTALSQKGPASGVQII 26

RESULT 2

AD2809

hypothetical protein Atul1894 [imported] - Agrobacterium tumefaciens (strain C58, Dupont

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AD2809

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McGle1

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AD2809

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-48 <KUR>

A/Cross-references: UNIPROT:Q8UB67; UNIPARC:UPI00000D1CF5; GB:AE008688; PIDN:AAL42890.1

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A;Gene: Atul894

A;Map position: circular chromosome

Query Match 19.1%; Score 39.5; DB 2; Length 48;

Best Local Similarity 45.0%; Pred. No. 1.9e+02;

Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 18 CCGLAGGVEQFIS---DICP 34

Db 12 CCGCGGQGVQFPTGGIGICP 31

RESULT 3

S33484

hypothetical protein 38 - Xanthomonas campestris phage phi-Lf

C;Species: Xanthomonas campestris phage phi-Lf

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S33484

R;Wen, F.S.; Tseng, Y.H.

submitted to the EMBL Data Library, February 1993

A;Description: Single e-stranded DNA binding protein and major coat protein of filamentous

A;Reference number: S33482

A;Accession: S33484

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-38 <WEN>

A;Cross-references: UNIPROT:Q07484; UNIPARC:UPI0000127C91; EMBL:X70331; NID:g311543; PID

Query Match 18.8%; Score 39; DB 2; Length 38;

Best Local Similarity 28.9%; Pred. No. 1.8e+02;

Matches 11; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 4 PORETLKAHYALNCCG-----LAGGVEQFISD 31

Db 2 PSQE--DAVAMSTGCCGLVIVFWVLGRLAGSVAGMFND 37

RESULT 4

PH1481

T-cell receptor beta chain (clone A24/PEG2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1481

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1481

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Cross-references: UNIPARC:UPI000017C79D

A;Experimental source: cytolytic T-lymphocyte

A;Note: the authors translated the codon GGT for residue 2 as Ala and GCT for residue 3

C;Keywords: receptor; T-cell

Query Match 18.4%; Score 38; DB 2; Length 12;

Best Local Similarity 70.0%; Pred. No. 81;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 19 CGLAGGVEQF 28

Db 1 CGAEGAEQF 10

RESULT 5

A24074

pyricularia thionin - oil nut

C;Species: Pyricularia pubera (oil nut, buffalo nut)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004

C;Accession: A24074

R;Vernon, L.P.; Evtett, G.E.; Zeikus, R.D.; Gray, W.R.

Arch. Biochem. Biophys. 238, 18-29, 1985

A;Title: A toxic thionin from Pyricularia pubera: purification, properties, and amino acid

A;Reference number: A24074; MUID:85173323; PMID:3985614

A;Accession: A24074

A;Molecule type: protein

A;Residues: 1-47 <VER>

A;Cross-references: UNIPROT:P07504; UNIPARC:UPI0000136EC3

C;Superfamily: hordothionin precursor

Query Match 18.4%; Score 38; DB 1; Length 47;

Best Local Similarity 38.5%; Pred. No. 2.9e+02;

Matches 10; Conservative 4; Mismatches 6; Indels 6; Gaps 2;

QY 14 YALNC---CGLAGGVEQFISDICPKK 36

Db 8 WARNCYNVCRLPGTISR---EICAKK 30

RESULT 6

A82772

hypothetical protein XF0722 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: A82772

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: A82772

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-50 <SIM>

A;Cross-references: UNIPROT:Q9PFE8; UNIPARC:UPI00000C24E3; GB:AE003849; NI

R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir,

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve

M.; Tshuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0722

Query Match 18.4%; Score 38; DB 2; Length 50;

Best Local Similarity 29.6%; Pred. No. 3.1e+02;

Matches 8; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 7 ETILKAHYALNCCGLAGGVEQFISDIC 33

Db 22 CQGLGGTHRAVSCGFSIAFLLSVTDIC 48

RESULT 7

S29216

neurotoxin Tx2 - spider (Phoneutria nigriventer)

C;Species: Phoneutria nigriventer

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S29216

R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Bickstedt,

FEBB Lett. 310, 153-156, 1992

A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the ven

A;Reference number: S29214; MUID:93011905; PMID:1397265

A;Accession: S29216

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-48 <COR>

A;Cross-references: UNIPROT:P29425; UNIPARC:UPI00001766CE
C;Superfamily: curtatoxin

Query Match	18.1%	Score 37.5;	DB 2;	Length 48;
Best Local Similarity	34.8%	Pred. NO. 3.5e+02;		
Matches 8;	Conservative 4;	Mismatches 4;	Indels 7;	Gaps 1;

Qy 1 KDEPQRETLKAIHYALNCCGLAG 23
 :|:|:|:
Dd 6 QDQPCKET-----CDCCGERG 21

RESULT 8

I22565
R-phycoerythrin gamma-D chain - red alga (Gastrocloonium coulteri) (fragment)
C;Species: Gastrocloonium coulteri
C;date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
C;Accession: I22565
J;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: I22565
A;Molecule type: protein
A;Residues: 1-33 <KLO>

A; Cross-references: UNIPROT:Q7M269; UNIPARC:UPI00001792E6
C; Superfamily: Aglaothamnion neglectum R-phycoerythrin gene

Query Match 17.6%; Score 36.5; DB 2; Length 33;
Best Local Similarity 38.5%; Pred. No. 3.4e+02;
Matches 10; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Qy 2 DEPQRETLKAIHYALNCCGLAGVEQ 27
| | : | | : | | :
Dd 9 DFPVAPSL-AGHYSLTNCGPQSGASK 33

RESULT 9

S66586
hypothetical protein 33 - Escherichia coli cryptic lambdaoid prophage DLP12
C:Species: Escherichia coli
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: S66586
R:Mahdi, A.A.; Sharples, G.J.; Mandal, T.N.; Lloyd, R.G.
J. Mol. Biol. 257, 561-573, 1996
A:Title: Holliday junction resolvases encoded by homologous *rusA* genes in *Escherichia coli*
A:Reference number: S66579; MUID:96196428; PMID:8648624
A:Accession: S66586
A:Molecule type: DNA
A:Residues: 1-33 <MAH>
A:Cross-references: UNIPROT:Q47268; UNIPARC:UPI000013B802; EMBL:X92587; NID:gl051136; PT
C:Genetics:
A:Map position: 12 min
A:Genome: prophage
C:Superfamily: phage 82 hypothetical protein 33

```
Query Match      17.4%; Score 36; DB 1; Length 33;
Best Local Similarity 37.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

QY 5 QRETLKAHYALNCCG 20
 | : | : | : | :
Db 15 QKCTCNSLHLAFDLCG 30

RESULT 10

A05136
neurotoxin IX - scorpion (Buthus occitanus) (fragment)
C-Species: Buthus occitanus tunetanus
C-Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C-Accession: A05136
R: Martin, M.F.; Rochat, H.
Toxicon 22, 279-291, 1984

A:Title: Purification of thirteen toxins active on mice from the venom of the North African scorpion *Androctonus crassipalpis* (Hymenoptera: Scorpiones)
A:Reference: number: A94316; MUID:84224814; PMID:6779843
A:Accession: A05136
A:Molecule type: protein
A:Residues: 1-33 <MAP>
A:Cross-references: UNIPROT:P04099; UNIPARC:UPI000001356F3
C:Superfamily: scorpion neurotoxin
C:Keywords: neurotoxin

Query Match	17.1%	Score 35.5;	DB 2;	Length 33;
Best Local Similarity	36.0%;	Pred. No. 4.6e+02;		
Matches	9;	Conservative	4;	Mismatches 5;
				Indels 7;
				Gaps 2;

Qy	12	IHYALNC---	CGLAGV	EQFISD	IC	33
Db	10	IVYPNNCVYH	CGL----	DPYCND	LC	30

RESULT 11

T16032
hypothetical protein F11D5.6 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16032
R:Nhan, M.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid F11D5.
A/Reference number: Z18449

A/Accession: T16032
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-48
A/Cross-references: UNIPROT:Q9GVP8; UNIPARC:UPI000007E1
C/Genetics:
A/Gene: CESP:F11D5.6
A/Introns: 30/1

Query Match 17.1%; Score 35.5; DB 2; Length 48;
Best Local Similarity 47.1%; Pred. No. 6.6e+02;
Matches 8; Conservative 2; Mismatches 6; Indels

Qy	3	EPQRET	KA	IHYAL	NCC	19
			:			
Db	7	ENQKET	-AYI	HFIY	CC	22

RESULT 12

6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.16)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: I46940
 R:Sakata, J.; Uyeda, K.
 Biochem. Biophys. Res. Commun. 180, 470-474, 1991
 A:Title: Characterization of two isozymic forms of heart fructose 6-phosphate, 2-kinase
 A:Reference number: I46940; MUID:92062062; PMID:1659398
 A:Accession: I46940
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-20 <SAK>

A; Keywords: 1-20 <SAK>
A; Cross-references: UNIPROT:Q28830; UNIPARC:UPI00000876C7; GB:
C; Superfamily: 6-phosphofructo-2-kinase / fructose-2,6-bisphos-
C; Keywords: phosphoric monoester hydrolase; phosphotransferase

Query Match	16.9%	Score 35;	DB 2;	Length 20;
Best Local Similarity	46.2%	Pred. No.	3.4e+02;	
Matches 6;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	KDEPQRETLKAIH	13
		: : :	
Db	6	RDKPTAETSRAAH	18

RESULT 18

Tl8202

hypothetical protein - Bacillus sp. (fragment)

C/Species: Bacillus sp.

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: Tl8202

R;van Waasbergen, L.G.; Hildebrand, M.; Tebo, B.M.

J. Bacteriol. 178, 3517-3530, 1996

A/Title: Identification and characterization of a gene cluster involved in manganese oxidation

A/Reference number: Z18825; MUID:96256605; PMID:8655549

A/Accession: Tl8202

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-41 <V>

A/Cross-references: UNIPROT:P70956; UNIPARC:UPI00000B345A; EMBL:U31081; NID:G942616; NID:G942616

Query Match 15.9%; Score 33; DB 2; Length 41;

Best Local Similarity 35.7%; Pred. No. 1.2e+03;

Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PORETLKAHYALN 17

| | | | |

| | | | |

Db 9 PHRTISGIYWTYN 22

RESULT 19

B81717

hypothetical protein TC0307 [imported] - Chlamydia muridarum (strain Nigg)

C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: B81717

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.; et al. Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A/Reference number: A81500; MUID:20150255; PMID:10684935

A/Accession: B81717

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-46 <T>

A/Cross-references: UNIPROT:Q9P0L1; UNIPARC:UPI0000057893; GB:AE002298; GB:AE002160; NID:G942616

A/Experimental source: strain Nigg (MoPn)

C/Genetics:

A/Gene: TC0307

Query Match 15.9%; Score 33; DB 2; Length 46;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ALNCCGLA 22

| | | | |

| | | | |

Db 37 ALNCSGVA 44

RESULT 20

A59487

parabutoxin 2 - Parabuthus villosus

C/Species: Parabuthus villosus

C/Date: 02-Jun-2003 #sequence_revision 02-Jun-2003 #text_change 02-Jun-2003

C/Accession: A59487

R;Tytgat, J.

submitted to the Protein Sequence Database, April 2003

A/Description: Acidic short chain K+ channel toxins from Parabuthus venom.

A/Reference number: A59487

A/Accession: A59487

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-37 <Y>

A/Note: potassium channel toxin

F;8-27/Disulfide bonds: #status predicted

F;13-33/Disulfide bonds: #status predicted

F;17-35/Disulfide bonds: #status predicted


```
Query Match      15.0%; Score 31; DB 2; Length 34;
Best Local Similarity 30.4%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 10 KAIHYALNCCGLAGGVQFISDI 32
Db 8 KSNINIRICGLDSPPTQFLKRI 30

RESULT 34
JX0200
gummarin - Gymnema sylvestre
N;Alternate names: sweet-taste-suppressing peptide
C;Species: Gymnema sylvestre
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: JX0200
R;Kamei, K.; Takano, R.; Miyasaka, A.; Imoto, T.; Hara, S.
J. Biochem. 111, 109-112, 1992
A;Title: Amino acid sequence of sweet-taste-suppressing peptide (gummarin) from the leav
A;Reference number: JX0200; MUID:92299642; PMID:1607357
A;Accession: JX0200
A;Molecule type: protein
A;Residues: 1-35 <KAM>
A;Cross-references: UNIPROT:P25810; UNIPARC:UPI000012BE09
A;Experimental source: leaf
C;Comment: This protein suppresses sweet taste.
C;Keywords: pyroglutamic acid; sweet taste
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      15.0%; Score 31; DB 2; Length 35;
Best Local Similarity 42.1%; Pred. No. 2e+03;
Matches 8; Conservative 1; Mismatches 4; Indels 6; Gaps 1;

QY 1 KDEPQRETLKAIHYALNCC 19
Db 6 KDE-----LCIPYLDCC 18

RESULT 35
PH1751
IG heavy chain V region (clone NP-12-17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1751
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1751
A;Molecule type: mRNA
A;Residues: 1-36 <MCH>
A;Cross-references: UNIPARC:UPI0000176A99
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match      15.0%; Score 31; DB 2; Length 36;
Best Local Similarity 26.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCC 19
Db 14 KSKPSMQSTERYHYGSSC 32

RESULT 36
S04184
fixC protein - Bradyrhizobium japonicum (fragment)
C;Species: Bradyrhizobium japonicum
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04184
R;Gubler, M.; Zuercher, T.; Hennecke, H.
```

```
Mol. Microbiol. 3, 141-148, 1989
A;Title: The Bradyrhizobium japonicum fixBCX operon: identification of fixX and of a 5'
A;Reference number: S04182; MUID:89343618; PMID:2503674
A;Accession: S04184
A;Molecule type: DNA
A;Residues: 1-36 <GUB>
A;Cross-references: UNIPROT:P10331; UNIPARC:UPI000016BE6FC; EMBL:X13144; NID:g39519; PID:
C;Genetics:
A;Gene: fixC
C;Superfamily: fixC protein

Query Match      15.0%; Score 31; DB 2; Length 36;
Best Local Similarity 28.6%; Pred. No. 2.1e+03;
Matches 8; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVQF 28
Db 4 KVEKEKASLKSPFKTRSWGLVGDAVRP 31

RESULT 37
A49591
spike protein - porcine epidemic diarrhea virus (fragment)
C;Species: porcine epidemic diarrhea virus
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A49591; S37435
R;Duarte, M.; Tobler, K.; Bridgen, A.; Raeschaert, D.; Ackermann, M.; Laude, H.
Virology 198, 466-476, 1994
A;Title: Sequence analysis of the porcine epidemic diarrhea virus genome between the nu
A;Reference number: A49591; MUID:94120721; PMID:8291230
A;Accession: A49591
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-37 <DUA>
A;Cross-references: UNIPROT:Q84707; UNIPARC:UPI00000F555B; EMBL:Z24733; NID:g406754; PI
C;Genetics:
A;Gene: S
C;Superfamily: coronavirus E2 glycoprotein

Query Match      15.0%; Score 31; DB 2; Length 37;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 6; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 18 CCGLAGGVQFISDIC 33
Db 5 CCGCGCGCGAGCFGCC 20

RESULT 38
PS0131
H-2 class I histocompatibility antigen T3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: PS0131
R;Bronson, K.A.; Hunt III, S.W.; Hunkapiller, T.; Sun, Y.H.; Cheroutre, H.; Nickerson,
J. Exp. Med. 170, 1837-1858, 1989
A;Title: Comparison of exon 5 sequences from 35 class I genes of the BALB/c mouse.
A;Reference number: PS0114; MUID:90063453; PMID:2584927
A;Accession: PS0131
A;Molecule type: DNA
A;Residues: 1-37 <BRO>
A;Cross-references: UNIPROT:Q60678; UNIPARC:UPI0000176F4F
A;Experimental source: strain BALB/c
A;Note: this sequence is encoded by exon 5
C;Comment: This protein is a surface glycoprotein noncovalently associated with beta 2-
C;Superfamily: immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein; transplantation antigen
F;1-1/Domain: connecting peptide #status predicted <COP>
F;12-32/Domain: transmembrane #status predicted <TRS>
F;33-37/Domain: intracellular #status predicted <INT>

Query Match      15.0%; Score 31; DB 2; Length 37;
Best Local Similarity 33.3%; Pred. No. 2.1e+03;
```

Matches 7; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 PORETKAIHYALNCCGLAGG 24
| | | | | | | | | |
Db 7 PNRITVRALLGAMITLGFMSG 27

RESULT 39

C37264
E2 glycoprotein - Barmah Forest virus (fragment)
C:Species: Barmah Forest virus
C>Date: 30-Aug-1991 #sequence_revision 30-Jan-1993 #text_change 31-Dec-2004
C:Accession: C37264
R:Bell, J.R.; Kinney, R.M.; Trent, D.W.; Strauss, E.G.; Strauss, J.H.
Proc. Natl. Acad. Sci. U.S.A. 81, 4702-4706, 1984
A:Title: An evolutionary tree relating eight alphaviruses, based on amino-terminal sequences
A:Reference number: A21774; MUID:84272701; PMID:6087344
A:Accession: C37264
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-39 <BEL>
A:Cross-references: UNIPROT:P89946; UNIPARC:UPI000017855E
C:Keywords: glycoprotein

Query Match 15.0%; Score 31; DB 2; Length 39;
Best Local Similarity 43.8%; Pred. No. 2.2e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

Qy 19 CGLAGGVEQFIISDIP 34
| | | | | | | | | |
Db 21 CGLAGS-----CP 28

RESULT 40

S77773
Probable thymidine kinase - Mycoplasma capricolum (fragment)
N:Alternate names: protein MC375
C:Species: Mycoplasma capricolum
C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S77773; S48624
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77773
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-45 <BOR>
A:Cross-references: UNIPROT:Q49069; UNIPARC:UPI000000AF9FF; EMBL:Z33279; NID:9541724; PID:
A:Experimental source: ATCC 27343
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: thymidine kinase
C:Keywords: ATP; phosphotransferase

Query Match 15.0%; Score 31; DB 2; Length 45;
Best Local Similarity 54.5%; Pred. No. 2.5e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 19 CGLAGGVEQFI 29
| | | | | | | | | |
Db 26 CMFAGKTEEFI 36

Search completed: January 20, 2006, 17:34:26
Job time : 16.0741 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:22:44 ; Search time 82.5679 Seconds
(without alignments)
324.703 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207
Sequence: 1 KDPQRETLKAIHYALNCCGLAGVQVFISDIPKRDV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	22.2	36	2	Q5P857_AZOSE
2	45.5	22.0	45	2	Q5WG86_BACSK
3	45	21.7	37	2	Q72VY5_BACCL
4	45	21.7	37	2	Q81KH9_EACAN
5	43.5	21.0	39	2	Q9BF50_CONAE
6	43	20.8	35	2	Q5C273_SCHJA
7	43	20.8	44	2	Q4X8W4_PLACH
8	42	20.3	44	2	Q5BZF7_SCHJA
9	41	19.8	19	2	Q86DB6_HALRO
10	41	19.8	41	2	Q4R921_WACFA
11	41	19.8	46	1	SP12_SEGFL
12	40	19.3	33	2	Q29066_PIG
13	40	19.3	33	2	Q9W7N9_MORGA
14	39.5	19.1	48	2	Q8UB67_AGRTS
15	39	18.8	36	2	Q4YB36_PLABE
16	39	18.8	38	1	COAT3_BPPL
17	39	18.8	38	1	COAT3_XANCP
18	39	18.8	38	2	Q4UUU6_XANCP
19	39	18.8	44	1	YDAG_ECOLI
20	39	18.8	50	2	Q51AA2_ENTHI
21	38.5	18.6	36	2	Q4Z513_PLABE
22	38	18.4	37	2	Q5C5J9_SCHJA
23	38	18.4	37	2	Q4X2T4_PLACH
24	38	18.4	42	2	Q4Y419_PLACH
25	38	18.4	43	2	Q6J506_PIG
26	38	18.4	43	1	LEBCEB_VIPLE
27	38	18.4	47	1	THN_PYRU
28	38	18.4	48	2	Q4RC82_TETNG
29	38	18.4	50	2	Q7N8J8_PHOHL
30	38	18.4	50	2	Q9PFE8_XYLFA
31	37	17.9	30	2	Q86DN6_9CAEN

32	37	17.9	44	2	Q9WMD8_9FLAV	Q9wmd8 gb virus c/
33	37	17.9	49	2	Q5C4E6_SCHJA	Q5c4e6 schistosoma
34	37	17.9	50	2	Q787S5_9FLAV	Q787s5 gb virus c/
35	37	17.9	50	2	Q787T7_9FLAV	Q787t7 gb virus c/
36	37	17.9	50	2	Q787R8_9FLAV	Q787r8 gb virus c/
37	37	17.9	50	2	Q9WA37_9FLAV	Q9wa37 gb virus c/
38	37	17.9	50	2	Q9YIK7_9FLAV	Q9yik7 gb virus c/
39	37	17.9	50	2	Q9Z039_9FLAV	Q9z039 gb virus c/
40	36.5	17.6	33	2	Q7M269_GASCO	Q7m269 gastrocloni
41	36.5	17.6	34	2	Q71798_9HIVI	Q71798 human immun
42	36.5	17.6	35	2	Q9IPX9_9HIVI	Q9ipx9 human immun
43	36.5	17.6	35	2	Q9IPY1_9HIVI	Q9ipy1 human immun
44	36.5	17.6	47	1	TX32_PHORI	TX3204 phoneutria
45	36.5	17.6	49	2	Q8CIW8_MOUSE	Q8ciw8 mus musculus
46	36	17.4	25	2	Q7Z6N6_HUMAN	Q7z6n6 homo sapien
47	36	17.4	30	1	CX2A_CONBE	P58625 conus betul
48	36	17.4	33	1	YLCH_ECOLI	Q47288 escherichia
49	36	17.4	33	1	Q9NGN0_STRPU	Q9ngn0 strongyloce
50	36	17.4	37	2	Q81RS9_BACAN	Q81rs9 bacillus an

ALIGNMENTS

RESULT 1

Q5P857_AZOSE
ID Q5P857_AZOSE PRELIMINARY; PRT; 36 AA.
AC Q5P857_AZOSE PRELIMINARY; PRT; 36 AA.
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=AZOSEA03820; ORFNames=eBA749;
OS Azocarcus sp. (strain EbN1).
OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC Rhodocyclaceae; Azocarcus.
OX NCBI_TaxID=76114;
RN [1]
RP NUCLEOTIDE SEQUENCES.
RC STRAIN=EbN1.
RX PubMed=15551059; DOI=10.1007/s00203-004-0742-9;
RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel F., Reinhardt R.;
RA "The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1."
RL Arch. Microbiol. 183:27-36(2005).
RL Arch. Microbiol. 183:27-36(2005).
DR EMBL; CR555306; CA06504.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 36 AA; 4153 MW; 38E2D62BA024C649 CRC64;

Query Match 22.2%; Score 46; DB 2; Length 36;
Best Local Similarity 47.8%; Pred. No. 56;
Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 2 DEPORETLKAIHYALNCC--CG 20
||||| : : : : :
DB 16 DEPORETLTPSSFLHCGRCG 36

RESULT 2

Q5WG86_BACSK
ID Q5WG86_BACSK PRELIMINARY; PRT; 45 AA.
AC Q5WG86_BACSK PRELIMINARY; PRT; 45 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=ABC2084;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCES.


```
AC Q5C273;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY810363; AAX26252.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 3872 MW; 6D7F796482D9952B CRC64;

Query Match 20.8%; Score 43; DB 2; Length 35;
Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 12 IHVALNCCGLAGGVQFISDICPKDV 38
DB 2 IQSAFNYKLSGLDVTQNVVPTKV 28

RESULT 7
ID Q4X8W4 PLACH PRELIMINARY; PRT; 44 AA.
AC Q4X8W4;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC404818.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RA transcriptomic, and proteomic analyses."
RA Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01008748; CAH86662.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 44
FT NON TER 44
SQ SEQUENCE 44 AA; 4905 MW; D77C3404234DDF50 CRC64;

Query Match 20.8%; Score 43; DB 2; Length 44;
Best Local Similarity 37.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 8 TLKAIHYALNCCGLAGGVQFISDICP 34
DB 6 TIPITENAINCLFSISIEFTFSDIIP 32

RESULT 8
ID Q5BZF7 SCHJA PRELIMINARY; PRT; 44 AA.
AC Q5BZF7;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
```

```
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY811329; AAX27218.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 44 AA; 5266 MW; 4EBCF906ED28BD18 CRC64;

Query Match 20.3%; Score 42; DB 2; Length 44;
Best Local Similarity 46.7%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 DEPORETLKAIHYAL 16
DB 10 DQPTQEMVKNLHFAL 24

RESULT 9
ID Q86DB6 HALRO PRELIMINARY; PRT; 19 AA.
AC Q86DB6;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 25, Last annotation update)
DE Homeobox protein Otx (Fragment).
GN Name=Hroth;
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22586101; PubMed=12701103; DOI=10.1002/dvdy.10295;
RA Oda-Ishii I., Saiga H.;
RT "Genomic organization and promoter and transcription regulatory
RT regions for the expression in the anterior brain (sensory vesicle) of
RT Hroth, the otx homologue of the ascidian, Halocynthia roretzi.";
RL Dev. Dyn. 227:104-113(2003).
DR EMBL; AB104851; BAC76068.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON TER 19
FT NON TER 19
SQ SEQUENCE 19 AA; 2041 MW; 2D9CAB7036EAP8D CRC64;

Query Match 19.8%; Score 41; DB 2; Length 19;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 LKAIHYALNCCGL 21
DB 4 LKSHYAMNGLGL 16

RESULT 10
ID Q4R921 MACFA PRELIMINARY; PRT; 41 AA.
AC Q4R921;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Testis cDNA clone: Ota-10904, similar to human tudor domain
DE containing 6 protein (LOC388929).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
```

```

RN NUCLEOTIDE SEQUENCE.
RP International consortium for macaque cDNA sequencing, analysis;
RA "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RP Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RL Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB168276; BAB00400.1; -; mRNA.
SQ SEQUENCE 41 AA; 4624 MW; EBD6F0E219C7FD2 CRC64;

Query Match 19.8%; Score 41; DB 2; Length 41;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 24 GVEQFISDICKP 35
DB 28 GIEEFSSSCPQ 39

RESULT 11
ID12 SEGFL STANDARD; PRT; 46 AA.
AC P61096;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Toxin SFI 2 (FS.7).
OS Segestria florentina (tube-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Haplogynae; Dyderoidea; Segestriidae; Segestria.
OX NCBI_TaxID=31925;
RN [1]
RN NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 1-18, MASS SPECTROMETRY, AND
RP LETHAL DOSE.
RA TISSUE=Venom, and Venom gland;
RX PubMed=11689233; DOI=10.1016/S0041-0101(01)00181-7;
RA Lipkin A., Kozlov S., Nosyreva E., Blake A., Windass J.D., Grishin E.;
RT "Novel insecticidal toxins from the venom of the spider Segestria
RL florentina.";
RL Toxinon 40:125-130(2002).
CC -1- FUNCTION: Causes complete flaccid paralysis on H. virescens larvae
CC and death with larger doses. Is inactive on mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- PTM: Contains four disulfide bonds (probable).
CC -1- MASS SPECTROMETRY: MW=4993; METHOD=MALDI; RANGE=1-46; NOTE=Ref.1.
CC -1- TOXIC DOSE: LD50 is 7 mg/kg on H. virescens larvae.
CC -1- SIMILARITY: Belongs to the spider toxin SFI family.
CC -1- CAUTION: Mass spectrometry experiment was done on the entire
CC protein whose the sequence known is incomplete (sequence of 1-18).
CC The difference between measured (4993) and calculated (5136) mass
CC resides in the fact that the sequence of this entire protein is
CC maybe not identical to the sequence shown.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC InterPro: IPR012633; Toxin_28.
DR Pfam: PF08115; Toxin_28; 1.
KW Direct protein sequencing; Multigene family; Toxin.
SQ SEQUENCE 46 AA; 5136 MW; CBFC66F6292D8F6 CRC64;

Query Match 19.8%; Score 41; DB 1; Length 46;
Best Local Similarity 57.1%; Pred. No. 4e+02;

```

```

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 ETLKAHYALNCCG 20
DB 7 ETVCIYIHNHNNCCG 20

RESULT 12
Q29066_PIG PRELIMINARY; PRT; 33 AA.
ID Q29066_PIG PRELIMINARY; PRT; 33 AA.
AC Q29066;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RX MEDLINE=94294418; PubMed=8022818;
RA Benet W.M., Hasson T., Wirth J.A., Cheney R.E., Mooseker M.S.;
RT "Identification and overlapping expression of multiple unconventional
RL myosin genes in vertebrate cell types.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:6549-6553(1994).
DR EMBL; L29135; AAA20920.1; -; mRNA.
DR PIR; I46600; I46600.
FT NON_TER 1
FT NON_TER 33
SQ SEQUENCE 33 AA; 3448 MW; 2EAD4B56F22A40C7 CRC64;

Query Match 19.3%; Score 40; DB 2; Length 33;
Best Local Similarity 55.0%; Pred. No. 3.8e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 12 IHV--ALNCCGLAGGVEQFI 29
DB 7 IHHLTALSQKFGASGVEQII 26

RESULT 13
Q9W7N9_MORSA PRELIMINARY; PRT; 33 AA.
ID Q9W7N9_MORSA PRELIMINARY; PRT; 33 AA.
AC Q9W7N9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Class 9A myosin (Fragment).
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=RPE;
RA Hillman D.W., Bost-Usinger L., Cheng J., Burnside B.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002868; AAD41449.1; -; mRNA.
FT NON_TER 1
FT NON_TER 33
SQ SEQUENCE 33 AA; 3476 MW; 2BBFFCA6F22A40C7 CRC64;

Query Match 19.3%; Score 40; DB 2; Length 33;
Best Local Similarity 55.0%; Pred. No. 3.8e+02;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 12 IHV--ALNCCGLAGGVEQFI 29
DB 7 IHHLTALSQKFGASGVEQII 26

```


Db 7 IHHLTALSQRGPASGVBEQII 26

RESULT 14

Q8UE67_AGRTS PRELIMINARY; PRT; 48 AA.

AC Q8UE67;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein Atu1894.

GN OrderedLocuNames=Atu1894;

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

OX NCBI_TaxID=176299;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Dupont;

RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

RA Chapman P., Clendenning J., Decherage G., Gillet W., Grant C.,

RA Kutayavin T., Levy R., Li M.-J., McLelland E., Palmieri A.,

RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

RT C58.";

RL Science 294:2317-2323(2001).

RL EMBL; AR009143; AAL42890.1; -; Genomic_DNA.

DR PIR; AD2809; AD2809.

SK Complete proteome; Hypothetical protein.

QW SEQUENCE 48 AA; 5156 MW; F14474E058E50D58 CRC64;

Query Match 19.1%; Score 39.5; DB 2; Length 48;

Best Local Similarity 45.0%; Pred. No. 6.9e+02;

Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 18 CCGAGGVQFIS---DIPC 34

Db 12 CCGCSQGVQFPPTGGIGICP 31

RESULT 15

Q4YB36_PLABE PRELIMINARY; PRT; 36 AA.

AC Q4YB36;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

GN ORFNames=PB107877.00.0;

OS Plasmodium berghei.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5821;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,

RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos P.C.,

RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

RT transcriptomic, and proteomic analyses.";

RL Science 307:82-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAAI01006880; CAI04941.1; -; Genomic_DNA.

KW Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 36 AA; 4525 MW; 480B6A796A4FCCF2 CRC64;

Query Match 18.8%; Score 39; DB 2; Length 36;

Best Local Similarity 75.0%; Pred. No. 5.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 HYALNCCG 20

Db 25 HYCLNLCG 32

RESULT 16

COAT3_BPPHL STANDARD; PRT; 38 AA.

ID COAT3_BPPHL

AC P68672; Q07484;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Putative minor coat protein (ORF38).

OS Bacteriophage phi-Lf.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=28365;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RX MEDLINE=94157455; PubMed=8113723;

RA Wen F.-S., Tseng Y.-H.;

RT "Nucleotide sequence determination, characterization and purification

RT of the single-stranded DNA-binding protein and major coat protein of

RT filamentous phage phi-Lf of Xanthomonas campestris pv. campestris.";

RL J. Gen. Virol. 75:15-22(1994).

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; X70331; CAA49798.1; -; Genomic_DNA.

DR PIR; S33484; S33484.

KW Capsid protein; Structural protein.

SQ SEQUENCE 38 AA; 4045 MW; 7ADEB1D8AB6AF6C CRC64;

Query Match 18.8%; Score 39; DB 1; Length 38;

Best Local Similarity 28.9%; Pred. No. 6.3e+02;

Matches 11; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 4 PORETKATHYALNCCG-----LAGGVQFISD 31

Db 2 PSQE--DAVAMSTGCCGLVIVWFVGLGRLAGSVAGMFND 37

RESULT 17

COAT3_XANCP STANDARD; PRT; 38 AA.

ID COAT3_XANCP

AC P68671; Q07484;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Phi-Lf prophage-derived putative minor coat protein.

GN Name=gix-1; OrderedLocuNames=XCC2061;

GN and

GN Name=gix-2; OrderedLocuNames=XCC2072;

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB01000145; EAL49778.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 50 AA; 5555 MW; 7A0DBFE92F5D87F3 CRC64;

Query Match 18.8%; Score 39; DB 2; Length 50;
Best Local Similarity 28.6%; Pred. No. 8.5e+02;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 12 IHVALNCCGLAGGV 25
:|: :|:|:
DB 13 LHFLIGCSIVGGI 26

RESULT 21

Q4Z5I3_PLABE
ID Q4Z5I3_PLABE PRELIMINARY; PRT; 36 AA.
AC Q4Z5I3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB101071.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CRAI01000450; CAH94448.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 36
SQ SEQUENCE 36 AA; 4208 MW; D45F4F460D25CA49 CRC64;

Query Match 18.6%; Score 38.5; DB 2; Length 36;
Best Local Similarity 35.5%; Pred. No. 7e+02;
Matches 11; Conservative 5; Mismatches 6; Indels 9; Gaps 1;

QY 8 TLKAIHYALNCCGLAGGVQFISDIPCKDV 38
||:|:|:|:|:|:
DB 14 TLESLEALN-----QMIDDLVYKDV 35

RESULT 22

Q5C5J9_SCHJA
ID Q5C5J9_SCHJA PRELIMINARY; PRT; 37 AA.
AC Q5C5J9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY809186; AAX25075.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 37 AA; 4561 MW; D7A9D69B68E1790D CRC64;

Query Match 18.4%; Score 38; DB 2; Length 37;
Best Local Similarity 71.4%; Pred. No. 8.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 HYALNCC 19
||:|:|:
DB 20 HYVTNCC 26

RESULT 23

Q4X2T4_PLACH
ID Q4X2T4_PLACH PRELIMINARY; PRT; 37 AA.
AC Q4X2T4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC405189.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01010581; CAH89048.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 37 AA; 4339 MW; 8F915E9C2E5CCDD2 CRC64;

Query Match 18.4%; Score 38; DB 2; Length 37;
Best Local Similarity 28.6%; Pred. No. 8.5e+02;
Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 YALNCCGLAGGVQFISDIP 34
||:|:|:|:|:|:
DB 5 YSLKLVRLVLSYISFVNITCP 25

RESULT 24

Q4Y419_PLACH
ID Q4Y419_PLACH PRELIMINARY; PRT; 42 AA.
AC Q4Y419;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC102095.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

OX	NCBI_TaxID=8709;
RN	[1]
RP	PROTEIN SEQUENCE, FUNCTION, COPACTOR, SUBUNIT, TISSUE SPECIFICITY,
RP	SUBCELLULAR LOCATION, GLYCOSYLATION, AND MASS SPECTROMETRY.
RP	TISSUE=Venom;
RX	PubMed=14499586; DOI=10.1016/S1570-9639(03)00232-2;
RA	Sarraz S., Strali N., Hatmi N., Luis J., Louzir H., Regaya I.,
RA	Slema H., Marvaldi J., El Ayeib M., Marrakchi N.;
RT	"Lebecetin, a potent antiplatelet C-type lectin from Macrovipera
RT	lebetina venom.";
RL	Biochim. Biophys. Acta 1651:30-40(2003).
CC	-I- FUNCTION: Binds to the platelet GPIb/IX receptor system and
CC	-I- inhibits ristocetin-induced platelet agglutination in human
CC	platelet-rich plasma. Strongly inhibits platelet aggregation
CC	induced by ADP, calcium ionophore, thrombin and collagen. Does not
CC	inhibit U46613-induced platelet aggregation.
CC	-I- COPACTOR: Calcium.
CC	-I- SUBUNIT: Heterodimer of an alpha and a beta subunit; disulfide-
CC	linked.
CC	-I- SUBCELLULAR LOCATION: Secreted.
CC	-I- TISSUE SPECIFICITY: Expressed by the venom gland.
CC	-I- PTM: Glycosylated.
CC	-I- MASS SPECTROMETRY: MW=16295.4; METHOD=MALDI; RANGE=1-?;
CC	NOTE=Ref.1.
CC	-I- SIMILARITY: Contains 1 C-type lectin domain.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	-----
DR	InterPro: IPR001304; Lectin C.
DR	PROSITE; P800615; C_TYPE LECTIN 1; PARTIAL.
DR	PROSITE; P850041; C_TYPE LECTIN 2; PARTIAL.
DR	Blood coagulation; Calcium; Cell adhesion; Direct protein sequencing;
KW	Glycoprotein; Lectin.
FT	DOMAIN 1 >43 C-type lectin.
FT	DISULFID 4 16 By similarity.
FT	NON_TER 43 43
FT	SEQUENCE 43 AA; 4703 MW; D89603CD1304CCES CRC64;
FT	-----
QY	Query Match 18.4%; Score 38; DB 1; Length 43;
DB	Best Local Similarity 45.8%; Pred. No. 1e+03;
DB	Matches 11; Conservative 3; Mismatches 6; Indels 4; Gaps 2;
DB	1 ALNCASGWSGGYDQHCHYKVFDDIPP 24
DB	15 ALNCC-GLAGVGEQF---ISDIPC 34
DB	: : :
DB	1 ALNCASGWSGGYDQHCHYKVFDDIPP 24
DB	-----
RESULT 27	
ID	THN PYRPU STANDARD; PRT; 47 AA.
THN	AC P07504;
AC	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DT	Thionin.
DE	Thionin.
GN	Names=Thi1;
OS	Pyricularia pubera (Rabbitwood) (Buffalo nut).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC	Santalales; Santalaceae; Pyricularia.
OX	NCBI_TaxID=3960;
OX	[1]
RP	PROTEIN SEQUENCE.
RX	MEDLINE=8517323; PubMed=3985614;
RA	Vernon L.P., Brett G.B., Zeikus R.D., Gray W.R.;
RA	"A toxic thionin from Pyricularia pubera: purification, properties, and
RT	amino acid sequence.";
RT	Arch. Biochem. Biophys. 238:18-29(1985).
CC	-I- FUNCTION: Thionins are small plant proteins which are toxic to

CC animal cells. They seem to exert their toxic effect at the level
CC of the cell membrane. Their precise function is not known.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the plant thionin (TC 1.C.44) family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A24074; A24074.
DR HSP; P01538; IED0.
DR InterPro; IPR001010; Thionin.
DR Pfam; PF00321; Thionin; 1.
DR PRINTS; PR00287; THIONIN.
DR PROSITE; PS00271; THIONIN; 1.
KW Direct protein sequencing; Plant defense; Plant toxin; Thionin; Toxin.
FT DISULFID 3 41 By similarity.
FT DISULFID 4 31 By similarity.
FT DISULFID 16 27 By similarity.
FT SQ SEQUENCE 47 AA; 5288 MW; 87E10460D8E4C6E1 CRC64;
SQ
Query Match 18.4%; Score 38; DB 1; Length 47;
Best Local Similarity 38.5%; Pred. No. 1.1e+03;
Matches 10; Conservative 4; Mismatches 6; Indels 6; Gaps 2;
QY 14 YALNC---CGLAGGVQFISDICPK 36
DB 8 WARCYNVCKLPGTISR---EICAK 30
RESULT 28
Q4RC82_TETNG
ID Q4RC82_TETNG PRELIMINARY; PRT; 48 AA.
AC Q4RC82;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAR19550, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0038161001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Basiliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellon V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01019550; CAG14001.1; -; Genomic_DNA.

FT NON TER 1 1
SQ SEQUENCE 48 AA; 5445 MW; 778C266C74DAC92B CRC64;
Query Match 18.4%; Score 38; DB 2; Length 48;
Best Local Similarity 28.6%; Pred. No. 1.1e+03;
Matches 8; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
QY 6 RETLKAHYALNCCGLAGGVQFISDIC 33
DB 8 RHPRPLSFNLVLAAGNVERWIAPAC 35
RESULT 29
Q7N8J8_PHOLL
ID Q7N8J8_PHOLL PRELIMINARY; PRT; 50 AA.
AC Q7N8J8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarities with unknown protein.
GN OrderedLocusNames=plu0724;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Ruenik C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens";
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571861; CAE13019.1; -; Genomic_DNA.
DR PhotoList; plu0724; -;
KW Complete proteome.
SQ SEQUENCE 50 AA; 5429 MW; 1B964C7A0DB14253 CRC64;
Query Match 18.4%; Score 38; DB 2; Length 50;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
Matches 7; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 17 NCCGLAGG--VEQFISD 31
DB 14 SCCALKGGTAINLFVRD 30
RESULT 30
Q9PF8_XYLFA
ID Q9PF8_XYLFA PRELIMINARY; PRT; 50 AA.
AC Q9PF8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf0722;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu P.A., Acencio M.,
RA Alvares M.H., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

```

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferri J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva P.R., Silva W.A. Jr.,
RA da Silveira J.P., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Teai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA "The genome sequence of the plant pathogen Xylella fastidiosa.";
RT Nature 406:151-159(2000).
DR EMBL; AF003914; AAF83532.1; -; Genomic_DNA.
DR PIR; A82772; A82772.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 50 AA; 5205 MW; CF370BD2D4647BDC CRC64;

Query Match 18.4%; Score 38; DB 2; Length 50;
Best Local Similarity 29.6%; Pred. No. 1.2e+03;
Matches 8; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 7 ETLKAIHYALNCCGLAGGVEQFISDIC 33
Db 22 QQLGGTHRAVSCGFSLAFLLSVTDIC 48

RESULT 31
Q86DN6_9CAEN PRELIMINARY; PRT; 30 AA.
AC Q86DN6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mitochondrial malate dehydrogenase (fragment).
GN Name=Mdh;
OS Natica alderi.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
OC Littorinimorpha; Naticoidea; Naticidae; Natica.
OX NCBI_TaxID=208833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14743317; DOI=10.1007/s00239-003-2528-0;
RA Kirby R.R.;
RT "Genetic variation in a cline in a living intertidal snail arose in
the Neogastropoda over 100 million years ago.";
RL J. Mol. Evol. 58:97-105(2004).
DR EMBL; AY138136; AAN23848.1; -; mRNA.
DR HSSP; Q9FD04; 2CMD.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008100; P:tricarboxylic acid cycle intermediate metab. . .; IEA.
DR InterPro; IPR001236; ldh.
DR Pfam; PF00056; Ldh_1_N; 1.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 30
FT NON_TER 30
SQ SEQUENCE 30 AA; 3192 MW; 640907AF5612A7DD CRC64;

Query Match 17.9%; Score 37; DB 2; Length 30;
Best Local Similarity 37.5%; Pred. No. 9.5e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 20 GLAGGVEQFISDICPK 35
Db 8 GIVRLVDIAIDVCPK 23

RESULT 32
Q9WMD8_9FLAV PRELIMINARY; PRT; 44 AA.
AC Q9WMD8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98154925; PubMed=9495537; DOI=10.1016/S0168-1702(97)00123-8;
RA Kondo Y., Mizokami M., Nakano T., Kato T., Ohba K., Orito E., Ueda R.,
RA Mukaide M., Hikiji K., Oyunsuren T., Cooksley W.G.;
RT "Genotype of GB virus C/hepatitis G virus by molecular evolutionary
analysis.",
RT analysis.
RL Virus Res. 52:221-230(1997).
DR EMBL; AB006146; BAA35134.1; -; Genomic_RNA.
KW Polyprotein.
FT NON_TER 44
FT NON_TER 44
SQ SEQUENCE 44 AA; 4558 MW; 34C6C10975CCE306 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 44;
Best Local Similarity 29.2%; Pred. No. 1.5e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDICPKKDV 38
Db 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 33
Q5C4E6_SCHJA PRELIMINARY; PRT; 49 AA.
AC Q5C4E6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY809590; AAX25479.1; -; mRNA.
DR InterPro; IPR000471; Interferon_abd.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5479 MW; 1491391F97B9E9FA CRC64;

Query Match 17.9%; Score 37; DB 2; Length 49;
Best Local Similarity 26.3%; Pred. No. 1.6e+03;
Matches 10; Conservative 4; Mismatches 14; Indels 10; Gaps 1;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
Db 3 KDFTEELFDVNVSSLVCCSL-----ICLGNDI 30

RESULT 34
Q787R5_9FLAV PRELIMINARY; PRT; 50 AA.
ID Q787R5_9FLAV
AC Q787R5_9FLAV

```

```
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE-98154925; PubMed-9495537; DOI=10.1016/S0168-1702(97)00123-8;
RA Kondo Y., Mizokami M., Nakano T., Ooba K., Orito E., Ueda R.,
RA Mukaida M., Hikiji K., Oyunsuren T., Cooksley W.G.;
RT "Genotype of GB virus C/Hepatitis G virus by molecular evolutionary
RT analysis.";
RL Virus Res. 52:221-230(1997).
DR EMBL; AB003545; BAA36157.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5083 MW; C77B505F1A2CE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 35
Q787R7_9FLAV
ID Q787R7_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q787R7_9FLAV PRELIMINARY; PRT; 50 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaida M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003538; BAA36188.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5083 MW; C77B505F1A2CE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 36
Q787R8_9FLAV
ID Q787R8_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q787R8_9FLAV PRELIMINARY; PRT; 50 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
```

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaida M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003535; BAA36185.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5117 MW; C77B5877B8AEE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 37
Q9WA37_9FLAV
ID Q9WA37_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q9WA37_9FLAV PRELIMINARY; PRT; 50 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaida M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003537; BAA36187.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5117 MW; C77B5877B8AEE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCKDV 38
DB 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 38
Q9YIK7_9FLAV
ID Q9YIK7_9FLAV PRELIMINARY; PRT; 50 AA.
AC Q9YIK7_9FLAV PRELIMINARY; PRT; 50 AA.
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Polypeptide (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kondo Y., Mizokami M., Nakano T., Ueda R., Mukaida M., Hikiji K.,
RA Kato T., Oyunsuren T., Rukibakiev R., Cooksley W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003539; BAA36189.1; -; Genomic_RNA.
KW Polypeptide.
FT NON_TER 50
SQ SEQUENCE 50 AA; 5083 MW; C77B505F1A2CE4C6 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
```

Best Local Similarity 29.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

Search completed: January 20, 2006, 17:33:46
Job time : 85.5679 secs

QY 15 ALNCCGLAGGVEQFISDIPCCKDV 38
| : || | : | : : : | : | :
Db 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 39

Q9Z039 9FLAV
ID Q9Z039 9FLAV PRELIMINARY; PRT; 50 AA.
AC Q9Z039;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Polypeptidein (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98154925; PubMed=9495537; DOI=10.1016/S0168-1702(97)00123-8;
RA Kondo Y., Mizokami M., Nakano T., Kato T., Ohba K., Orito E., Ueda R.,
RA Mukaide M., Hikiji K., Oyunsuren T., Cooksley W.G.;
RT "Genotype of GB virus C/hepatitis G virus by molecular evolutionary
RT analysis";
RL Virus Res. 52:221-230(1997).
DR EMBL; AB006145; BAA35133.1; -; Genomic_RNA.
KW Polypeptidein.
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5169 MW; DB0B587F900D3783 CRC64;

Query Match 17.9%; Score 37; DB 2; Length 50;
Best Local Similarity 29.2%; Pred. No. 1.7e+03;

Matches 7; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 15 ALNCCGLAGGVEQFISDIPCCKDV 38
| : || | : | : : : | : | :
Db 19 ATHACGANG--QYFLTNCCALEDI 40

RESULT 40

Q7M269 GASCO
ID Q7M269 GASCO PRELIMINARY; PRT; 33 AA.
AC Q7M269;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE R-phycoerythrin gamma-D chain (Fragment).
OS Gastroclonium coulteri (Red alga).
OC Eukaryota; Rhodophyta; Florideophyceae; Rhodomeniales; Champiaceae;
OC Gastroclonium.
OX NCBI_TaxID=2773;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=85182601; PubMed=3886644;
RA Klotz A.V., Glazer A.N.;
RT "Characterization of the bilin attachment sites in R-phycoerythrin.";
RL J. Biol. Chem. 260:4856-4863(1985).
DR PIR; I22565; I22565.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3211 MW; 58A7C5A2D52DA56B CRC64;

Query Match 17.6%; Score 36.5; DB 2; Length 33;
Best Local Similarity 38.5%; Pred. No. 1.2e+03;

Matches 10; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 2 DEPORETLKATHYALNCCGLAGGVEQ 27
| : || | : | : : : | : | :
Db 9 DFPVAPSL-AGHYSLTNCGQPSGASK 33

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:21:43 ; Search time 62.3457 Seconds
(without alignments)
176.187 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKQVLETFVKSCPDPAKEVFNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	25	8	ADJ57562 Human CD9
2	95	72.0	18	8	ADJ57563 Human CD9
3	61	46.2	30	6	ABU05051 Human exp
4	49	37.1	10	6	ABU03385 Human exp
5	46	34.8	44	4	AAM83184 Human imm
6	39	29.5	41	4	AU020329 Human nov
7	38	28.8	46	9	ADY51925 Phage SPO
8	36	27.3	33	4	ABB39440 Peptide #
9	36	27.3	33	4	AAM32967 Peptide #
10	36	27.3	33	4	AAM72739 Human bon
11	36	27.3	33	4	AAM60125 Human bra
12	36	27.3	33	4	ABG54437 Human liv
13	36	27.3	33	5	ABG42563 Human pep
14	36	27.3	34	3	AAY92549 Finger 2
15	36	27.3	34	3	AAB02778 Human TGF
16	36	27.3	36	2	AAB030357 Fragment
17	36	27.3	36	3	AAB09511 Human TGF
18	36	27.3	39	7	ADJ81051 INSP010 p
19	36	27.3	36	46	ADS06580 Staphyloc
20	35.5	26.9	39	3	AAY56422 Mycoplasma
21	35.5	26.9	41	4	AAM65372 Human bra
22	35.5	26.9	41	4	ABG59698 Human liv
23	35.5	26.9	42	8	ADJ97737 Protein e
24	35.5	26.9	43	4	ABB66998 Drosophil

25	35	26.5	28	4	AAM64295 Human bra
26	35	26.5	33	4	AAM18282 Peptide #
27	35	26.5	33	4	ABB37316 Peptide #
28	35	26.5	33	4	AAM30772 Peptide #
29	35	26.5	33	4	ABB32066 Peptide #
30	35	26.5	33	4	ABB22608 Protein #
31	35	26.5	33	4	AAM70450 Human bon
32	35	26.5	33	4	AAM58010 Human bra
33	35	26.5	33	4	ABG52136 Human liv
34	35	26.5	33	4	AAM05895 Peptide #
35	35	26.5	33	5	ABG40088 Human pep
36	35	26.5	38	4	ABB42598 Peptide #
37	35	26.5	38	4	AAM36414 Peptide #
38	35	26.5	38	4	AAM76304 Human bon
39	35	26.5	38	4	AAM63489 Human bra
40	35	26.5	38	4	ABG58014 Human liv
41	35	26.5	38	5	ABG45607 Human pep
42	35	26.5	50	2	AAR66211 Phi 29 in
43	34.5	26.1	18	7	ADC29648 Antioxi
44	34.5	26.1	35	4	AAM17469 Peptide #
45	34.5	26.1	35	4	ABB36490 Peptide #
46	34.5	26.1	35	4	AAM29988 Peptide #
47	34.5	26.1	35	4	ABB31285 Peptide #
48	34.5	26.1	35	4	ABB21834 Protein #
49	34.5	26.1	35	4	AAM69654 Human bon
50	34.5	26.1	35	4	AAM57255 Human bra

ALIGNMENTS

RESULT 1

ADJ57562

ID ADJ57562 standard; peptide; 25 AA.

XX

AC ADJ57562;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human CD9 fibronectin-binding domain peptide fragment.

XX

KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;

KW haemostatic; angiogenic; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2004007685-A2.

XX

PD 22-JAN-2004.

XX

PF 14-JUL-2003; 2003WO-US022050.

XX

PR 12-JUL-2002; 2002US-0395864P.

XX

PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;

PI Crossno JT, Lu Y,

XX

DR WPI; 2004-122924/12.

XX

PT Interfering with CD9 binding to fibronectin by binding a fibronectin-

PT binding domain of the CD9 protein or polypeptide, useful in treating

PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis

PT and cancers.

XX

PS Claim 7; SEQ ID NO 5; 126pp; English.

XX

CC The present sequence is that of a peptide fragment from the fibronectin-

CC binding domain of human CD9 ADJ57558. The peptide, or an antibody that

CC binds to it, is used in claimed methods for: interfering with CD9 binding

CC to fibronectin; modifying adhesion, motility or spreading of a CD9-

CC expressing cell on fibronectin; inhibiting proliferation or survival of

CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix
 CC ; and modifying cell-to-cell interaction. The methods are based on the
 CC finding that increased CD9 expression is implicated in (i) decreased
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1
 CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 25 AA;

Query Match 100.0%; Score 132; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETTVKSCPDAIKEVFDNK 25
 |||||
 DB 1 PKQVLETTVKSCPDAIKEVFDNK 25

RESULT 2
 ADJ57563
 ID ADJ57563 standard; peptide; 18 AA.
 XX
 AC ADJ57563;

XX DT 06-MAY-2004 (first entry)
 XX DE Human CD9 fibronectin-binding domain peptide fragment.
 XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
 KW haemostatic; antiangiogenic; cytostatic.
 KW
 XX Homo sapiens.
 XX WO2004007685-A2.
 XX 22-JAN-2004.

XX PF 14-JUL-2003; 2003WO-US022050.
 XX PR 12-JUL-2002; 2002US-0395864P.
 XX PA (UYTE-) UNIV TENNESSEE RES FOUND.
 XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW,
 PI Croeseno JT, Lu Y;
 PI WPI; 2004-122924/12.
 DR
 XX
 XX Interfering with CD9 binding to fibronectin by binding a fibronectin-
 PT binding domain of the CD9 protein or polypeptide, useful in treating
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
 PT and cancers.
 XX
 PS Claim 7; SEQ ID NO 6; 126pp; English.

XX The present sequence is that of a peptide fragment from the fibronectin-
 CC binding domain of human CD9 ADJ57563. The peptide, or an antibody that
 CC binds to it, is used in claimed methods for: interfering with CD9 binding
 CC to fibronectin; modifying adhesion, motility or spreading of a CD9-
 CC expressing cell on fibronectin; inhibiting proliferation or survival of
 CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix
 CC ; and modifying cell-to-cell interaction. The methods are based on the
 CC finding that increased CD9 expression is implicated in (i) decreased
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1

CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 18 AA;

Query Match 72.0%; Score 95; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETTVKSCPDAI 18
 |||||
 DB 1 PKQVLETTVKSCPDAI 18

RESULT 3
 ABU05051
 ID ABU05051 standard; protein; 30 AA.
 XX
 AC ABU05051;

XX DT 29-JAN-2003 (first entry)
 XX DE Human expressed protein tag (EPT) #1717.
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX WO200278524-A2.
 XX 10-OCT-2002.
 XX PF 28-MAR-2002; 2002WO-US009671.
 XX PR 28-MAR-2001; 2001US-0279495P.
 XX PR 21-MAY-2001; 2001US-0292544P.
 XX PR 08-AUG-2001; 2001US-0310801P.
 XX PR 01-OCT-2001; 2001US-0326370P.
 XX PR 04-DEC-2001; 2001US-0336780P.
 XX PR 20-FEB-2002; 2002US-0358985P.
 XX (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;
 XX WPI; 2003-040607/03.
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1717; 134pp; English.
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 30 AA;

Query Match 46.2%; Score 61; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PKDVLFTFTVK 12
 |||||
 Db 19 PKDVLFTFTVK 30

RESULT 4
 ABU03385
 ID ABU03385 standard; protein; 10 AA.
 XX
 AC ABU03385;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #165.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX

(ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;
 XX
 XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX

PS Claim 10; SEQ ID NO 165; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 10 AA;

Query Match 37.1%; Score 49; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KDVLEFTFTVK 12
 |||||
 Db 1 KDVLEFTFTVK 10

RESULT 5
 AAM83184
 ID AAM83184 standard; protein; 44 AA.
 XX
 AC AAM83184;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen SEQ ID NO:10777.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184564P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.

PR	22-AUG-2000;	2000US-02266811P.
PR	22-AUG-2000;	2000US-02266868P.
PR	22-AUG-2000;	2000US-0227182P.
PR	23-AUG-2000;	2000US-02270092P.
PR	30-AUG-2000;	2000US-0228794P.
PR	01-SEP-2000;	2000US-0229287P.
PR	01-SEP-2000;	2000US-0229343P.
PR	01-SEP-2000;	2000US-0229344P.
PR	05-SEP-2000;	2000US-0229345P.
PR	05-SEP-2000;	2000US-0229509P.
PR	06-SEP-2000;	2000US-0229513P.
PR	06-SEP-2000;	2000US-0230437P.
PR	08-SEP-2000;	2000US-0230438P.
PR	08-SEP-2000;	2000US-0231242P.
PR	08-SEP-2000;	2000US-0231243P.
PR	08-SEP-2000;	2000US-0231244P.
PR	08-SEP-2000;	2000US-0231413P.
PR	08-SEP-2000;	2000US-0231414P.
PR	08-SEP-2000;	2000US-0232080P.
PR	08-SEP-2000;	2000US-0232081P.
PR	14-SEP-2000;	2000US-0233196P.
PR	14-SEP-2000;	2000US-02332397P.
PR	14-SEP-2000;	2000US-02333064P.
PR	14-SEP-2000;	2000US-02333065P.
PR	21-SEP-2000;	2000US-0234223P.
PR	21-SEP-2000;	2000US-0234224P.
PR	25-SEP-2000;	2000US-0234597P.
PR	25-SEP-2000;	2000US-0234598P.
PR	25-SEP-2000;	2000US-0234599P.
PR	26-SEP-2000;	2000US-0234844P.
PR	27-SEP-2000;	2000US-0235634P.
PR	27-SEP-2000;	2000US-0235636P.
PR	29-SEP-2000;	2000US-0236327P.
PR	29-SEP-2000;	2000US-0236367P.
PR	29-SEP-2000;	2000US-0236368P.
PR	29-SEP-2000;	2000US-0236369P.
PR	29-SEP-2000;	2000US-0236370P.
PR	02-OCT-2000;	2000US-0236802P.
PR	02-OCT-2000;	2000US-0237037P.
PR	02-OCT-2000;	2000US-0237038P.
PR	02-OCT-2000;	2000US-0237039P.
PR	02-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239353P.
PR	13-OCT-2000;	2000US-0239337P.
PR	20-OCT-2000;	2000US-0240960P.
PR	20-OCT-2000;	2000US-0241221P.
PR	20-OCT-2000;	2000US-0241785P.
PR	20-OCT-2000;	2000US-0241786P.
PR	20-OCT-2000;	2000US-0241787P.
PR	20-OCT-2000;	2000US-0241808P.
PR	20-OCT-2000;	2000US-0241809P.
PR	01-NOV-2000;	2000US-0241826P.
PR	01-NOV-2000;	2000US-0244617P.
PR	08-NOV-2000;	2000US-0246474P.
PR	08-NOV-2000;	2000US-0246475P.
PR	08-NOV-2000;	2000US-0246476P.
PR	08-NOV-2000;	2000US-0246477P.
PR	08-NOV-2000;	2000US-0246478P.
PR	08-NOV-2000;	2000US-0246523P.
PR	08-NOV-2000;	2000US-0246524P.
PR	08-NOV-2000;	2000US-0246525P.
PR	08-NOV-2000;	2000US-0246526P.
PR	08-NOV-2000;	2000US-0246527P.
PR	08-NOV-2000;	2000US-0246528P.
PR	08-NOV-2000;	2000US-0246532P.
PR	08-NOV-2000;	2000US-0246609P.
PR	08-NOV-2000;	2000US-0246610P.
PR	08-NOV-2000;	2000US-0246611P.
PR	08-NOV-2000;	2000US-0246613P.

PR	17-NOV-2000;	2000US-02492007P.
PR	17-NOV-2000;	2000US-02492008P.
PR	17-NOV-2000;	2000US-02492009P.
PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
PR	17-NOV-2000;	2000US-0249213P.
PR	17-NOV-2000;	2000US-0249214P.
PR	17-NOV-2000;	2000US-0249215P.
PR	17-NOV-2000;	2000US-0249216P.
PR	17-NOV-2000;	2000US-0249217P.
PR	17-NOV-2000;	2000US-0249218P.
PR	17-NOV-2000;	2000US-0249244P.
PR	17-NOV-2000;	2000US-0249245P.
PR	17-NOV-2000;	2000US-0249264P.
PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249297P.
PR	17-NOV-2000;	2000US-0249299P.
PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0254179P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0253678P.

2

RESULT 6
AAU20329
ID AAU20329 standard; protein; 41 AA.
XX
AC AAU20329;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human novel endocrine antigen, SEQ ID No 386.
XX
KW Human; endocrine antigen; cytostatic; antiinfertility; antidiabetic;
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;
KW antisense-therapy; antibody; endocrine disorder; hormone imbalance;
KW reproductive disorder; endocrine cancer; pancreatic disorder;
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.
XX
OS Homo sapiens.
XX
PN WO200155319-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001335.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227109P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.

XX DE Peptide #6946 encoded by human foetal liver single exon probe.
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX OS Homo sapiens.
 XX PN WO200157277-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000669.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PF WPI; 2001-483447/52.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
 XX PS Claim 27; SEQ ID NO 32075; 639pp + Sequence Listing; English.
 XX CC The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 33 AA;
 Query Match 27.3%; Score 36; DB 4; Length 33;
 Best Local Similarity 36.8%; Pred. No. 4.1e+02;
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 4 DVLETFVTKSCPDPAIKEVF 22
 Db 3 NMLSTASITMLPFGLKEVF 21
 RESULT 9
 AAM32967
 ID AAM32967 standard; protein; 33 AA.
 XX AC AAM32967;
 XX DT 17-OCT-2001 (first entry)
 XX DE Peptide #7004 encoded by probe for measuring placental gene expression.
 XX KW Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200157272-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000663.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PF WPI; 2001-488997/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
 XX PS Claim 27; SEQ ID NO 33236; 654pp; English.
 XX CC The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
 XX SQ Sequence 33 AA;
 Query Match 27.3%; Score 36; DB 4; Length 33;
 Best Local Similarity 36.8%; Pred. No. 4.1e+02;
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 4 DVLETFVTKSCPDPAIKEVF 22
 Db 3 NMLSTASITMLPFGLKEVF 21
 RESULT 10
 AAM72739
 ID AAM72739 standard; protein; 33 AA.
 XX AC AAM72739;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33045.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
 XX OS Homo sapiens.
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000668.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PF WPI; 2001-488900/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

```
PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 33045; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX CC Sequence 33 AA;
SQ

Query Match          27.3%; Score 36; DB 4; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22
   ::||::|::|::|::|
Db 3 NMLSTASITMLPFGLEKEVF 21

RESULT 11
AAM60125
ID AAM60125 standard; protein; 33 AA.
XX AC AAM60125;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32230.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-483446/52.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-483446/52.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX CC Sequence 33 AA;
SQ

Query Match          27.3%; Score 36; DB 4; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22
   ::||::|::|::|::|
Db 3 NMLSTASITMLPFGLEKEVF 21

PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 33045; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX CC Sequence 33 AA;
SQ

Query Match          27.3%; Score 36; DB 4; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22
   ::||::|::|::|::|
Db 3 NMLSTASITMLPFGLEKEVF 21

Best Local Similarity 36.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22
   ::||::|::|::|::|
Db 3 NMLSTASITMLPFGLEKEVF 21

RESULT 12
ABG54437
ID ABG54437 standard; peptide; 33 AA.
XX AC ABG54437;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID NO 33085.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-488898/53.
XX PR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 33085; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX CC Sequence 33 AA;
SQ

Query Match          27.3%; Score 36; DB 4; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAIKEVF 22
   ::||::|::|::|::|
Db 3 NMLSTASITMLPFGLEKEVF 21
```


RESULT 13
ABG42563
ID ABG42563 standard; peptide; 33 AA.
XX
AC ABG42563;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32228.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PP 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLB-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 27; SEQ ID NO 32228; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 33 AA;
XX
Query Match 27.3%; Score 36; DB 5; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 4 DVLETFVKSCPDALKEVF 22
DB 3 NMLSTASITWLPGLKEVF 21
XX
RESULT 14
AA92549
ID AA92549 standard; peptide; 34 AA.
XX
AC AA92549;
XX
DT 10-AUG-2000 (first entry)
XX
DE Finger 2 subdomain of TGF-beta3.
XX
KW finger 2 subdomain; BMP; TGF-beta family; protein refolding;
KW fusion protein; osteopathic; antibacterial; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200020449-A2.
XX
PD 13-APR-2000.
XX
PP 07-OCT-1999; 99WO-US023372.
XX
PR 07-OCT-1998; 98US-0103418P.
PR 16-AUG-1999; 99US-00375333.
XX
XX (STYC) STRYKER CORP.
XX
PI Oppermann H, Tai M, McCartney J;
XX
XX WPI; 2000-303743/26.
XX
PT A biologically active TGF-beta family member fusion protein competent to
PT refold, comprising a C-terminal linked TGF-beta family protein.
XX
PS Disclosure; Page 131; 160pp; English.
XX
CC AA92519-53 are C-terminal residues of the finger 2 subdomain of various
CC known members of the BMP and TGF-beta families, starting with the first
CC residue following the cysteine doublet. Novel proteins comprise
CC biologically active TGF-beta family member fusion proteins competent to
CC refold under suitable refolding conditions. The fusion proteins comprise:
CC (1) a TGF-beta family protein C-terminal seven cysteine domain,
CC comprising finger 1, finger 2 and heel subdomains; and (2) a heterologous
CC leader sequence domain operatively linked to the C-terminal domain.
CC Truncations, heterodimers and mutants of these fusion proteins and
CC methods of purifying the heterodimers are also claimed. The TGF-beta
CC family proteins can be used to induce the full cascade of morphogenic
CC events which culminate in skeletal tissue formation, including cartilage
CC and endochondral bone formation. They are useful in the binding of fibrin

CC and fibronectin to the implanted matrix, chemotaxis of cells.
 CC proliferation of fibroblasts, differentiation into chondroblasts,
 CC cartilage formation, vascular invasion, bone formation, remodeling, and
 CC bone marrow differentiation. The proteins have improved physical
 CC properties such as solubility and stability, improved biological
 CC activity, including altered receptor binding and improved targeting
 CC capabilities

XX SQ Sequence 34 AA;
 Query Match 27.3%; Score 36; DB 3; Length 34;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETTFTVKSC 14
 || : | ||||
 Db 18 PKVEQLSNMVKSC 31

RESULT 15
 AAB02778
 ID AAB02778 standard; protein; 34 AA.

XX AC AAB02778;
 XX DT 22-AUG-2000 (first entry)

DE Human TGF-beta3 finger 2 sub-domain sequence SEQ ID NO:31.

XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
 KW bone morphogenic protein; osteogenic protein; mutant; modified;
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
 KW tissue repair; regeneration; proliferation; differentiation.

XX OS Homo sapiens.

XX WO200020591-A2.

PN 13-APR-2000.

XX 07-OCT-1999; 99WO-US023370.

XX 07-OCT-1998; 98US-0103418P.

PR 16-AUG-1999; 99US-00374936.

XX (STYC) STRYKER CORP.

XX Oppermann H, Tai M, Mccartney J;

XX WPI; 2000-303776/26.

XX Novel TGF-beta superfamily mutant chimeric protein, useful for inducing
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one
 PT monomer containing domains from two family members.

XX Disclosure; Page 120; 149pp; English.

XX The present invention describes a tumour growth factor beta (TGF-beta)
 CC superfamily chimeric protein (I) derived from at least 2 different
 CC members of the superfamily comprising a dimer with one monomer that
 CC contains a finger 2 domain derived from a first family member and a
 CC finger 1 domain and heel domain, both derived from a second family
 CC member. The monomer further comprises a conserved C-terminal cysteine
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair
 CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised
 CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve
 CC and for inducing the proliferation and differentiation of uncommitted
 CC progenitor cells in a tissue-specific manner to support new tissue
 CC formation. AAA29887 to AAA29897 and AAB02748 to AAB02824 represent
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 34 AA;
 Query Match 27.3%; Score 36; DB 3; Length 34;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETTFTVKSC 14
 || : | ||||
 Db 18 PKVEQLSNMVKSC 31

RESULT 16
 AAW30357
 ID AAW30357 standard; peptide; 36 AA.

XX AC AAW30357;

XX DT 11-FEB-1998 (first entry)

DE Fragment #2 of growth factor TGFbeta3.

XX Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopaenia;
 KW acute spinal cord injury; multiple sclerosis; eosinopaenia; lymphopaenia;
 KW monocytopenia; neutropaenia; anaemia; thrombocytopenia; neuroblastoma;
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta3;
 KW growth factor; hybrid protein.

XX OS Homo sapiens.

XX WO9708196-A1.

XX 06-MAR-1997.

XX 27-AUG-1996; 96WO-US014065.

XX 28-AUG-1995; 95US-00519777.

XX (UNIW) UNIV WASHINGTON.

XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;

XX WPI; 1997-179176/16.

XX A novel growth factor Neurturin - used to treat neuro-degenerative and
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and
 PT eosinopenia.

XX Claim 92; Fig 18; 206pp; English.

XX AAW30355-W30377 represent growth factor fragments that are used in a
 CC hybrid polypeptide of the invention. These sequences form a hybrid with
 CC the human neurturin (NT) fragment shown in AAW30354. NT promotes the
 CC growth and differentiation of haematopoietic and neuronal cells, and
 CC their stem cells. The NT gene and protein are used to prevent or treat
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,
 CC nervous system tumours, multiple sclerosis and infection; and
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopaenia,
 CC lymphopaenia, monocytopenia, neutropaenia, anaemia, thrombocytopenia
 CC and stem cell insufficiencies. The NT protein and gene are also useful to
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or
 CC flanking a target sequence) can be used for detecting NT in a sample or
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene
 CC are used to treat diseases promoted by NT expression e.g. obesity

XX Sequence 36 AA;

Query Match 27.3%; Score 36; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVVKSC 14
||| : |||||
Db 20 PKVEQLSNMVKSC 33

RESULT 17
AAB09511
ID AAB09511 standard; peptide; 36 AA.
XX AAB09511;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human TGF-beta 3 finger 2 subdomain.
XX
KW TGF-beta superfamily; transforming growth factor-beta;
KW developmental regulation; finger 2 subdomain; basic region;
KW protein refolding; stability; solubility; osteogenic protein; OP;
KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
KW connective tissue; cartilage; vulvular.
XX
OS Homo sapiens.
XX
XX W0200020607-A2.
XX
XX 13-APR-2000.
XX
XX 07-OCT-1999; 99WO-US023371.
XX
XX 07-OCT-1998; 98US-0103418P.
XX
XX 16-AUG-1999; 99US-00374958.
XX
XX (STYC) STRYKER CORP.
XX
XX Oppermann H, Tai M, McCartney J;
XX
XX WPI; 2000-303787/26.
XX
XX
XX Transforming growth factor-beta superfamily member mutant induces tissue
XX morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
XX tissue and connective tissue and comprises a substitution in a region of
XX the finger 2 domain.
XX
XX Disclosure; Fig 1; 162pp; English.

CC The invention relates to mutant TGF-beta (transforming growth factor-
CC beta) superfamily members. These mutants comprise one or more amino acid
CC substitutions in the base region of the finger 2 subdomain, and a C-
CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
CC beta superfamily proteins regulate developmental processes and include
CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibitors.
CC Specific examples of TGF-beta superfamily mutants encompassed by the
CC invention are the finger 2 subdomain mutants of human osteogenic protein-
CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,
CC dental tissue, connective tissue, brain, liver and nerve tissue. The
CC proteins can be used in conjunction with a biocompatible matrix e.g.,
CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
CC cartilage and/or other mineralised skeletal or connective tissues e.g.,
CC ligament, tendon, muscle, fibrocartilage, joint capsule and
CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
CC damaged mammalian tissue and to prevent or substantially inhibit
CC immune/inflammatory response-mediated tissue damage and scar tissue
CC formation following an injury. Compared to the wild-type TGF-beta

CC superfamily members, the mutant proteins have improved in vitro refolding
CC properties in a pH range of 6-9, increased solubility in aqueous solution
CC and improved stability and/or activity. Sequences AAB09481-B09516
CC represent wild-type finger 2 subdomains from a variety of TGF-beta
CC superfamily proteins referred to in the specification

XX
SQ Sequence 36 AA;

Query Match 27.3%; Score 36; DB 3; Length 36;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVVKSC 14
||| : |||||
Db 20 PKVEQLSNMVKSC 33

RESULT 18
ADJ81051
ID ADJ81051 standard; protein; 39 AA.
XX
XX AC ADJ81051;
XX
XX 06-MAY-2004 (first entry)
XX
XX INSP010 protein sequence exon 29.
XX
XX
XX cytostatic; immunosuppressive; antiinflammatory; cardiant;
KW neuroprotective; antimicrobial; gene therapy; mucin-like protein;
KW cystine knot; diagnosis; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; cardiovascular disorder;
KW neurological disorder; developmental disorder; metabolic disorder.
XX
XX Homo sapiens.
XX
XX W02003051919-A1.
XX
XX 26-JUN-2003.
XX
XX 19-DEC-2002; 2002WO-GB005811.
XX
XX 19-DEC-2001; 2001GB-00030384.
XX
XX (ARES-) ARES TRADING SA.
XX
XX Davies MD, Fegan RJ, Phelps CB, Power C;
XX
XX WPI; 2003-532999/50.
XX
XX N-PSDB; ADJ81050.
XX
XX
XX Novel isolated INSP010 polypeptide which is a secreted protein of the
XX mucin subfamily of cystine knot containing proteins useful for treating
XX cell proliferative disorders, autoimmune/inflammatory disorders.
XX
XX Example 2; SEQ ID NO 110; 147pp; English.

CC The invention relates to secreted mucin-like protein (INSP009, INSP010
CC and INSP011), members of a mucin subfamily of cystine knot containing
CC proteins. The proteins are useful for therapy or diagnosis of a disease
CC such as cell proliferative disorders, autoimmune/inflammatory disorders,
CC cardiovascular disorders, neurological disorders, developmental
CC disorders, metabolic disorders, infections and other pathological
CC conditions. This sequence corresponds to a protein sequence of the
CC invention.

XX
SQ Sequence 39 AA;

Query Match 27.3%; Score 36; DB 7; Length 39;
Best Local Similarity 41.2%; Pred. No. 5e+02;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 7 EFTTVKSCPDAIKEVPD 23
||| : |||:

DT 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 37477.
DE Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
KW Homo sapiens.
OS WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000667.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
PT Example 4; SEQ ID NO 37477; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 41 AA;
Query Match 26.9%; Score 35.5; DB 4; Length 41;
Best Local Similarity 42.9%; Pred. No. 6.4e+02;
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
QY 1 PKKDVLETF-TVKSCPDIAKE 20
||:|||||:|:|:|:
Db 19 PKEDHLEGFLEVQAKKEAVKD 39
RESULT 22
ABG59698
ID ABG59698 standard; peptide; 41 AA.
XX ABG59698;
XX 25-FEB-2003 (first entry)
DT Human liver peptide, SEQ ID NO 38346.
DE Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
KW Homo sapiens.
OS WO200157273-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 05-NOV-2001 (first entry)
PR Human brain expressed single exon probe encoded protein SEQ ID NO: 37477.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488898/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT Claim 27; SEQ ID NO 38346; 658pp; English.
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 41 AA;
Query Match 26.9%; Score 35.5; DB 4; Length 41;
Best Local Similarity 42.9%; Pred. No. 6.4e+02;
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
QY 1 PKKDVLETF-TVKSCPDIAKE 20
||:|||||:|:|:|:
Db 19 PKEDHLEGFLEVQAKKEAVKD 39
RESULT 23
ADL97737
ID ADL97737 standard; protein; 42 AA.
XX ADL97737;
AC ADL97737;
XX 17-JUN-2004 (first entry)
DT Protein encoded by human transporter/channel protein INPIONCH10 exon 7.
DE Protein encoded by human transporter/channel protein INPIONCH10 exon 7.
XX contraindicative; antiinflammatory; gastrointestinal; cardiac; antiangiinal;
KW anorectic; antidiabetic; vasotropic; nephrotropic; antiinfertility;
KW cytostatic; endocrine; gene therapy; vaccine; transporter;
KW channel protein; diagnosis; contraceptive; colitis; hypertrophy;
KW fibrosis; heart failure; myocardial infarction; angina; obesity;
KW hyperinulinemia; vascular disease; renal disease; fertility disorder;
KW infertility; testosterone deficiency; testosterone-related disorder;
KW testicular cancer; sexual dysfunction; exon.
XX Homo sapiens.
OS WO2004026905-A2.
XX 01-APR-2004.
XX 17-SEP-2003; 2003WO-GB004014.
XX

PR 17-SEP-2002; 2002GB-00021567.
PR 09-JAN-2003; 2003GB-00000506.
XX (INPH-) INPHARMATICA LTD.
XX Lobley AE, Michalovich D, Pierron VN, Leake KL;
PI WPI; 2004-295386/27.
DR N-PSDB; ADL97736.
XX New transporter/channel proteins (e.g. INPIONCH07 or INPIONCH08) useful
PT as contraceptives or for diagnosing, preventing or treating diseases such
PT as heart failure, angina, obesity, renal disease, infertility or
PT testicular cancer.
XX Claim 21; SEQ ID NO 144; 133pp; English.
XX The invention relates to novel polypeptides termed INPIONCH07,
CC INPIONCH08, INPIONCH09 and INPIONCH10, which are identified as
CC transporter/channel proteins. The pharmaceutical composition is useful in
CC the therapy or diagnosis of diseases or as a contraceptive. This may also
CC be used in manufacturing a medicament for the treatment of diseases or
CC disorders such as colitis, hypertrophy, fibrosis, heart failure,
CC myocardial infarction, angina, obesity, hyperinsulinemia, vascular
CC disease, renal disease, fertility disorders, infertility, testosterone
CC deficiency, testosterone-related disorder, testicular cancer or sexual
CC dysfunction. This sequence represents the amino acid sequence encoded by
CC an exon from the INPIONCH10 gene.
XX
SQ Sequence 42 AA;
Query Match 26.9%; Score 35.5; DB 8; Length 42;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;
Matches 8; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
QY 2 KKVLETFVVKSPDAIKV 21
Db 3 QBEITHQVK-CPDCNKEI 21
RESULT 24
ABB66998
ID ABB66998 standard; protein; 43 AA.
XX
AC ABB66998;
XX
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 27786.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL11101.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions.
XX
XX Disclosure; SEQ ID NO 27786; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 43 AA;
Query Match 26.9%; Score 35.5; DB 4; Length 43;
Best Local Similarity 43.8%; Pred. No. 6.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
QY 11 VKSCPDAIK-RVFDNK 25
Db 7 LESCDDVMKWTMSNE 22
RESULT 25
AAM64295
ID AAM64295 standard; protein; 28 AA.
XX
XX AAM64295;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 36400.
DE
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX Homo sapiens.
OS
XX WO200157275-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000667.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
PT
XX Example 4; SEQ ID NO 36400; 650pp + Sequence Listing; English.
PS
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention

```
XX SQ Sequence 28 AA;
Query Match 26.5%; Score 35; DB 4; Length 28;
Best Local Similarity 45.8%; Pred. No. 4.8e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 2; Gaps 1;

QY 1 PKQDVLETFVKSCPDAIKEVFDN 24
DB 5 PKLD--EYTECSLEDTICEAATN 26

RESULT 26
AAM18282
ID AAM18282 standard; protein; 33 AA.
XX AC AAM18282;
XX DT 12-OCT-2001 (first entry)
XX DE Peptide #4716 encoded by probe for measuring cervical gene expression.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488901/53.
XX XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human cervical epithelial cells.
Claim 27; SEQ ID NO 23108; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENPs: see Aa10068-AA128459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 33 AA;

Query Match 26.5%; Score 35; DB 4; Length 33;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 6 LETFTVKSCPDAIKEVFDNK 25
DB 1 LQTTTFWLCPPYMKRKRDsk 20

RESULT 28
AAM30772
ID AAM30772 standard; protein; 33 AA.
XX AC AAM30772;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #4809 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX XX
```

```
RESULT 27
ABB37316
ID ABB37316 standard; peptide; 33 AA.
XX AC ABB37316;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #4822 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483447/52.
XX XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human fetal liver.
Claim 27; SEQ ID NO 29951; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human fetal liver. The
XX CC present sequence is a peptide encoded by a single exon nucleic acid probe
XX CC of the invention. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 33 AA;

Query Match 26.5%; Score 35; DB 4; Length 33;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 6 LETFTVKSCPDAIKEVFDNK 25
DB 1 LQTTTFWLCPPYMKRKRDsk 20

RESULT 28
AAM30772
ID AAM30772 standard; protein; 33 AA.
XX AC AAM30772;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #4809 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX XX
```



```
QY      6 LETFTVKSCPDAIKEVFNK 25
Db      1 LQTTFWLCPYMKRKRDsk 20

RESULT 33
ABG52136
ID      ABG52136 standard; peptide; 33 AA.
AC      ABG52136;
XX      25-FEB-2003 (first entry)
DT      Human liver peptide, SEQ ID No 30784.
DE      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW      hypercholesterolaemia; coronary heart disease.
XX      Homo sapiens.
XX      WO200157273-A2.
XX      09-AUG-2001.
XX      30-JAN-2001; 2001WO-US000664.
XX      04-FEB-2000; 2000US-0180312P.
XX      26-MAY-2000; 2000US-0207456P.
XX      30-JUN-2000; 2000US-00608408.
XX      03-AUG-2000; 2000US-00632366.
XX      21-SEP-2000; 2000US-0234687P.
XX      27-SEP-2000; 2000US-0236359P.
XX      04-OCT-2000; 2000GB-00024263.
XX      (MOLE-) MOLECULAR DYNAMICS INC.
XX      Penn SG, Hanzel DK, Chen W, Rank DR;
PI      WPI; 2001-48898/53.
XX      Human genome-derived single exon nucleic acid probes useful for analyzing
PT      gene expression in human adult liver.
XX      Claim 27; SEQ ID NO 30784; 658pp; English.
XX      The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC      measuring human gene expression in a sample derived from human adult
CC      liver, comprising one of 13109 defined nucleotide sequences given in the
CC      specification (or complements/ fragments). The probe hybridises at high
CC      stringency to a nucleic acid molecule expressed in the human adult liver.
CC      (i) may be used for predicting, measuring and displaying gene expression
CC      in samples derived from human adult liver. The genes identified may be
CC      involved in genetic liver diseases such as cirrhosis,
CC      hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC      associated with coronary heart disease. ABG47348-ABG59930 represent human
CC      liver single exon encoded peptides of the invention. Note: The sequence
CC      information for this patent does not appear in the printed specification
CC      but was obtained in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 33 AA;
XX      Query Match      26.5%; Score 35; DB 4; Length 33;
XX      Best Local Similarity 40.0%; Pred. No. 5.9e+02;
XX      Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      6 LETFTVKSCPDAIKEVFNK 25
Db      1 LQTTFWLCPYMKRKRDsk 20

RESULT 34
ABG52136
ID      ABG52136 standard; peptide; 33 AA.
AC      ABG40088;
XX      19-AUG-2002 (first entry)
DT      Human peptide encoded by genome-derived single exon probe SEQ ID 29753.
DE      Human peptide encoded by genome-derived single exon probe SEQ ID 29753.
```

```
AAM05895
ID      AAM05895 standard; protein; 33 AA.
AC      AAM05895;
XX      09-OCT-2001 (first entry)
DT      Peptide #4577 encoded by probe for measuring breast gene expression.
DE      Probe; human; breast disease; breast cancer; development disorder;
KW      inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX      Homo sapiens.
XX      WO200157270-A2.
XX      09-AUG-2001.
XX      29-JAN-2001; 2001WO-US000661.
XX      04-FEB-2000; 2000US-0180312P.
XX      26-MAY-2000; 2000US-0207456P.
XX      30-JUN-2000; 2000US-00608408.
XX      03-AUG-2000; 2000US-00632366.
XX      21-SEP-2000; 2000US-0234687P.
XX      27-SEP-2000; 2000US-0236359P.
XX      04-OCT-2000; 2000GB-00024263.
XX      (MOLE-) MOLECULAR DYNAMICS INC.
XX      Penn SG, Hanzel DK, Chen W, Rank DR;
PI      WPI; 2001-476286/51.
XX      Novel single exon nucleic acid probe used to measuring gene expression in
PT      a human breast.
XX      Claim 27; SEQ ID NO 14635; 322pp; English.
XX      The present invention relates to novel single exon nucleic acid probes
CC      (see AI100010-AA110067). The present sequence is a peptide encoded by one
CC      such probe. The probes are useful for measuring human gene expression in
CC      a human breast sample, where the probe hybridises at high stringency to a
CC      nucleic acid expressed in the human breast. The probes are useful for
CC      predicting, diagnosing, grading, staging, monitoring and prognosing
CC      diseases of the human breast, particularly those diseases with polygenic
CC      aetiology. The diseases include: breast cancer, disorders of development,
CC      inflammatory diseases of the breast, fibrocystic changes, proliferative
CC      breast disease and non-carcinoma tumours. Note: The sequence data for
CC      this patent did not form part of the printed specification, but was
CC      obtained in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 33 AA;
XX      Query Match      26.5%; Score 35; DB 4; Length 33;
XX      Best Local Similarity 40.0%; Pred. No. 5.9e+02;
XX      Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      6 LETFTVKSCPDAIKEVFNK 25
Db      1 LQTTFWLCPYMKRKRDsk 20

RESULT 35
ABG40088
ID      ABG40088 standard; peptide; 33 AA.
AC      ABG40088;
XX      19-AUG-2002 (first entry)
DT      Human peptide encoded by genome-derived single exon probe SEQ ID 29753.
DE      Human peptide encoded by genome-derived single exon probe SEQ ID 29753.
```

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX Homo sapiens.
XX WO200186003-A2.
XX 15-NOV-2001.
XX 30-JAN-2001; 2001WO-US000665.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX Claim 27; SEQ ID NO 29753; 634pp; English.
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of

CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 33 AA;
SQ
Query Match 26.5%; Score 35; DB 5; Length 33;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
QY 6 LETFTVKSCPDALKEVFDNK 25
DB 1 LQTTTFWLCFYVMVKRDKS 20
RESULT 36
ABB42598
ID ABB42598 standard; peptide; 38 AA.
XX AC ABB42598;
XX 04-FEB-2002 (first entry)
XX Peptide #10104 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX Claim 27; SEQ ID NO 35233; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 38 AA;
SQ
Query Match 26.5%; Score 35; DB 4; Length 38;
Best Local Similarity 37.5%; Pred. No. 7e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 10 TVKSCPDALKEVFDNK 25
DB 3 TLKGCPSSSNNMFYKK 18

RESULT 37	WO200157276-A2.
AAM36414	
ID	AAM36414 standard; protein; 38 AA.
XX	
AC	AAM36414;
XX	
DT	17-OCT-2001 (first entry)
XX	
DE	Peptide #10451 encoded by probe for measuring placental gene expression.
XX	
KW	Probe; microarray; human; placenta; antenatal diagnosis;
KW	genetic disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200157272-A2.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000663.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-48897/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing
PT	gene expression in human placenta.
XX	
PS	Claim 27; SEQ ID NO 36683; 654pp; English.
XX	
CC	The present invention relates to single exon nucleic acid probes (SENP;
CC	see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC	such probe. The probes are useful for producing a microarray for
CC	predicting, measuring and displaying gene expression in samples derived
CC	from human placenta. The probes are useful for antenatal diagnosis of
CC	human genetic disorders
XX	
SQ	Sequence 38 AA;
Query Match 26.5%; Score 35; DB 4; Length 38;	
Best Local Similarity 37.5%; Pred. No. 7e+02;	
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;	
QY	10 TVKSCPDATKEVFDNK 25
Db	3 TLKGCPSSSNNMFYK 18
: :	
: :	
RESULT 38	
AAM76304	
ID	AAM76304 standard; protein; 38 AA.
XX	
AC	AAM76304;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human bone marrow expressed probe encoded protein SEQ ID NO: 36610.
XX	
KW	Human; bone marrow expressed exon; gene expression analysis; probe;
KW	microarray; cancer; leukaemia; lymphoma; myeloma.
XX	
OS	Homo sapiens.
XX	
PN	WO200157275-A2.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000667.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-48897/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing
PT	gene expression in human placenta.
XX	
PS	Claim 27; SEQ ID NO 36683; 654pp; English.
XX	
CC	The present invention relates to single exon nucleic acid probes (SENP;
CC	see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC	such probe. The probes are useful for producing a microarray for
CC	predicting, measuring and displaying gene expression in samples derived
CC	from human placenta. The probes are useful for antenatal diagnosis of
CC	human genetic disorders
XX	
SQ	Sequence 38 AA;
Query Match 26.5%; Score 35; DB 4; Length 38;	
Best Local Similarity 37.5%; Pred. No. 7e+02;	
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;	
QY	10 TVKSCPDATKEVFDNK 25
Db	3 TLKGCPSSSNNMFYK 18
: :	
: :	
RESULT 39	
AAM63489	
ID	AAM63489 standard; protein; 38 AA.
XX	
AC	AAM63489;
XX	
DT	05-NOV-2001 (first entry)
XX	
DE	Human brain expressed single exon probe encoded protein SEQ ID NO: 35594.
XX	
KW	Human; brain expressed exon; gene expression analysis; probe; microarray;
KW	Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO200157275-A2.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000667.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-488900/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing
PT	gene expression in human bone marrow.
XX	
PS	Example 4; SEQ ID NO 36610; 658pp + Sequence Listing; English.
XX	
CC	The present invention provides a number of single exon nucleic acid
CC	probes which are derived from genomic sequences expressed in the human
CC	bone marrow. They can be used to measure gene expression in bone marrow
CC	samples, which may enable the improved diagnosis and treatment of cancers
CC	such as lymphoma, leukaemia and myeloma. The present sequence is a
CC	protein encoded by one of the probes of the invention
XX	
SQ	Sequence 38 AA;
Query Match 26.5%; Score 35; DB 4; Length 38;	
Best Local Similarity 37.5%; Pred. No. 7e+02;	
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;	
QY	10 TVKSCPDATKEVFDNK 25
Db	3 TLKGCPSSSNNMFYK 18
: :	
: :	

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
XX Example 4; SEQ ID NO 35594; 650pp + Sequence Listing; English.
XX
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 38 AA;
XX
Query Match 26.5%; Score 35; DB 4; Length 38;
Best Local Similarity 37.5%; Pred. NO. 7e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 10 TVKSCPDPAIKEVFDNK 25
Db 3 TLKGCPSSSSNMVYKK 18
XX
RESULT 40
ABG58014
ID ABG58014 standard; peptide; 38 AA.
XX
AC ABG58014;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver peptide, SEQ ID No 36662.
XX
XX Human, liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX
XX Claim 27; SEQ ID NO 36662; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 38 AA;
XX
Query Match 26.5%; Score 35; DB 4; Length 38;
Best Local Similarity 37.5%; Pred. NO. 7e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 10 TVKSCPDPAIKEVFDNK 25
Db 3 TLKGCPSSSSNMVYKK 18
XX
Search completed: January 20, 2006, 17:30:41
Job time : 65.3457 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:26:44 ; Search time 17.284 Seconds
(without alignments)
119.584 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKQVLETFVKSCPDPAKEVFNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	29	1	US-08-254-493-6
2	132	100.0	29	1	US-08-408-222B-6
3	38	28.8	30	1	US-08-193-977-11
4	36	27.3	28	1	US-08-310-912A-154
5	36	27.3	28	2	US-09-301-085-154
6	36	27.3	28	4	PCT-US95-04589-154
7	36	27.3	31	1	US-08-486-057B-38
8	36	27.3	31	1	US-08-789-588-38
9	36	27.3	32	6	5262319-9
10	36	27.3	34	2	US-09-374-958C-31
11	36	27.3	34	2	US-09-374-936-31
12	36	27.3	42	2	US-09-848-664A-14
13	35	26.5	17	2	US-08-974-549A-100
14	35	26.5	17	2	US-08-912-951-100
15	35	26.5	17	2	US-09-402-181B-100
16	35	26.5	17	2	US-09-721-456-100
17	35	26.5	26	2	US-08-851-843A-140
18	35	26.5	26	2	US-08-974-549A-258
19	35	26.5	26	2	US-08-854-050-140
20	35	26.5	26	2	US-09-430-323-140
21	35	26.5	26	2	US-09-402-181B-258
22	35	26.5	26	2	US-09-721-456-258
23	35	26.5	26	2	US-09-766-253-140
24	35	26.5	26	2	US-10-054-295-140
25	35	26.5	26	2	US-09-438-486A-140
26	35	26.5	27	2	US-08-851-843A-156
27	35	26.5	27	2	US-08-851-843A-162

28	35	26.5	27	2	US-08-974-549A-276	Sequence 276, App
29	35	26.5	27	2	US-08-974-549A-282	Sequence 282, App
30	35	26.5	27	2	US-08-854-050-156	Sequence 156, App
31	35	26.5	27	2	US-08-854-050-162	Sequence 162, App
32	35	26.5	27	2	US-09-430-323-156	Sequence 156, App
33	35	26.5	27	2	US-09-430-323-162	Sequence 162, App
34	35	26.5	27	2	US-09-402-181B-276	Sequence 276, App
35	35	26.5	27	2	US-09-402-181B-282	Sequence 282, App
36	35	26.5	27	2	US-09-721-456-276	Sequence 276, App
37	35	26.5	27	2	US-09-721-456-282	Sequence 282, App
38	35	26.5	27	2	US-09-766-253-156	Sequence 156, App
39	35	26.5	27	2	US-09-766-253-162	Sequence 162, App
40	35	26.5	27	2	US-10-054-295-156	Sequence 156, App
41	35	26.5	27	2	US-10-054-295-162	Sequence 162, App
42	35	26.5	27	2	US-09-438-486A-156	Sequence 156, App
43	35	26.5	27	2	US-09-438-486A-162	Sequence 162, App
44	35	26.5	32	2	US-09-082-358B-57	Sequence 57, Appl
45	35	26.5	34	2	US-08-974-549A-26	Sequence 26, Appl
46	35	26.5	34	2	US-08-974-549A-45	Sequence 45, Appl
47	35	26.5	34	2	US-08-912-951-26	Sequence 26, Appl
48	35	26.5	34	2	US-08-912-951-45	Sequence 45, Appl
49	35	26.5	34	2	US-09-402-181B-25	Sequence 25, Appl
50	35	26.5	34	2	US-09-402-181B-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: Koyama, Masaru
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:

```

;
; TELEPHONE: (617) 523-3400
;
; TELEFAX: (617) 523-6440
;
; TELEX: 200291 SYR UR
;
; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 29 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-254-493-6

```

```
Query Match      100.0%; Score 132; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels
```

Qy	1	P	25
D_b	5	P	29

RESULT 2
US-08-408-222B-6
; Sequence 6, Application US/08408222B
; Patent No. 5776727
; GENERAL INVENTION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masauyuki
; APPLICANT: Senco, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

```

, MIT: 02109
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: Diskette
,
, COMPUTER: IBM Compatible
,
, OPERATING SYSTEM: DOS
,
, SOFTWARE: FastSQL Version 1.5
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/408,222B
,
, FILING DATE: 22-MAR-1995
,
, CLASSIFICATION: 536
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: 08/254,493
,
, FILING DATE: 06-JUN-1994
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: JP-079996-1991
,
, FILING DATE: 12-APR-1991
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: JP-085396-1991
,
, FILING DATE: 14-APR-1991
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: JP-022321-1992
,
, FILING DATE: 07-FEB-1994
,
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Renick, David S.

```

```

? NAME: RESNICK, DAVID S.
? REGISTRATION NUMBER: 34,235
? REFERENCE/DOCKET NUMBER: 41777-DIV
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-523-3400
? TELEFAX: 617-523-6440
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 29 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?

```

US-08-408-222B-6

```
Query Match      100.0%; Score 132; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	P	25
D_b	5	P	29

RESULT 3

US-08-193-977-11
Sequence 11, Application US/08193977
Patent No. 5625031
GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193.977

FILING DATE: 08-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: ROBINS, ROBERTA L.
 REGISTRATION NUMBER: 33,208
 REFERENCE/DOCKET NUMBER: 5998-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 617-8999
 TELEFAX: (415) 327-3231
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-193-977-11

Query Match 28.8%; Score 38; DB 1; Length 30;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAIKE 20
||: ||| :|:
Db 3 FTLVHCPSDLMKD 14

RESULT 4

US-08-310-912A-154
; Sequence 134, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Kataciri, Fumiaki


```
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-310-912A-154

Query Match      27.3%; Score 36; DB 1; Length 28;
Best Local Similarity 35.0%; Pred. No. 78;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY      1 PKQVLETFVTKSCPDAIKE 20
      ||:|:|:|:|:|:|:|:|
Db      1 PKLEVIEFDCEIEBELISE 20

RESULT 5
US-09-301-085-154
; Sequence 154, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-301-085-154

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 35.0%; Pred. No. 78;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY      1 PKQVLETFVTKSCPDAIKE 20
      ||:|:|:|:|:|:|:|:|
Db      1 PKLEVIEFDCEIEBELISE 20

RESULT 6
PCT-US95-04589-154
; Sequence 154, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 201
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04589
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04589-154

Query Match      27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 35.0%; Pred. No. 78;
Matches 7; Conservative 4; Mismatches 9; Indels 9; Gaps 0;

QY      1 PKQVLETFVTKSCPDAIKE 20
      ||:|:|:|:|:|:|:|:|
Db      1 PKLEVIEFDCEIEBELISE 20
```

```
RESULT 7
US-08-486-057B-38
; Sequence 38, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-057B-38

Query Match 27.3%; Score 36; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSC 14
||:|
Db 15 PKVEQLSNMVKSC 28

RESULT 8
US-08-789-588-38
; Sequence 38, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-38

Query Match 27.3%; Score 36; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSC 14
||:|
Db 15 PKVEQLSNMVKSC 28

RESULT 9
5262319-9
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-38

Query Match 27.3%; Score 36; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSC 14
||:|
Db 15 PKVEQLSNMVKSC 28
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO: 9
; LENGTH: 32
5262319-9

Query Match      27.3%; Score 36; DB 6; Length 32;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKQVLETFVVKSC 14
DB      19 PKVEQLSNMVKSC 32

RESULT 10
US-09-374-958C-31
; Sequence 31, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Morphogenic Proteins
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-09-374-958C-31

Query Match      27.3%; Score 36; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKQVLETFVVKSC 14
DB      18 PKVEQLSNMVKSC 31

RESULT 11
US-09-374-936-31
; Sequence 31, Application US/09374936
; Patent No. 6846906
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-077
; CURRENT APPLICATION NUMBER: US/09/374,936
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO: 9
; LENGTH: 32
5262319-9

Query Match      27.3%; Score 36; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKQVLETFVVKSC 14
DB      18 PKVEQLSNMVKSC 31

RESULT 12
US-09-848-664A-14
; Sequence 14, Application US/09848664A
; Patent No. 6723344
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Elbert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664A
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US/09/298,084A
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-09-848-664A-14

Query Match      27.3%; Score 36; DB 2; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKQVLETFVVKSC 14
DB      26 PKVEQLSNMVKSC 39

RESULT 13
US-08-974-549A-100
; Sequence 100, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
```

```
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; OTHER INFORMATION: peptide from Saccharomyces
; OTHER INFORMATION: cerevisiae EST2"
US-08-974-549A-100

Query Match 26.5%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 14
US-08-912-951-100
; Sequence 100, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.

; FILING DATE: 19-NOV-1997
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; OTHER INFORMATION: peptide from Saccharomyces
; OTHER INFORMATION: cerevisiae EST2"
US-08-912-951-100

Query Match 26.5%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 15
```

US-09-402-181B-100
; Sequence 100, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-402-181B-100

Query Match 26.5%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 62;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17
RESULT 16
US-09-721-456-100
; Sequence 100, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-721-456-100

Query Match 26.5%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | |
DB 8 FDKSCYDSI 17

RESULT 17
US-08-851-843A-140
; Sequence 140, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
US-08-851-843A-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | |
DB 7 FDKSCYDSI 16

RESULT 18
US-08-974-549A-258
; Sequence 258, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
US-08-974-549A-258

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | | | |
Db 7 FDKSCYDSI 16

RESULT 19
US-08-854-050-140
Sequence 140, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
US-08-854-050-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | | | |
Db 7 FDKSCYDSI 16

RESULT 20
US-09-430-323-140
Sequence 140, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-430-323-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
DB 7 FDVKSICYDSI 16

RESULT 21
US-09-402-181B-258
Sequence 258, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-09-402-181B-258

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
DB 7 FDVKSICYDSI 16

RESULT 22
US-09-721-456-258
Sequence 258, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000

CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-09-721-456-258

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDKSCYDSI 16

RESULT 23
US-09-766-253-140
Sequence 140, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-766-253-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDKSCYDSI 16

RESULT 24
US-10-054-295-140
Sequence 140, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
FILE DESCRIPTION: SEQ ID NO: 140:
US-10-054-295-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | : |
Db 7 FDKVSCYDSI 16

RESULT 25
US-09-438-486A-140
Sequence 140, Application US/09438486A
Patent No. 6927285
GENERAL INFORMATION:
APPLICANT: CECCH, THOMAS R.
APPLICANT: LINGNER, JOACHIM
APPLICANT: NAKAMURA, TORU
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: MORIN, GREGG B.
APPLICANT: HARLEY, CALVIN
APPLICANT: ANDREWS, WILLIAM H.
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/851,843
PRIOR FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 223
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 140

LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant
US-09-438-486A-140

Query Match 26.5%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | : |
Db 7 FDKVSCYDSI 16

RESULT 26
US-08-851-843A-156
Sequence 156, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

```
;
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Schizosaccharomyces pombe tez1"
; US-08-851-843A-156

Query Match      26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. NO. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KDVLETFVTKSCPDALKE 20
Db 1 RKKYFVRIDIKSCYDRIKQ 19

RESULT 27
US-08-851-843A-162
; Sequence 162, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
```

```
;
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
; US-08-851-843A-162

Query Match      26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. NO. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 28
US-08-974-549A-276
; Sequence 276, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Schizosaccharomyces pombe tez1"
US-08-974-549A-276

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSCPDAIKE 20
Db 1 RKKYFVRIDIKSCYDRIKQ 19

RESULT 29
US-08-974-549A-282
; Sequence 282, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
```

```
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-974-549A-282

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18
Db 8 FDKSCYDSI 17

RESULT 30
US-08-854-050-156
; Sequence 156, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Schizosaccharomyces pombe tezl"
US-08-854-050-156

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KDVLETFTVKSCPDALKE 20
Db 1 RKKYFVRIDIKSCVDRIKQ 19

RESULT 31
US-08-854-050-162
Sequence 162, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"
US-08-854-050-162

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17

RESULT 32
US-09-430-323-156
Sequence 156, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from Schizosaccharomyces pombe te21"
SEQUENCE DESCRIPTION: SEQ ID NO: 156:
US-09-430-323-156
Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
QY 2 KKVLETFVTKSCPDAIKE 20
DB 1 RKKYFVRIDIKSCYDIKQ 19
RESULT 33
US-09-430-323-162
Sequence 162, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California

COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-430-323-162
Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAI 18
DB 8 FDKSCYDSI 17
RESULT 34
US-09-402-181B-276
Sequence 276, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

```
;
;
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Schizosaccharomyces pombe tezi"
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-09-402-181B-276
Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
QY 2 KQDVLETFVKSCPDAIKE 20
Db 1 RKXVFVRIDIKSCVDRIKQ 19
RESULT 35
US-09-402-181B-282
; Sequence 282, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
```

```
;
;
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-09-402-181B-282
Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17
RESULT 36
US-09-721-456-276
; Sequence 276, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
```



```

; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-09-721-456-282

```

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels

Qy	9	F	T	V	K	S	C	P	D	A	I	18
									:			
Db	8	F	D	V	K	S	C	Y	D	S	I	17

RESULT 38
US-09-766-253-156
; Sequence 156, Application US/09766253
; Patent No. 680880
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 680880e1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029200S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

```

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Schizosaccharomyces pombe test1"
SEQUENCE DESCRIPTION: SEQ ID NO: 156:
US-09-766-253-156

```

```

Query Match      26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 9; Indels

QY 2 KKDVLFTFTVKSPDAIKE 20
   : ||| | :
Db 1 RKKYFVRIDIKSCYDRIKO 19

```

RESULT 39
US-09-766-253-162
; Sequence 162, Application US/09766253
; Patent No. 6808880

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MC-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/766,253
? FILING DATE: 19-Jan-2001
? CLASSIFICATION: <Unknown>
?
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-00292005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 162:

```

;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 27 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: <Unknown>
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; FEATURE:
;
; NAME/KEY: Peptide
;
; LOCATION: 1..27
;
; OTHER INFORMATION: /note="motif A peptide from
;
; Saccharomyces cerevisiae EST2"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-766-253-162

```

Query Match 26.5%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7: Conservative 1; Mismatches 2; Indels

Qy 9 FTVKSCPAI 18
| | | | | : |
Db 8 FDKSCYDSI 17

Job time : 18.284 secs

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:27:09 ; Search time 47.8395 Seconds
(without alignments)
218.350 Million cell updates/sec

Title: US-10-619-323-5
Perfect score: 132
Sequence: 1 PKKDVLETFVKSCPDPAKEVFDNK 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	25	4	US-10-619-323-5
2	95	72.0	18	4	US-10-619-323-6
3	61	46.2	30	5	US-10-473-127-1717
4	49	37.1	10	5	US-10-473-127-165
5	39.5	29.9	50	4	US-10-425-115-244355
6	39	29.5	41	4	US-10-074-024-386
7	39	29.5	49	4	US-10-424-599-278211
8	39	29.5	50	4	US-10-424-599-165124
9	38.5	29.2	40	4	US-10-424-599-162982
10	38.5	29.2	50	4	US-10-437-963-136536
11	38	28.8	43	4	US-10-425-115-193153
12	38	28.8	46	5	US-10-809-761-18
13	37	28.0	46	4	US-10-437-963-170639
14	36	27.3	28	3	US-09-867-852-154
15	36	27.3	28	4	US-10-613-472-154
16	36	27.3	28	4	US-10-613-765-154
17	36	27.3	33	3	US-09-864-761-43932
18	36	27.3	42	3	US-09-848-664-14
19	36	27.3	46	4	US-10-724-972A-5875
20	35.5	26.9	41	3	US-09-864-761-46252
21	35.5	26.9	42	4	US-10-425-115-209264
22	35.5	26.9	43	6	US-11-097-143-27786
23	35	26.5	17	4	US-10-044-692-100
24	35	26.5	17	4	US-10-044-539-100
25	35	26.5	17	4	US-10-325-810-100
26	35	26.5	17	5	US-10-877-124-100
27	35	26.5	17	5	US-10-877-022-100

ALIGNMENTS

RESULT 1

US-10-619-323-5
; Sequence 5, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-5

Query Match 100.0%; Score 132; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDPAKEVFDNK 25

Db 1 PKKDVLETFVKSCPDPAKEVFDNK 25

RESULT 2

US-10-619-323-6
; Sequence 6, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.

```
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Cressno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-6

Query Match 72.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSQDAI 18
Db 1 PKKDVLFTFTVKSQDAI 18
|||||

RESULT 3
US-10-473-127-1717
; Sequence 1717, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1717
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1717

Query Match 46.2%; Score 61; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVK 12
Db 19 PKKDVLFTFTVK 30
|||||

RESULT 4
US-10-473-127-165
; Sequence 165, Application US/10473127
```

```
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-165

Query Match 37.1%; Score 49; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDVLETFTVK 12
Db 1 KDVLETFTVK 10
|||||

RESULT 5
US-10-425-115-244355
; Sequence 244355, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 244355
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_154437C.1.pep
US-10-425-115-244355

Query Match 29.9%; Score 39.5; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 8 TFTVKS-CPDAIKYFDN 24
Db 26 TFMRLTDLDPAMKEAFIN 43
|||||

RESULT 6
US-10-074-024-386
; Sequence 386, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
```

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC001C1
CURRENT APPLICATION NUMBER: US/10/074,024
CURRENT FILING DATE: 2002-02-14
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 879
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 386
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
US-10-074-024-386

Query Match 29.5%; Score 39; DB 4; Length 41;
Best Local Similarity 28.6%; Pred. No. 2e+02;
Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKSCPDPAIKEV 21
| : : | : : | : :
Db 5 PHREIFYFFTLRPADPVSKHL 25

RESULT 7
US-10-424-599-278211
Sequence 278211, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 278211
LENGTH: 49
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(49)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_93248C.1.pap
US-10-424-599-278211

Query Match 29.5%; Score 39; DB 4; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 ETFVTKSCPDPA 17
| : : | : : | : :
Db 9 ETFDVEGCPTA 19

RESULT 8
US-10-424-599-165124
Sequence 165124, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165124
LENGTH: 50
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_120122C.1.pap
US-10-424-599-165124

Query Match 29.5%; Score 39; DB 4; Length 50;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCPDPA 17
| : : | : : | : :
Db 36 LESKTLKTCPSA 47

RESULT 9
US-10-424-599-162982
Sequence 162982, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 162982
LENGTH: 40
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_118190C.1.pap
US-10-424-599-162982

Query Match 29.2%; Score 38.5; DB 4; Length 40;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 6 LETFTVKSC-PDAIKE 20
| : : | : : | : :
Db 15 LASLAVKSCPPQALKE 30

RESULT 10
US-10-437-963-136536
Sequence 136536, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 136536
LENGTH: 50
TYPE: PRT
ORGANISM: Oryza sativa

Matches 7; **Conservative** 4; **Mismatches** 9; **Indels** 0; **Gaps** 0;

Qy 1 PKKDVLFTFTVKSCPDAlKE 20
||:|:|:|:|:|:|
Db 1 PKLEVIelfDCREIEELISE 20

RESULT 15

```

US-10-613-472-154
; Sequence 154, Application US/10613472
; Publication No. US20040088756A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254004
; CURRENT APPLICATION NUMBER: US/10/613,472
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-472-154

```

Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 35.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 4; Mismatches 9; Indels

Qy 1 P K K D V L E T F T V K S C P D A I K E 20
 || : | : | : |
D b 1 P K L E V I E L F D C R E I E E L I S E 20

RESULT 16

```

US-10-613-765-154
; Sequence 154, Application US/10613765
; Publication No. US20040172673A1
; GENERAL INFORMATION:
; APPLICANT: AUSUBEL, FREDERICK M.
; APPLICANT: STASKAWICZ, BRIAN J.
; APPLICANT: KATAGIRI, FUMIAKI
; APPLICANT: KUNKEL, BARBARA N.
; APPLICANT: MINDRINOS, MICHAEL N.
; APPLICANT: YU, GUO-LIANG
; APPLICANT: BAKER, BARBARA
; APPLICANT: ELLIS, JEFFREY
; APPLICANT: SALMERON, JOHN
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254005
; CURRENT APPLICATION NUMBER: US/10/613,765
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28

```

```
; SEQ ID NO 43932
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005586.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.81
US-09-864-761-43932

Query Match      27.3%; Score 36; DB 3; Length 33;
Best Local Similarity 36.8%; Pred. No. 4.4e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 DVLETFVTKSCPDAIKEVF 22
Db 3 NMLSTASITWLPGLKEVF 21

RESULT 18
US-09-848-664-14
; Sequence 14, Application US/09848664
; Patent No. US20020146414A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Elbert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/298,084
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664-14

Query Match      27.3%; Score 36; DB 3; Length 42;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKDVLETFVTKSC 14
Db 26 PKVEQLSNMVKSC 39

RESULT 19
US-10-724-972A-5875
; Sequence 5875, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
```

```
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 5875
; LENGTH: 46
; TYPE: PRT
; ORGANISM: S.epidermidis
US-10-724-972A-5875

Query Match      27.3%; Score 36; DB 4; Length 46;
Best Local Similarity 35.3%; Pred. No. 6.5e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXDVLETFVTKSCPDAI 18
Db 4 KEDMNTYRLKECDIL 20

RESULT 20
US-09-864-761-46252
; Sequence 46252, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aewmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46252
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
```


;
; FEATURE:
; OTHER INFORMATION: MAP TO AC023154.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 62
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EST HUMAN HIT: T56807.1, EVALUATE 4.80e-01
; OTHER INFORMATION: SWISSPROT HIT: P17980, EVALUATE 1.90e-01
US-09-864-761-46252

Query Match 26.9%; Score 35.5; DB 3; Length 41;
Best Local Similarity 42.9%; Pred. No. 6.8e+02;
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 PKDVLTP-TVKSCPDPAIKE 20
||:|||||:|:|:|:
Db 19 PKEDHLEGFLEVOAKKEAVKD 39

RESULT 21
US-10-425-115-209264
; Sequence 209264, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 209264
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_122443C.1.pep
US-10-425-115-209264

Query Match 26.9%; Score 35.5; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 6 LETFTVKSCPDPAIKEVFD 23
|||:|:|:|:|:|:
Db 17 LETWLYYCKEA-KEKFD 33

RESULT 22
US-11-097-143-27786
; Sequence 27786, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693

;
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27786
; LENGTH: 43
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-27786

Query Match 26.9%; Score 35.5; DB 6; Length 43;
Best Local Similarity 43.8%; Pred. No. 7.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 11 VKSCPDPAIK-EVFDNK 25
:|||||:|:|:
Db 7 LKSCPDVWKWETMSNE 22

RESULT 23
US-10-044-692-100
; Sequence 100, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Hazley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

```
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..17
;     OTHER INFORMATION: /note= "telomerase RT finger motif A
;     peptide from Saccharomyces
;     cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-692-100

Query Match      26.5%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 24
US-10-044-539-100
; Sequence 100, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin
;   Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;   THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94111
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/044,539
;   FILING DATE: 11-Jan-2002
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/912,951
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..17
;     OTHER INFORMATION: /note= "telomerase RT finger motif A
;     peptide from Saccharomyces
;     cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-539-100

Query Match      26.5%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 25
US-10-325-810-100
; Sequence 100, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/325,810
;   FILING DATE: 20-Dec-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/402,181
;   FILING DATE: 29-Sep-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
```

APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-325-810-100
Query Match 26.5%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
| | | | | | | | | | | | | | | | | | | | | |
DB 8 FDKSCYDSI 17
RESULT 26
US-10-877-124-100
Sequence 100, Application US/10877124
Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-124-100
Query Match 26.5%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
| | | | | | | | | | | | | | | | | | | | | |
DB 8 FDKSCYDSI 17
RESULT 27
US-10-877-022-100
Sequence 100, Application US/10877022
Publication No. US20040247613A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-022-100

Query Match 26.5%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 28
US-10-877-146-100
Sequence 100, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.

Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-146-100

Query Match 26.5%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

```
RESULT 29
US-09-843-676-140
; Sequence 140, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Morin, Gregg B.
;               Harley, Calvin
;               Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
;               Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-843-676-140

Query Match      26.5%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 FTVKSCPDAl 18
      ||||| |
Db      7 FDVKSCYDSI 16

RESULT 30
US-09-843-676-140
; Sequence 140, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
;               Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-843-676-140

Query Match      26.5%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 FTVKSCPDAl 18
      ||||| |
Db      7 FDVKSCYDSI 16

RESULT 31
US-09-438-486-140
; Sequence 140, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
;               Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-766-253-140

Query Match      26.5%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 FTVKSCPDAl 18
      ||||| |
Db      7 FDVKSCYDSI 16

RESULT 31
US-09-438-486-140
; Sequence 140, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
```

APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"

Query Match 26.5%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | |
Db 7 FDVKSCYDSI 16

RESULT 32
US-10-053-758-140
; Sequence 140, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"

SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-053-758-140

Query Match 26.5%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | |
Db 7 FDVKSCYDSI 16

RESULT 33
US-10-054-295-140
; Sequence 140, Application US/10054295
; Publication No. US2003004953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim

;/ Nakamura, Toru
;/ Chapman, Karen B.
;/ Morin, Gregg B.
;/ Harley, Calvin
;/ Andrews, William H.
;/ TITLE OF INVENTION: No. US20030044953alel Telomerase
;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/10/054,295
;/ FILING DATE: 18-Jan-2002
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/854,050
;/ FILING DATE: <Unknown>
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 140:
;/ LENGTH: 26 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FEATURE:
;/ NAME/KEY: Peptide
;/ LOCATION: 1..26
;/ OTHER INFORMATION: /note= "motif 3(A) peptide from
;/ Saccharomyces cerevisiae EST2p"
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:
;/ US-10-054-295-140

Query Match 26.5%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDVKSVDSI 16

RESULT 34
US-10-054-611-140
;/ Sequence 140, Application US/10054611
;/ Publication No. US20030059787A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cech, Thomas R.
;/ Lingner, Joachim
;/ Nakamura, Toru
;/ Chapman, Karen B.
;/ Morin, Gregg B.

;/ Harley, Calvin
;/ Andrews, William H.
;/ TITLE OF INVENTION: No. US20030059787Alel Telomerase
;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/10/054,611
;/ FILING DATE: 18-Jan-2002
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/854,050
;/ FILING DATE: <Unknown>
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 140:
;/ LENGTH: 26 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FEATURE:
;/ NAME/KEY: Peptide
;/ LOCATION: 1..26
;/ OTHER INFORMATION: /note= "motif 3(A) peptide from
;/ Saccharomyces cerevisiae EST2p"
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:
;/ US-10-054-611-140

Query Match 26.5%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 7 FDVKSVDSI 16

RESULT 35
US-10-325-810-258
;/ Sequence 258, Application US/10325810
;/ Publication No. US20030204069A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cech, Thomas R.
;/ Lingner, Joachim
;/ Nakamura, Toru
;/ Chapman, Karen B.
;/ Morin, Gregg B.
;/ Harley, Calvin B.
;/ Andrews, William H.
;/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit

```

;
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausehus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-325-810-258

Query Match 26.5%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18
Db 7 FDKVSCYDSI 16

RESULT 36
US-10-877-124-258
; Sequence 258, Application US/10877124
; Publication No. US20040242529A1

;
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-877-124-258

Query Match 26.5%; Score 35; DB 5; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
;

```



```
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 9 FTVKSCPDAl 18
| | | | | | |
Db 7 FDKSCYDSI 16

RESULT 37
US-10-877-022-258
; Sequence 258, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 9 FTVKSCPDAl 18
| | | | | | |
Db 7 FDKSCYDSI 16

Query Match 26.5%; Score 35; DB 5; Length 26;
Best Local Similarity 70.0%; Pred. NO. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
US-10-877-022-258
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
; Saccharomyces cerevisiae EST2p
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; LOCATION: 1..26
; NAME/KEY: Peptide
; FEATURE:
; MOLECULE TYPE: peptide
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
```

/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 258:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..26
/ OTHER INFORMATION: /note= "motif 3(A) peptide from
/ Saccharomyces cerevisiae EST2p"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-877-146-258

Query Match 26.5%; Score 35; DB 5; Length 26;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 7 FDKSCYDSI 16

RESULT 39
US-09-843-676-156
; Sequence 156, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 156:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..27
/ OTHER INFORMATION: /note= "motif A peptide from
/ Schizosaccharomyces pombe tez1"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 156:
US-09-843-676-156

Query Match 26.5%; Score 35; DB 3; Length 27;
Best Local Similarity 36.8%; Pred. No. 5e+02;
Matches 7; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KQVLETFVKSQDAIKE 20
Db 1 RKKYFVRIDIKSCYDRIKQ 19

RESULT 40
US-09-843-676-162
; Sequence 162, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-843-676-162

```

```

Query Match      26.5% Score 35; DB 3; Length 27;
Best Local Similarity 70.0%; Pred. No. 5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 9 FTVKSCPDAI 18
   | | | | |
Db 8 FDVKSCYDSI 17

```

Search completed: January 20, 2006, 17:38:19
Job time : 48.8395 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:30:50 ; Search time 4.32099 Seconds
(without alignments)
58.632 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKQVLETFVTKSPDAKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 41278

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	27.3	34	6	US-10-816-768-31
2	34	25.8	34	6	US-10-816-768-30
3	34	25.8	37	6	US-10-957-351-6
4	33	25.0	43	6	US-10-952-535A-39
5	32	24.2	32	6	US-10-957-351-196
6	32	24.2	34	6	US-10-816-768-29
7	32	24.2	35	6	US-10-957-351-34
8	32	24.2	35	6	US-10-957-351-195
9	31	23.5	35	6	US-10-957-351-112
10	31	23.5	38	6	US-10-957-351-32
11	31	23.5	38	7	US-11-093-118-6
12	31	23.5	44	6	US-10-986-501-356
13	30	22.7	30	6	US-10-467-657-6336
14	30	22.7	33	6	US-10-957-351-183
15	29.5	22.3	33	6	US-10-504-879-63
16	29.5	22.3	33	7	US-11-121-301-50
17	29.5	22.3	48	6	US-10-504-879-62
18	29	22.0	38	6	US-10-957-351-155
19	29	22.0	47	6	US-11-123-896-453
20	28	21.2	19	6	US-10-503-575-243
21	28	21.2	20	7	US-11-022-562-157
22	28	21.2	20	7	US-11-022-562-158
23	28	21.2	24	7	US-11-006-119-30
24	28	21.2	24	7	US-11-033-116-4
25	28	21.2	34	7	US-11-033-116-6

26	28	21.2	35	6	US-10-957-351-329	Sequence 329, App
27	28	21.2	44	6	US-10-467-657-1118	Sequence 1118, App
28	28	21.2	44	6	US-10-957-887B-278	Sequence 278, App
29	28	21.2	46	6	US-10-957-887B-258	Sequence 258, App
30	27	20.5	9	6	US-10-859-643-2	Sequence 2, Appli
31	27	20.5	9	6	US-10-859-643-254	Sequence 254, App
32	27	20.5	9	6	US-10-859-643-690	Sequence 690, App
33	27	20.5	9	7	US-11-097-864-2	Sequence 2, Appli
34	27	20.5	9	7	US-11-097-864-254	Sequence 254, App
35	27	20.5	9	7	US-11-097-864-690	Sequence 690, App
36	27	20.5	9	7	US-11-097-912-2	Sequence 2, Appli
37	27	20.5	9	7	US-11-097-912-254	Sequence 254, App
38	27	20.5	9	7	US-11-097-912-690	Sequence 690, App
39	27	20.5	10	6	US-10-859-643-350	Sequence 350, App
40	27	20.5	10	7	US-11-097-864-350	Sequence 350, App
41	27	20.5	10	7	US-11-097-912-350	Sequence 350, App
42	27	20.5	15	7	US-11-019-894A-28	Sequence 28, Appl
43	27	20.5	16	7	US-11-060-646-10	Sequence 10, Appl
44	27	20.5	17	6	US-10-723-207-72	Sequence 72, Appl
45	27	20.5	19	6	US-10-503-575-192	Sequence 192, App
46	27	20.5	21	6	US-10-467-657-3848	Sequence 3848, App
47	27	20.5	30	6	US-10-467-657-5752	Sequence 5752, App
48	27	20.5	33	6	US-10-821-234-995	Sequence 995, App
49	27	20.5	35	6	US-10-467-657-7362	Sequence 7362, App
50	27	20.5	35	6	US-10-467-657-8218	Sequence 8218, App

ALIGNMENTS

RESULT 1
US-10-816-768-31
; Sequence 31, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-10-816-768-31

Query Match 27.3%; Score 36; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSC 14
|||:|
DB 18 PKVEQLSNMVKSC 31

RESULT 2
US-10-816-768-30
; Sequence 30, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02

```
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-10-816-768-30

Query Match      25.8%; Score 34; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQDVLETFVSK 14
   |||:|:|
Db 18 PKIEQLSNMIVKSC 31

RESULT 3
US-10-957-351-6
; Sequence 6, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-6

Query Match      25.8%; Score 34; DB 6; Length 37;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 KSCPDPAIKE 20
   |||||
Db 26 KSCPDGADE 34

RESULT 4
US-10-952-535A-39
; Sequence 39, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 43
; TYPE: PRT

; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-10-816-768-30

Query Match      25.0%; Score 33; DB 6; Length 43;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 KQDVLETFVSKCPDAIKEVF 22
   |||:|:|
Db 1 KKEYVELYTWRIIVDRVQEQF 21

RESULT 5
US-10-957-351-196
; Sequence 196, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-196

Query Match      24.2%; Score 32; DB 6; Length 32;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 VKSCPDPAIKE 20
   |||||
Db 20 VKDCPGLDE 29

RESULT 6
US-10-816-768-29
; Sequence 29, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 29
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Betal
US-10-816-768-29

Query Match      24.2%; Score 32; DB 6; Length 34;
Best Local Similarity 42.9%; Pred. No. 61;
```

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PKDVLFTFTVKSC 14
|| : | : ||
Db 18 PKVEQLSNMIVRSC 31

RESULT 7
US-10-957-351-34
; Sequence 34, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-34

Query Match 24.2%; Score 32; DB 6; Length 35;
Best Local Similarity 46.7%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 6 LETFTVKSCPDATKE 20
|| : || : ||
Db 18 LECDDTPNCPDASDE 32

RESULT 8
US-10-957-351-195
; Sequence 195, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-195

Query Match 24.2%; Score 32; DB 6; Length 35;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 11 VKSCPDATKEVP 22
|| : || : ||
Db 23 VQCCPDGSDSEDF 34

RESULT 9
US-10-957-351-112
; Sequence 112, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-112

Query Match 23.5%; Score 31; DB 6; Length 35;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 11 VKSCPDATKE 20
|| : || : ||
Db 23 VRDCPDGADSE 32

RESULT 10
US-10-957-351-32
; Sequence 32, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-32

Query Match 23.5%; Score 31; DB 6; Length 38;
Best Local Similarity 53.8%; Pred. No. 98;
Matches 7; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 13 SCPDAIKEVFDNK 25
|| : || : ||
Db 26 NCPDGSDE--DNK 36

RESULT 11
US-11-093-118-6
; Sequence 6, Application US/11093118

```

; Publication No. US2006000820A1
;
; GENERAL INFORMATION:
; APPLICANT: Theodore M. Klein
; APPLICANT: Zude Weng
; APPLICANT: Rebecca E. Cahoon
; APPLICANT: Karlene H. Bueller
; TITLE OF INVENTION: Cell Cycle Genes In Plants
; FILE REFERENCE: BB1345
; CURRENT APPLICATION NUMBER: US/11/093,118
; CURRENT FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US/09/958,110
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/128,192
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Glycine max
; US-11-093-118-6

```

Query Match 23.5%; Score 31; DB 7; Length 38;
Best Local Similarity 35.0%; Pred. No. 98;
Matches 7; Conservative 5; Mismatches 8; Indels

Qy 2 KKDVLFTFTVKSCPDAIKEV 21
:|:|:|:|:|:|:|:|
Db 6 EKDIQRFQDKYNYDIVKDV 25

```

RESULT 12
US-10-986-501-356
; Sequence 356, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19

```

Query Match 23.5%; Score 31; DB 6; Length 44;
Best Local Similarity 35.7%; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 5; Indels

Qy	6	LETFTVKSCPDAIK	19
		:::	:::
Db	28	IOTRTAVSCVDGR	41

```

RESULT 13
US-10-467-657-6336
; Sequence 6336, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6336
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6336

```

Query Match 22.7%; Score 30; DB 6; Length 30;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy	9	FTVKSCPD	AIKEVF	22
	:	:	:	:
Db	17	YSVLKLPD	TTKVVF	30

```

RESULT 14
US-10-957-351-183
; Sequence 183, Application US/10957351
; Publication No. US2006008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Sacyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 183
; LENGTH: 38
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-183

```

Query Match	22.7%	Score 30;	DB 6;	Length 38;
Best Local Similarity	50.0%;	Pred. No. 1.4e+02;		
Matches 5; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	11	VKSCPD	AIKE	20
		:		
Db	24	VRQCPD	GSDE	33


```
RESULT 15
US-10-504-879-63
; Sequence 63, Application US/10504879
; Publication No. US20060008801A1
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, Kouji et al.
; TITLE OF INVENTION: MOLECULE ASSOCIATING WITH INTRACELLULAR C-TERMINAL DOMAIN OF RECH
; FILE REFERENCE: 1752-0167PUS1
; CURRENT APPLICATION NUMBER: US/10/504,879
; CURRENT FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: PCT/JP03/01699
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-504-879-63

Query Match      22.3%; Score 29.5; DB 6; Length 33;
Best Local Similarity 31.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY      2 KKVLETFVTKSCPDAIKEVFD 23
Db      13 RKHITKRF-CKQCPVFYRETVD 33

RESULT 16
US-11-121-301-50
; Sequence 50, Application US/11121301
; Publication No. US20050277176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USD1
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-121-301-50

Query Match      22.3%; Score 29.5; DB 7; Length 33;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      7 ETFTVKSCPD 17
Db      18 ETF-MHLCPD 27

RESULT 17
US-10-504-879-62
; Sequence 62, Application US/10504879
; Publication No. US20060008801A1
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, Kouji et al.
; TITLE OF INVENTION: MOLECULE ASSOCIATING WITH INTRACELLULAR C-TERMINAL DOMAIN OF RECH
; FILE REFERENCE: 1752-0167PUS1
; CURRENT APPLICATION NUMBER: US/10/504,879
; CURRENT FILING DATE: 2004-08-17
```

```
; PRIOR APPLICATION NUMBER: PCT/JP03/01699
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-504-879-62

Query Match      22.3%; Score 29.5; DB 6; Length 48;
Best Local Similarity 31.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY      2 KKVLETFVTKSCPDAIKEVFD 23
Db      13 RKHITKRF-CKQCPVFYRETVD 33

RESULT 18
US-10-957-351-155
; Sequence 155, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satval, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 155
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-155

Query Match      22.0%; Score 29; DB 6; Length 38;
Best Local Similarity 55.8%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      12 KSCPDAIKE 20
Db      26 KDCPDGSD 34

RESULT 19
US-11-123-496-453
; Sequence 453, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McOutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
```



```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N-terminal 28.7
; OTHER INFORMATION: kDa fragment of fibronectin Chagas disease
; OTHER INFORMATION: biomarker tryptic digest fragment peptide
US-11-006-119-30

Query Match      21.2%; Score 28; DB 7; Length 24;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY  9 FTVKSCPDAIKEYVD 23
Db   2 FNCESKPEABETCFD 16

RESULT 24
US-11-033-116-4
; Sequence 4, Application US/11033116
; Publication No. US20050288224A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Yoshimitsu et al.
; TITLE OF INVENTION: A NOVEL PROTEIN, A GENE CODING THEREFOR AND A METHOD OF USING THE
; FILE REFERENCE: 0230-0157P
; CURRENT APPLICATION NUMBER: US/11/033,116
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US/05/856,327
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Lyophyllum shimeji
US-11-033-116-4

Query Match      21.2%; Score 28; DB 7; Length 24;
Best Local Similarity 27.8%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY  3 KQVLEFTFKSCPDAYKE 20
Db   4 ESIRHTLVLSRLQDAYKD 21

RESULT 25
US-11-033-116-6
; Sequence 6, Application US/11033116
; Publication No. US20050288224A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Yoshimitsu et al.
; TITLE OF INVENTION: A NOVEL PROTEIN, A GENE CODING THEREFOR AND A METHOD OF USING THE
; FILE REFERENCE: 0230-0157P
; CURRENT APPLICATION NUMBER: US/11/033,116
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US/05/856,327
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Lyophyllum shimeji
US-11-033-116-6

Query Match      21.2%; Score 28; DB 7; Length 34;
Best Local Similarity 27.8%; Pred. No. 2.5e+02;
Matches 5; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY  3 KQVLEFTFKSCPDAYKE 20
Db  14 ESIRHTLVLSRLQDAYKD 31
```

```
RESULT 26
US-10-957-351-329
; Sequence 329, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlioth, D. Victor
; APPLICANT: Satval, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 329
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DH3/2 selected clone 2
US-10-957-351-329

Query Match      21.2%; Score 28; DB 6; Length 35;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  11 VKSCPDIAKEV 21
Db  23 VGDCPDSDSEV 33

RESULT 27
US-10-467-657-1118
; Sequence 1118, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1118
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1118

Query Match      21.2%; Score 28; DB 6; Length 44;
Best Local Similarity 38.9%; Pred. No. 3.4e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY  1 PKQVLEFTFKS--CPD 16
Db  25 PRLAVLSVLAAASRCPD 42

RESULT 28
US-10-957-887B-278
; Sequence 278, Application US/10957887B
; Publication No. US20050272677A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Friesen, Robert H. E.
/ APPLICANT: Leenhouts, Cornelius J.
/ APPLICANT: Hektor, Harm
/ APPLICANT: van Esch, Johannes H.
/ APPLICANT: Heeres, Andre
/ TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
/ FILE REFERENCE: 2183-6668US
/ CURRENT APPLICATION NUMBER: US/10/957,887B
/ PRIOR FILING DATE: 2004-10-04
/ PRIOR APPLICATION NUMBER: PCT/NL/00256
/ NUMBER OF SEQ ID NOS: 309
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 278
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Sinorhizobium meliloti
US-10-957-887B-278

Query Match      21.2%; Score 28; DB 6; Length 44;
Best Local Similarity 38.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 PKQVLETFVK 13
Db      19 PEKEILKANGLKS 31

RESULT 29
US-10-957-887B-258
/ Sequence 258, Application US/10957887B
/ Publication No. US2005027267A1
/ GENERAL INFORMATION:
/ APPLICANT: Friesen, Robert H. E.
/ APPLICANT: Leenhouts, Cornelius J.
/ APPLICANT: Hektor, Harm
/ APPLICANT: van Esch, Johannes H.
/ APPLICANT: Heeres, Andre
/ TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
/ FILE REFERENCE: 2183-6668US
/ CURRENT APPLICATION NUMBER: US/10/957,887B
/ CURRENT FILING DATE: 2004-10-04
/ PRIOR APPLICATION NUMBER: PCT/NL/00256
/ PRIOR FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 309
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 258
/ LENGTH: 46
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-957-887B-258

Query Match      21.2%; Score 28; DB 6; Length 46;
Best Local Similarity 41.2%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      3 KDVLETFVKSCPD 19
Db      22 KDILNPRVANPDIK 38

RESULT 30
US-10-859-643-2
/ Sequence 2, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-2

Query Match      20.5%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
Db      2 VESCP 7

RESULT 31
US-10-859-643-254
/ Sequence 254, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 254
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-254

Query Match      20.5%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKSCPD 16
Db      2 VESCP 7

RESULT 32
US-10-859-643-690
/ Sequence 690, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Eid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
```

; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE OF INVENTION: Cancer
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-690

Query Match 20.5%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 33

US-11-097-864-2
; Sequence 2, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-2

Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 34

US-11-097-864-254
; Sequence 254, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-254

Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 35

US-11-097-864-690
; Sequence 690, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-690

Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 36

US-11-097-912-2
; Sequence 2, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-2

Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 37
US-11-097-912-254
; Sequence 254, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-254

Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 38
US-11-097-912-690
; Sequence 690, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-690

Query Match 20.5%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 39
US-10-859-643-350
; Sequence 350, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-350

Query Match 20.5%; Score 27; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 3 VESCP 8

RESULT 40
US-11-097-864-350
; Sequence 350, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick

```

; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-350

```

```

Query Match      20.5%; Score 27; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VKSCPD 16
        |::|||:
Db       3 VESCP 8

```

Search completed: January 20, 2006, 17:38:43
Job time : 4.32099 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:23:49 ; Search time 9.25926 Seconds
(without alignments)
259.785 Million cell updates/sec

Title: US-10-619-323-5
Perfect score: 132
Sequence: 1 PKKDVLFTVKSQDAIKEVFDNK 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	34.1	25	2	PC4445
2	35	26.5	43	2	S30362
3	34	25.8	15	2	S03353
4	33	25.0	29	2	B84144
5	33	25.0	30	2	S55462
6	33	25.0	41	2	G72312
7	33	25.0	44	2	AD1753
8	33	25.0	49	2	JQ1600
9	32.5	24.6	50	2	H70224
10	32	24.2	49	2	S72793
11	31.5	23.9	47	2	E97894
12	31	23.5	21	2	B33600
13	31	23.5	38	2	S12409
14	31	23.5	50	2	AB0925
15	30.5	23.1	48	2	A38882
16	30	22.7	31	2	B60507
17	30	22.7	35	2	T15602
18	30	22.7	42	2	D22102
19	30	22.7	44	2	E85849
20	30	22.7	48	2	G89944
21	30	22.7	50	2	A81546
22	29	22.0	12	2	A61309
23	29	22.0	25	2	S30361
24	29	22.0	28	2	A60698
25	29	22.0	32	2	S11610
26	29	22.0	34	2	S42051
27	29	22.0	34	2	E49754
28	29	22.0	34	2	F95187
29	28.5	21.6	28	2	A23691

30	28.5	21.6	36	1	WISMAA
31	28.5	21.6	44	2	S32316
32	28.5	21.6	44	2	E85938
33	28	21.2	17	2	S09507
34	28	21.2	30	2	A27375
35	28	21.2	33	2	A60507
36	28	21.2	33	2	A60601
37	28	21.2	34	2	S42050
38	28	21.2	34	2	G95151
39	28	21.2	34	2	B97082
40	28	21.2	38	2	I70022
41	28	21.2	42	2	T07581
42	28	21.2	43	2	A34071
43	28	21.2	44	2	T07537
44	28	21.2	45	2	S36709
45	28	21.2	46	2	H71262
46	28	21.2	48	2	A32457
47	28	21.2	48	2	H64322
48	28	21.2	49	2	T07580
49	28	21.2	50	2	I39746
50	27.5	20.8	41	2	C39558

ALIGNMENTS

RESULT 1

PC4445

L-ascorbate peroxidase (EC 1.11.1.11) - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Mar-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: PC4445

R;Wada, N.; Kinoshita, S.; Matsuo, M.; Amako, K.; Miyake, C.; Asada, K.

Biochem. Biophys. Res. Commun. 242, 256-261, 1998

A;Title: Purification and molecular properties of ascorbate peroxidase from bovine eye.

A;Reference number: PC4445; MUID:98113338; PMID:9446780

A;Accession: PC4445

A;Molecule type: protein

A;Residues: 1-25 <WAD>

A;Cross-references: UNIPROT:Q7M3G0; UNIPARC:UPI000017C53D

C;Comment: This hydrogen peroxide-scavenging peroxidase plays a role in the protection

C;Keywords: oxidoreductase

Query Match 34.1%; Score 45; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 5 4;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDAIKEVFDN 24

Db 8 LENCRAIKELFEN 21

RESULT 2

S30362

1,2-alpha-D-mannosidase - Penicillium citrinum

C;Species: Penicillium citrinum

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S30362

R;Yoshida, T.; Inoue, T.; Ichishima, E.

Biochem. J. 290, 349-354, 1993

A;Title: 1,2-alpha-D-mannosidase from Penicillium citrinum: molecular and enzymic prop

A;Reference number: S30361; MUID:93199503; PMID:8452520

A;Accession: S30362

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-43 <YOS>

A;Cross-references: UNIPROT:P31723; UNIPARC:UPI000017B3EB

Query Match 26.5%; Score 35; DB 2; Length 43;

Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 16 DAIKEVFDN 24

Db 7 DAVKEAFQN 15

||:|||||

RESULT 3

S03353

plastocyanin - Microcystis aeruginosa (fragment)

C:Species: Microcystis aeruginosa

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C:Accession: S03353

R;Tan, S.; Ho, K.K.

Biochim. Biophys. Acta 973, 111-117, 1989

A:Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.

A:Reference number: S03353; MUID:89134784; PMID:2537099

A:Accession: S03353

A:Molecule type: protein

A:Residues: 1-15 <TAN>

A:Cross-references: UNIPROT:P10625; UNIPARC:UPI00001131BAF

Query Match 25.8%; Score 34; DB 2; Length 15;

Best Local Similarity 72.7%; Pred. No. 1.4e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 17

|||||||

Db 1 ETFTVKMGDD 11

RESULT 4

B84144

hypothetical protein BH3954 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: B84144

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hara

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B84144

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-29 <STO>

A:Cross-references: UNIPROT:Q9K5Y2; UNIPARC:UPI00000C435A; GB:AP001520; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH3954

Query Match 25.0%; Score 33; DB 2; Length 29;

Best Local Similarity 42.9%; Pred. No. 3.7e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 FTVKSCPDAIKEYF 22

|||||

Db 3 FVLKGPDPYFEKVF 16

RESULT 5

S55462

mer5 protein homolog - human (fragment)

N:Alternate names: humer

C:Species: Homo sapiens (man)

C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S55462

R;Oberbaumer, I.

submitted to the EMBL Data Library, March 1995

A:Description: A new member of the highly conserved multigene family of thiol-specific a

As by their 3' untranslated regions.

A:Reference number: S55462

A:Accession: S55462

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-30 <OBE>

A:Cross-references: UNIPROT:Q14579; UNIPARC:UPI000006D89A; EMBL:X85129; NID:g854125; PID

C:Genetics:

A:Gene: mer5

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

Query Match 25.0%; Score 33; DB 2; Length 30;

Best Local Similarity 53.8%; Pred. No. 3.8e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 10 TVKSCPDAIKEYF 22

|||||

Db 13 TIKPSPAASKEYF 25

RESULT 6

G72312

hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: G72312

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: G72312

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-41 <ARN>

A:Cross-references: UNIPROT:Q9X065; UNIPARC:UPI00000C1340; GB:AE001759; GB:AE000512; NI

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TW0970

Query Match 25.0%; Score 33; DB 2; Length 41;

Best Local Similarity 54.5%; Pred. No. 5.2e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 DVLETFTVKSC 14

|||||

Db 23 EVLETHTSQTC 33

RESULT 7

AD1753

Lactococcus lactis prophage pi2 protein 41 homolog lin2569 [imported] - Listeria innocua

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD1753

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krefit, J.; Kuhn, M.; Kunet, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1753

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-44 <GLA>

A:Cross-references: UNIPROT:Q928G6; UNIPARC:UPI00000CC8BF; GB:AL592022; PIDN:CAC97796.1.1;

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lin2569

Query Match 25.0%; Score 33; DB 2; Length 44;

Best Local Similarity 47.1%; Pred. No. 5.5e+02;

Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 DVLETFTVKSCPDIAKE 20

|||||

Db 4 DDLEMTLGSCLDYFAE 20

RESULT 8
JQ1600
NepC' protein - Clostridium butyricum plasmid pCB101
N;Alternate names: hypochemical 5.6K protein; hypochemical protein C'
C;Species: Clostridium butyricum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1600; S18113
R;Brehm, J.K.; Pennock, A.; Bullman, H.M.S.; Young, M.; Oultram, J.D.; Minton, N.P.
Plasmid 28, 1-13, 1992
A;Title: Physical characterization of the replication origin of the cryptic plasmid pCB1
A;Reference number: PQ0372; MUID:92390513; PMID:1518909
A;Accession: JQ1600
A;Molecule type: DNA
A;Residues: 1-49 <BRE>
A;Cross-references: UNIPROT:Q45960; UNIPARC:UPI00000B3E35; EMBL:X62684; NID:g40399; PIDN
A;Experimental source: strain NCIB7423
C;Genetics:
A;Genome: plasmid

Query Match 25.0%; Score 33; DB 2; Length 49;
Best Local Similarity 41.7%; Pred. No. 6.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 13 SCPDAIKEVPDN 24
|||:|:|:
Db 6 SIPDEVKQFPED 17

RESULT 9
H70224
hypochemical protein BBR05 - Lyme disease spirochete plasmid E/1p25
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: H70224
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70224
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-50 <KLE>
A;Cross-references: UNIPROT:O50701; UNIPARC:UPI0000056836; GB:AE000785; NID:g2689951; PI
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match 24.6%; Score 32.5; DB 2; Length 50;
Best Local Similarity 47.6%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 3 KDVLFTFTKSCPDATKEVPD 23
|||:|:|:|:|:|:|:
Db 17 KGVEEKYKVKSPDLISEVLN 36

RESULT 10
S72793
cysteine synthase (EC 4.2.99.8) B - Mycobacterium leprae
N;Alternate names: B1549_C3_238 protein; O-Acetylserine sulphydrolase B
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72793
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1549.
A;Reference number: S72582
A;Accession: S72793

Query Match 23.5%; Score 31; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 5.3e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 11 VKSCPDATKEVPDN 24
:|:|:|:|:|:
Db 1 MKTAKDVLKSIKDN 14

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-49 <SMI>
A;Cross-references: UNIPROT:Q59529; UNIPARC:UPI00000B1374; EMBL:U00014; NID:g466903; PI
C;Genetics:
A;Gene: cysM
C;Keywords: carbon-oxygen lyase

Query Match 24.2%; Score 32; DB 2; Length 49;
Best Local Similarity 33.3%; Pred. No. 8.6e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 KDVLFTFTKSC 14
|||:|:|:|:
Db 38 KDLFPSTYTRTC 49

RESULT 11
E97894
orf47 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E97894
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: E97894
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <KUR>
A;Cross-references: UNIPROT:Q8DR08; UNIPARC:UPI00000E33D7; GB:AE007317; PIDN:AAK989895.1
C;Genetics:
A;Gene: orf47

Query Match 23.9%; Score 31.5; DB 2; Length 47;
Best Local Similarity 46.7%; Pred. No. 9.8e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 6 LETFTVKSCPDATKE 20
:|:|:|:|:|:|:
Db 24 IETP-VLCKCKSLKQ 37

RESULT 12
B33600
glutamate-ammonia ligase (EC 6.3.1.2) - Bradyrhizobium japonicum (fragment)
C;Species: Bradyrhizobium japonicum
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: B33600
R;Martin, G.B.; Thomashow, M.P.; Chelms, B.K.
J. Bacteriol. 171, 5638-5645, 1989
A;Title: Bradyrhizobium japonicum glnB, a putative nitrogen-regulatory gene, is regulat
A;Reference number: A33600; MUID:90008805; PMID:2793830
A;Accession: B33600
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-21 <MAR>
A;Cross-references: UNIPROT:P05457; UNIPARC:UPI000016E706; GB:M26753; NID:g152093; PIDN
C;Keywords: ligase

Query Match 23.5%; Score 31; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 5.3e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 11 VKSCPDATKEVPDN 24
:|:|:|:|:|:
Db 1 MKTAKDVLKSIKDN 14

```
RESULT 13
S12409
ribosomal protein S12 - wheat chloroplast (fragment)
C:Species: chloroplast Triticum aestivum (common wheat)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S12409
R:Gray, J.C.; Hird, S.M.; Dyer, T.A.
Plant Mol. Biol. 15, 947-950, 1990
A:title: Nucleotide sequence of a wheat chloroplast gene encoding the proteolytic subunit
A:Reference number: S12407; MUID:91355920; PMID:2103485
A:Accession: S12409
A:Molecule type: DNA
A:Residues: 1-38 <GRA>
A:Cross-references: UNIPROT:P24066; UNIPARC:UPI000016D3FB; EMBL:X54484; NID:g12334; PIDN
C:Genetics:
A:Gene: rps12
A:Genome: chloroplast
A:Superfamily: ribosomal protein S12
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match      23.5%; Score 31; DB 2; Length 38;
Best Local Similarity 33.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCP 15
| : : : : : : : : : :
Db 14 PIRNARKTAALKGCP 28

RESULT 14
AB0925
hypothetical protein STY3659 [imported] - Salmonella enterica subsp. enterica serovar Ty
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0925
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0925
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <PAR>
A:Cross-references: UNIPARC:UPI000005A5A3; GB:AL513382; PIDN:CAD09420.1; PID:g16504537;
C:Genetics:
A:Gene: STY3659

Query Match      23.5%; Score 31; DB 2; Length 50;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PKDVLLET 8
| : : : : :
Db 33 PKKSVLKT 40

RESULT 15
A38882
GTP-binding protein Cdc42 - mouse (fragment)
N:Alternate names: rab protein Cdc42
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A38882; JH0651
R:Chavrier, P.; Simons, K.; Zerial, M.
submitted to GenBank, June 1992
A:Reference number: A38879
A:Accession: A38882
A:Molecule type: mRNA
A:Residues: 1-48 <CHA>
```

```
A:Cross-references: UNIPROT:Q99JI7; UNIPARC:UPI00000E67CE; GB:M79301
R:Chavrier, P.; Simons, K.; Zerial, M.
Gene 112, 261-264, 1992
A:title: The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by
A:Reference number: JH0639; MUID:92210010; PMID:1555775
A:Accession: JH0651
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-41,'W',43-48 <CH2>
A:Cross-references: UNIPARC:UPI00000176444
A:Experimental source: kidney
C:Genetics:
A:Gene: Cdc42
A:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding

Query Match      23.1%; Score 30.5; DB 2; Length 48;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 8; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 2 KKDVLFTFTVKSCP-DAIKEVFDN 24
| : : : : : : : : : :
Db 2 KSCLLISVTNNKFPSEYVPTVFDN 25

RESULT 16
B60507
pepsin Iia (EC 3.4.23.-) - Atlantic cod (fragment)
C:Species: Gadus morhua (Atlantic cod)
C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 16-Aug-2004
C:Accession: B60507
R:Gildberg, A.; Olsen, R.L.; Bjarnason, J.B.
Comp. Biochem. Physiol. B 96, 323-330, 1990
A:title: Catalytic properties and chemical composition of pepsins from Atlantic cod (Ga
A:Reference number: A60507; MUID:90298622; PMID:2113846
A:Accession: B60507
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-31 <GIL>
A:Cross-references: UNIPROT:Q7LZP3; UNIPARC:UPI0000175D39
C:Superfamily: Pepsin
C:Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match      22.7%; Score 30; DB 2; Length 31;
Best Local Similarity 27.8%; Pred. No. 1.1e+03;
Matches 5; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 6 LETFTVKSCPDAIKEVED 23
| : : : : : : : : : :
Db 14 LGVISIGTPESFKVIFD 31

RESULT 17
T15602
hypothetical protein C25E10.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15602
R:Bradshaw, H.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid C25E10.
A:Reference number: Z18376
A:Accession: T15602
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-35 <BRA>
A:Cross-references: UNIPARC:UPI000007DDA7; EMBL:U50311; NID:g1226295; PID:g1226296; PIDN
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C25E10.6
A:Introns: 31/3

Query Match      22.7%; Score 30; DB 2; Length 35;
```

Best Local Similarity 33.3%; Pred. No. 1.2e+03; Mismatches 5; Indels 7; Gaps 0;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 3 KDVLETFVTKSCPDPAIKE 20
DB 11 KDTQNSFPINTELTKE 28

RESULT 18
D22102
phycoerythrin-545 alpha-2 chain - Cryptomonas sp. (fragment)
C:Species: Cryptomonas sp.
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Apr-1999
R:Sidler, W.; Kumpf, B.; Suter, F.; Morisset, W.; Wehrmeyer, W.; Zuber, H.
Biol. Chem. Hoppe-Seyler 366, 233-244, 1985
A:Title: Structural studies on cryptomonad biliprotein subunits. Two different alpha-sub
A:Reference number: A94645; MUID:85225953; PMID:4005040
A:Accession: D22102
A:Molecule type: protein
A:Residues: 1-42 <SID>
A:Cross-references: UNIPARC:UPI000017AED4
C:Keywords: chromoprotein; hydroxyllysine; phytochromobilin
P:4/Modified site: 4-hydroxyllysine (lys) #status experimental
F:19/Binding site: phycoerythrobilin (Cys) (covalent) #status experimental

Query Match 22.7%; Score 30; DB 2; Length 42;
Best Local Similarity 42.1%; Pred. No. 1.5e+03; Mismatches 10; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 2 KKDVLFTFVTKSCPDPAIKE 20
DB 7 KAPVLTFDHRGSRAPKE 25

RESULT 19
E85849
unknown protein encoded within prophage CP-933V [imported] - Escherichia coli (strain O1
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85849
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11204551
A:Accession: E85849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44 <STO>
A:Cross-references: UNIPROT:Q8X3K2; UNIPARC:UPI00000D0F04; GB:AE005174; NID:gl2516430; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3374

Query Match 22.7%; Score 30; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 1.5e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 14 CPDAIKEVFD 23
DB 28 CREVVKRMFD 37

RESULT 20
G89944
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89944
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-48 <KUR>
A:Cross-references: UNIPROT:Q99TW5; UNIPARC:UPI000005427D; GB:BA000018; PID:g13701422;
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS049

Query Match 22.7%; Score 30; DB 2; Length 48;
Best Local Similarity 37.5%; Pred. No. 1.7e+03; Mismatches 9; Conservative 2; Mismatches 7; Indels 6; Gaps 1;
Matches 9; Conservative 2; Mismatches 7; Indels 6; Gaps 1;
QY 3 KDVLETF-----TVKSCPDPAIKE 20
DB 8 KDAVEKFKNSDNEQVKNVKDKINE 31

RESULT 21
A81546
hypothetical protein CP0727 [imported] - Chlamydomophila pneumoniae (strain AR39)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: A81546
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: A81546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <REA>
A:Cross-references: UNIPARC:UPI000016560C; GB:AE002231; GB:AE002161; NID:g7189633; PIDN
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0727

Query Match 22.7%; Score 30; DB 2; Length 50;
Best Local Similarity 37.5%; Pred. No. 1.7e+03; Mismatches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 2 KKDVLFTFVTKSCPDPA 17
DB 23 KXDYELWVYIGSCPES 38

RESULT 22
A61309
Glycoprotein hormones alpha chain - hamster (fragment)
N:Alternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; lut
C:Species: Crictetinae gen. sp. (hamster)
C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C:Accession: A61309
R:Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.
Endocrinology 111, 1263-1269, 1982
A:Title: Isolation and characterization of hamster luteinizing hormone.
A:Reference number: A61309; MUID:83003498; PMID:6889489
A:Accession: A61309
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <GLE>
A:Cross-references: UNIPROT:Q7MOA7; UNIPARC:UPI00001765C7
C:Superfamily: glycoprotein hormones alpha chain
C:Keywords: glycoprotein

Query Match 22.0%; Score 29; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 6e+02; Mismatches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	9	FTVKSCP 15	
		::	
Db	6	FTWQGP 12	
RESULT 23			
		S30361	
		1,2-alpha-D-mannosidase - Penicillium citrinum	
		C;Species: Penicillium citrinum	
		C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004	
		C;Accession: S30361	
		R;Yoshida, T.; Inoue, T.; Ichishima, E.	
		Biochem. J. 290, 349-354, 1993	
		A;Title: 1,2-alpha-D-mannosidase from Penicillium citrinum: molecular and enzymic properties	
		A;Reference number: S30361; MUID:93199503; PMID:8452520	
		A;Accession: S30361	
		A;Status: preliminary	
		A;Molecule type: protein	
		A;Residues: 1-25 <YOS>	
		A;Cross-references: UNIPROT:Q7M527; UNIPARC:UPI000017B3EA	
Query Match 22.0%; Score 29; DB 2; Length 25;			
Best Local Similarity 71.4%; Pred. No. 1.2e+03;			
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	16	DAIKEVP 22	
		::	
Db	7	DAVKEAF 13	
RESULT 24			
		A60698	
		trichocyst protein 12 - Paramesium tetraurelia (fragment)	
		C;Species: Paramesium tetraurelia	
		C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-Dec-1999	
		C;Accession: A60698	
		R;Tindall, S.H.; Devito, L.D.; Nelson, D.L.	
		J. Cell Sci. 92, 441-447, 1989	
		A;Title: Biochemical characterization of the proteins of Paramesium secretory granules.	
		A;Reference number: A60698; MUID:90078398; PMID:2592449	
		A;Accession: A60698	
		A;Molecule type: protein	
		A;Residues: 1-28 <TIN>	
		A;Cross-references: UNIPARC:UPI000017B66F	
		C;Comment: This protein was purified from the extruded matrix (contents) of trichocysts	
		C;Genetics:	
		A;Genetic code: SGCS	
		C;Keywords: extracellular protein	
Query Match 22.0%; Score 29; DB 2; Length 28;			
Best Local Similarity 66.7%; Pred. No. 1.4e+03;			
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	16	DAIKEVPDN 24	
		::	
Db	4	DTIKGVLDN 12	
RESULT 25			
		S11610	
		ribosomal protein S4_eR [validated] - Halobacterium salinarum (fragment)	
		N;Alternate names: ribosomal protein HS5	
		C;Species: Halobacterium salinarum	
		C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004	
		C;Accession: S11610	
		R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.	
		Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982	
		A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea	
		A;Reference number: S11609	
		A;Accession: S11610	
		A;Molecule type: protein	
		A;Residues: 1-32 <YAG>	
		A;Cross-references: UNIPROT:Q7M553; UNIPARC:UPI000017725F	

A;Note: the protein is designated as ribosomal protein HS5			
A;Note: the source is designated as Halobacterium cutirubrum			
C;Superfamily: ribosomal protein S4			
C;Keywords: protein biosynthesis; ribosome			
Query Match 22.0%; Score 29; DB 2; Length 32;			
Best Local Similarity 53.8%; Pred. No. 1.6e+03;			
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;			
QY	1	PKKDVLETFVKS 13	
		: ::	
Db	14	PVZRRKTETSKS 26	
RESULT 26			
		S42051	
		GTP-binding protein (clone pSH-RHO2) - penaeid shrimp (Penaeus monodon) (fragment)	
		C;Species: Penaeus monodon	
		C;Date: 27-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004	
		C;Accession: S42051	
		R;Gendreau, S.; Lee, R.; Mialhe, E.	
		submitted to the EMBL Data Library, February 1994	
		A;Reference number: S42050	
		A;Accession: S42051	
		A;Molecule type: DNA	
		A;Residues: 1-34 <GEN>	
		A;Cross-references: UNIPROT:Q26078; UNIPARC:UPI000007DB98; EMBL:G454998; PIR	
		C;Superfamily: ras transforming protein; translation elongation factor Tu homology	
		C;Keywords: GTP binding; transforming protein	
Query Match 22.0%; Score 29; DB 2; Length 34;			
Best Local Similarity 40.9%; Pred. No. 1.7e+03;			
Matches 9; Conservative 5; Mismatches 6; Indels 2; Gaps 2;			
QY	1	PKKDV-LETFVKSCPDAIKEY 21	
		::	
Db	9	PDTDVILMCFSDS-PDSLENV 29	
RESULT 27			
		E49754	
		hypothetical protein I4 - Bacillus licheniformis (fragment)	
		C;Species: Bacillus licheniformis	
		C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004	
		C;Accession: E49754	
		R;Lee, J.W.K.; Edwards, C.W.; Hulett, F.M.	
		J. Gen. Microbiol. 137, 667-677, 1991	
		A;Title: Identification of four unique clones encoding 10 kDa proteins from Bacillus tha	
		A;Reference number: A49754; MUID:91237328; PMID:2033382	
		A;Accession: E49754	
		A;Status: preliminary	
		A;Molecule type: DNA	
		A;Residues: 1-34 <LEE>	
		A;Cross-references: UNIPROT:Q7M148; UNIPARC:UPI0000178E1B; GB:M37167	
		C;Superfamily: hypothetical protein b1540	
Query Match 22.0%; Score 29; DB 2; Length 34;			
Best Local Similarity 28.6%; Pred. No. 1.7e+03;			
Matches 6; Conservative 6; Mismatches 7; Indels 2; Gaps 1;			
QY	2	KKDVLETFVKSPPDAIKEYF 22	
		: ::	
Db	13	EKEISERYEVSRTP--VREAF 31	
RESULT 28			
		F95187	
		hypothetical protein SP1611 [imported] - Streptococcus pneumoniae (strain TIGR4)	
		C;Species: Streptococcus pneumoniae	
		C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004	
		C;Accession: F95187	
		R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei-	
		on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,	

nsen, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-34 <KOR>
A;Cross-references: UNIPROT:Q97PJ8; UNIPARC:UPI00000518FB; GB:AE005672; PIDN:AAK75695.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SPI611

Query Match 22.0%; Score 29; DB 2; Length 34;
Best Local Similarity 35.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSC 14
|:|:|:|:|
Db 12 PEEDIIVTGLPKYC 25

RESULT 29
A23691
apolipoprotein C-I - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C;Accession: A23691
R;Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 285, 22453-22459, 1990
A;Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-mig-
ceptor-related protein.
A;Reference number: A23691; MUID:91093092; PMID:2266137
A;Accession: A23691
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <WEI>
A;Cross-references: UNIPROT:P33047; UNIPARC:UPI0000125C1C
C;Superfamily: apolipoprotein A-I
C;Keywords: lipid binding; lipoprotein

Query Match 21.6%; Score 28.5; DB 2; Length 28;
Best Local Similarity 46.7%; Pred. No. 1.6e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 10 TVKSCPDPAIKVFDN 24
|:|:|:|:|
Db 6 TLELIPDKLKE-FGN 19

RESULT 30
WISMAA
alpha-amylase inhibitor AI-3688 - Streptomyces aureofaciens
C;Species: Streptomyces aureofaciens
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01331
R;Vertesy, L.; Tripiet, D.
FEBS Lett. 185, 187-190, 1985
A;Title: Isolation and structure elucidation of an alpha-amylase inhibitor, AI-3688, fr
A;Reference number: A01331; MUID:85204394; PMID:2581812
A;Accession: A01331
A;Molecule type: protein
A;Residues: 1-36 <VER>
A;Cross-references: UNIPROT:P04082; UNIPARC:UPI000012D0A7
A;Experimental source: FHL656, strain DSM 2790
C;Comment: This protein is an effective inhibitor of pancreatic alpha-amylase, forming a
does not inhibit the B. subtilis enzyme. Inhibition is pH-independent but does require
C;Superfamily: alpha-amylase inhibitor, Streptomyces type
C;Keywords: alpha-amylase inhibitor
F;4-18/Region: inhibitory #status predicted
F;9-25/Diulfide bonds: #status experimental

Query Match 21.6%; Score 28.5; DB 1; Length 36;
Best Local Similarity 28.6%; Pred. No. 2.1e+03;
Matches 8; Conservative 3; Mismatches 10; Indels 7; Gaps 1;

QY 1 PKQVLETF-----TVKSCPDPAIKV 21
|:|:|:|:|
Db 5 PAPDCVESFQSWRYTDVRNGCSDAVTV 32

RESULT 31
S32316
3,5-dichlorocatechol 1,2-dioxygenase (EC 1.13.11.1) - Pseudomonas cepacia (fragment)
C;Species: Pseudomonas cepacia
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S32316
R;Bhat, M.A.; Ishida, T.; Horike, K.; Vaidyanathan, C.S.; Nozaki, M.
Arch. Biochem. Biophys. 300, 738-746, 1993
A;Title: Purification of 3,5-dichlorocatechol 1,2-dioxygenase, a nonheme iron dioxygenase
as cepacia CSV90.
A;Reference number: S32316; MUID:93167864; PMID:7679568
A;Accession: S32316
A;Molecule type: protein
A;Residues: 1-44 <BHA>
A;Cross-references: UNIPROT:Q9RSD3; UNIPARC:UPI0000088F82
A;Experimental source: strain CSV90
C;Function:
A;Description: catalyzes intradiol cleavage of different catechol derivatives
A;Note: involved in degradation of the herbicide 2,4-dichlorophenoxyacetic acid
A;Note: a nonheme ferric dioxygenase
C;Superfamily: protocatechu 3,4-dioxygenase beta chain
C;Keywords: homodimer; oxidoreductase

Query Match 21.6%; Score 28.5; DB 2; Length 44;
Best Local Similarity 30.4%; Pred. No. 2.5e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 3 KDVLFTTVKSCPDPAIKVFDNK 25
|:|:|:|:|
Db 6 KDWDVAIVA-----AVQVLDQK 23

RESULT 32
E85938
hypothetical protein Z4177 [imported] - Escherichia coli (strain O157:H7, substrain EDL
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85938
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85938
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-44 <STO>
A;Cross-references: UNIPROT:Q8X3M1; UNIPARC:UPI00000D0EF2; GB:AE005174; NID:gl2517352;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4177

Query Match 21.6%; Score 28.5; DB 2; Length 44;
Best Local Similarity 31.6%; Pred. No. 2.5e+03;
Matches 6; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 7 EFTTVKSCPDPAIKVFDNK 25
|:|:|:|:|
Db 29 ELFIKAC-----VSHIFSTK 44

RESULT 33
S09607
phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Salmonella typhimurium (fragment)

C:Species: Salmonella typhimurium
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S09607
R:Li, Z.J.; Hillyard, D.; Higgins, P.
Nucleic Acids Res. 17, 8880, 1989
A:Title: Nucleotide sequence of the Salmonella typhimurium himA gene.
A:Reference number: S09607; MUID:90067874; PMID:2685752
A:Accession: S09607
A:Molecule type: DNA
A:Residues: 1-17 <LIZ>
A:Cross-references: UNIPROT:PI5434; UNIPARC:UPI000017035D; EMBL:X16739; NID:g47703; PIDN
C:Genetics: phet
A:Gene: phet
C:Function:
A:Description: catalyzes transfer of activated phenylalanine to phenylalanyl-tRNA
C:Superfamily: phenylalanine-tRNA ligase beta chain
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 21.2%; Score 28; DB 2; Length 17;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 14 CPDAIKVF 22
| : : | : |
Db 3 CVEALKRF 11

RESULT 34
A27375
Photosystem I iron-sulfur protein - barley chloroplast (fragment)
N:Alternate names: photosystem I 9K protein
C:Species: chloroplast Hordeum vulgare (barley)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 12-Jul-2004
C:Accession: A27375
R:Hoj, P.B.; Svendsen, I.; Scheller, H.V.; Moller, B.L.
J. Biol. Chem. 262, 12676-12684, 1987
A:Title: Identification of a chloroplast-encoded 9-kDa polypeptide as a 2[4Fe-4S] protein
A:Reference number: A27375; MUID:87308302; PMID:3305512
A:Accession: A27375
A:Molecule type: DNA
A:Residues: 1-30 <HOJ>
A:Cross-references: UNIPROT:PI0794; UNIPARC:UPI0000174DD7
C:Genetics: chloroplast
A:Genome: chloroplast
C:Keywords: 4Fe-4S; chloroplast; electron transfer; iron-sulfur protein; membrane-associ

Query Match 21.2%; Score 28; DB 2; Length 30;
Best Local Similarity 35.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 TPTVKSCPDPAKEV 21
| : : | : | : |
Db 14 TQCVRACTDVLDM 27

RESULT 35
A60507
pepsin I (EC 3.4.23.-) - Atlantic cod (fragment)
C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 16-Aug-2004
C:Accession: A60507
R:Glibberg, A.; Olsen, R.L.; Bjarnason, J.B.
Comp. Biochem. Physiol. B 96, 323-330, 1990
A:Title: Catalytic properties and chemical composition of pepsins from Atlantic cod (Gad
A:Reference number: A60507; MUID:90298622; PMID:2113846
A:Accession: A60507
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-33 <GL>
A:Cross-references: UNIPROT:Q7LZP5; UNIPARC:UPI0000175D37
C:Superfamily: Pepsin
C:Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 21.2%; Score 28; DB 2; Length 33;
Best Local Similarity 44.4%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 15 PDAIKEVFD 23
| : : | : | : |
Db 25 PESFKVIFD 33

RESULT 36
A60601
keratin, 55k, nuclear matrix - rat (fragments)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: A60601
R:Alique, R.; Bastos, R.; Serratos, J.; Enrich, C.; James, P.; Pujades, C.; Bachs, O.
Exp. Cell Res. 186, 346-353, 1990
A:Title: Increase in a 55-kDa keratin-like protein in the nuclear matrix of rat liver c
A:Reference number: A60601; MUID:90127112; PMID:1688805
A:Accession: A60601
A:Molecule type: protein
A:Residues: 1-33 <ALI>
A:Cross-references: UNIPROT:Q7MOB6; UNIPARC:UPI00001774C5
C:Superfamily: cytoskeletal keratin
C:Keywords: nuclear matrix; nucleus

Query Match 21.2%; Score 28; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KKVLETFVK 12
| : : | : | : |
Db 8 KKVDEAYXK 18

RESULT 37
S42050
GRP-binding protein (clone pSH-RH01) - penaeid shrimp (Penaeus monodon) (fragment)
C:Species: Penaeus monodon
C:Date: 27-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S42050
R:Gendreau, S.; Lee, R.; Mialhe, E.
submitted to the EMBL Data Library, February 1994
A:Reference number: S42050
A:Accession: S42050
A:Molecule type: DNA
A:Residues: 1-34 <GEN>
A:Cross-references: UNIPROT:Q26077; UNIPARC:UPI0000075244; EMBL:Z30080; NID:g454996; PII
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; transforming protein

Query Match 21.2%; Score 28; DB 2; Length 34;
Best Local Similarity 36.4%; Pred. No. 2.3e+03;
Matches 8; Conservative 6; Mismatches 6; Indels 2; Gaps 2;

QY 1 PKKDV-LFTFTVKSCPDPAKEV 21
| : : | : | : | : | : |
Db 9 PDTDVILMCFIDS-PDSLENI 29

RESULT 38
G95151
hypothetical protein SPI305 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95151
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
non, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: G95151
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1..34 <KUR>
A;Cross-references: UNIPROT:Q97QBS; UNIPARC:UPI00000517BF; GB:AE005672; PIDN:AAK75408.1-7
A;Experimental source: strain TIGR4
A;Genetics:
A;Gene: Spi305

```

Query Match      21.2%; Score 28; DB 2; Length 34;
Best Local Similarity 37.9%; Pred.No. 2.3e+03;
Matches 11; Conservative 3; Mismatches 9; Indels 6; Gaps 2;

Qy 3 KQVLET----FTVKSCPDAIKEY--FDNK 25
    | | | | | | | | | | : | | | |
Db 2 KEFLNFCFFETVKNSAIIINSYVIKYDNK 30

```

RESULT 39

B97082

hypothetical protein CAC1477 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: B97082

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97082

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-34 <R>

A:Cross-references: UNIPROT:Q97J09, UNIPARC:UPT00000CA1FC; GB:AB001437; PIDN:AAK79445.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1477

```

Query Match      21.2%; Score 28; DB 2; Length 34;
Best Local Similarity 44.4%; Fred.No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 SCPDAIKEV 21
    ||| : : |
Db 15 SCPOSVDKV 23

```

RESULT 40
I70022
kallikrein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C/Accession: I70022
R/Evans, B.A.; Drinkwater, C.C.; Richards, R.I.
J. Biol. Chem. 262, 8027-8034, 1987
A/Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of the
A/Reference number: I55260; MUID: 97250386; PMID: 3036794
A/Accession: I70022
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-38 <RES>
A/Cross-references: UNIPARC:UPI000016CE68; GB:M18530; NID:g198528; PIDN:AAA39352.1; PID:
C/Genetics:
A/Gene: KAL

```

Query Match      21.2%; Score 28; DB 2; Length 38;
Best Local Similarity 38.5%; Pred. NO. 2.6e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      4  DVLFTFTVKSCPD 16
      :||| ||| :
Db      9  ELLEDLTVRRIPN 21

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:22:44 ; Search time 54.321 Seconds
(without alignments)
324.703 Million cell updates/sec

Title: US-10-619-323-5
Perfect score: 132
Sequence: 1 PKXDLVTFVVKSPDAIKVFNK 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	34.1	25	Q7M3G0_BOVIN	Q7m3g0 bos taurus
2	43.5	33.0	48	Q4RC18_TETNG	Q4rc18 tetraodon n
3	41	31.1	44	Q8U2Q3_PYRPU	Q8u2q3 pyrococcus
4	40	30.3	45	Q5UZA6_HALWA	Q5uza6 haloarcula
5	39	29.5	47	Q8F5I4_LEPIN	Q8f5i4 leptospira
6	38.5	29.2	35	Q8E9Z3_SHEON	Q8e9z3 shewanella
7	38.5	29.2	43	Q8F6T4_LEPIN	Q8f6t4 leptospira
8	38	28.8	39	Q4RAQ9_TETNG	Q4raq9 tetraodon n
9	38	28.0	46	GP54_BFSP1	Q48408 bacterioph
10	37	28.0	45	Q6SH21_BACLD	Q6sh21 bacillus li
11	36	27.3	41	Q91G73_IRV6	Q91g73 chilo iride
12	36	27.3	43	Q87JQ4_VIBPA	Q87jq4 vibrio para
13	36	27.3	45	Q570A7_ARATH	Q570a7 arabidopsis
14	35	26.5	37	Q86B24_9CAEN	Q86b24 reishia cla
15	35	26.5	41	Q5FU93_LACAC	Q5fi93 lactobacill
16	35	26.5	44	Q8G001_BRUSU	Q8g001 brucella su
17	35	26.5	49	Q5C039_SCHJA	Q5c039 schistosoma
18	34.5	26.1	44	Q8U2Q2_PYRPU	Q8u2q2 pyrococcus
19	34.5	26.1	44	Q7S6Q7_NEUCR	Q7s6q7 neurospora
20	34	25.8	15	PLAS MICAE	P10625 microcystis
21	34	25.8	18	Q9XJQ5_9CAUD	Q9xjq5 bacterioph
22	34	25.8	30	Q83B13_COXBU	Q83b13 coxiella bu
23	34	25.8	42	Q5V7J5_HALWA	Q5v7j5 haloarcula
24	34	25.8	46	Q9NYL8_HUMAN	Q9nyl8 homo sapien
25	34	25.8	47	Q70UJ3_9BASI	Q70uj3 uncultured
26	33	25.0	18	Q63506_RAT	Q63506 rattus norv
27	33	25.0	29	Q9K5Y2_BACHD	Q9k5y2 bacillus ha
28	33	25.0	30	Q14579_HUMAN	Q14579 homo sapien
29	33	25.0	32	Q4XWD9_PLACH	Q4xwd9 plasmodium
30	33	25.0	33	Q8DWB4_STRMU	Q8dwb4 streptococc
31	33	25.0	34	Q4XE03_PLACH	Q4xe03 plasmodium

32	33	25.0	37	2	Q84TL9_BRARP	Q84tl9 brassica ra
33	33	25.0	41	2	Q8BX0_SHEON	Q8bx0 shewanella
34	33	25.0	41	2	Q9X065_THEMA	Q9x065 thermotoga
35	33	25.0	43	2	Q4XGQ9_PLACH	Q4xgq9 plasmodium
36	33	25.0	44	2	Q4W2C5_MYZAU	Q4w2c5 myzopoda au
37	33	25.0	44	2	Q928G6_LISTIN	Q928g6 listeria in
38	33	25.0	47	2	Q5XDQ6_STRP6	Q5xdq6 streptococc
39	33	25.0	48	2	Q4XVJ5_PLACH	Q4xvj5 plasmodium
40	33	25.0	49	2	Q45960_CLOBU	Q45960 clostridium
41	33	25.0	50	2	Q4X9P8_PLACH	Q4x9p8 plasmodium
42	32.5	24.6	22	2	Q6VQ25_9NEOP	Q6vq25 heliconius
43	32.5	24.6	32	2	Q8TGT3_YEAST	Q8tgt3 saccharomyc
44	32.5	24.6	35	2	Q8ZWX8_PYRAE	Q8zwx8 pyrobaculum
45	32.5	24.6	46	2	Q5V3C5_HALWA	Q5v3c5 haloarcula
46	32.5	24.6	49	2	Q71ID3_LACDL	Q71id3 lactobacill
47	32.5	24.6	50	2	Q4XNE0_PLACH	Q4xne0 plasmodium
48	32.5	24.6	50	2	Q50701_BORBU	Q50701 borrelia bu
49	32	24.2	22	2	Q5BT20_SCHJA	Q5bt20 schistosoma
50	32	24.2	27	2	Q9GIC1_9PHAE	Q9gic1 sargassum m

ALIGNMENTS

RESULT 1

Q7M3G0_BOVIN	Q7M3G0_BOVIN PRELIMINARY;	PRT;	25 AA.
AC	Q7M3G0;		
DT	01-MAR-2004 (TREMBLrel. 26, Created)		
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	L-ascorbate peroxidase (BC 1.11.1.11) (Fragment).		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;		
OC	Pecora; Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	PROTEIN SEQUENCE.		
RX	MEDLINE=98113338; PubMed=9446780; DOI=10.1006/bbrc.1997.7946;		
RT	Wada N., Kinoshita S., Matsuo M., Amako K., Miyake C., Asada K.;		
RT	"Purification and molecular properties of ascorbate peroxidase from		
RL	bovine eye."		
RL	Biochem. Biophys. Res. Commun. 242:256-261(1998).		
DR	PIR; PC4445; PC4445.		
DR	GO; GO:0016888; F:L-ascorbate peroxidase activity; IEA.		
FT	NON_TER 1 1		
FT	NON_TER 25 25		
SQ	SEQUENCE 25 AA; 2942 MW; 6355FFAF335709A8 CRC64;		

Query Match 34.1%; Score 45; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDATKEVPDN 24

Db 8 LENCRAIKELPEN 21

RESULT 2

Q4RC18_TETNG	Q4RC18_TETNG PRELIMINARY;	PRT;	48 AA.
ID	Q4RC18;		
AC	Q4RC18;		
DT	13-SEP-2005 (TREMBLrel. 31, Created)		
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)		
DE	Chromosome 5 SCAF18819, whole genome shotgun sequence.		
DE	(Fragment)		
GN	ORFNames=GSTENG00038457001;		
OS	Tetraodon nigroviridis (Green puffer).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		

OC	Tetradontoidae; Tetraodontidae; Tetraodon.
OX	[1]
RN	NBI_TaxID=99883;
RP	NUCLEOTIDE SEQUENCE.
RA	Jailon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA	Mauclai E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA	Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA	Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA	Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Goury J., Bosak S.,
RA	Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA	Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA	Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA	Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RT	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT	the early vertebrate proto-karyotype.";
RL	Nature 431:946-957(2004).
RN	[2]
RN	NUCLEOTIDE SEQUENCE.
RG	Genoscope; Whitehead Institute Centre for Genome Research;
RL	Submitted (FEB-2004) to the ENBL/GenBank/DBJ databases.
CC	-! CAUTION: The sequence shown here is derived from an
CC	ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
DR	EMBL; CAAB01018919; CAGI3895.1; -; Genomic_DNA.
FT	NON TER 1
FT	NON TER 48
FT	SEQUENCE 48 AA; 5561 MW; ABCB2CCE7B88813F CRC64;
SQ	
Query Match	33.0%; Score 43.5; DB 2; Length 48;
Best Local Similarity	40.0%; Pred. No. 1.3e+02;
Matches	10; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
Qy	1 PKKDVLTFYTKSCFDA-IKEVFON 24 : : : : : :
Db	13 PKASMWKVCVKACSDSTYKYIFDN 37 : : : : : :
RESULT 3	
Q8U2Q3 PYRFU	
ID	Q8U2Q3_PYRFU PRELIMINARY; PRT; 44 AA.
AC	Q8U2Q3;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Hypothetical protein PF0779.
GN	OrderedLocusNames=PF0779;
OS	Pyrrococcus furiosus.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC	Pyrrococcus.
NCBI TaxID=2261;	
[1]	
RN	NUCLEOTIDE SEQUENCE
RC	STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA	Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT	"The complete sequence of the Pyrococcus furiosus genome.";
RL	Submitted (FEB-2002) to the ENBL/GenBank/DBJ databases.
DR	EMBL; AE010195; AAL80903.1; -; Genomic_DNA.
DR	InterPro: IPR008203; DUF104.
DR	Pfam; PF01954; DUF104; 1.
KW	Complete proteome; Hypothetical protein.
SQ	SEQUENCE 44 AA; 5128 MW; C1CB029DB57D97A8 CRC64;
Query Match	31.1%; Score 41; DB 2; Length 44;
Best Local Similarity	36.4%; Pred. No. 2.7e+02;
Matches	8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
Qy	4 DVLEFTTVKSCPDAIKEVFNDK 25 : : : : : : :
Db	22 DILEKFSRKVDKDKVLEKPLEER 43 : : : : : : :


```
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Putative gene protein 54.
GN Name=54;
OS Bacteriophage SP01.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC SP01-like viruses.
OX NCBI_TaxID=10685;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=98327781; PubMed=9657951; DOI=10.1006/viro.1998.9197;
RA Stewart C.R., Gaslightwala I., Hinata K., Krolkowski K.A.;
RA Needleman D.S., Peng A.S.-Y., Peterman M.A., Tobias A., Wei P.;
RT "Genes and regulatory sites of the 'host-takeover module' in the
RT terminal redundancy of Bacillus subtilis bacteriophage SP01."
RL Virology 246:329-340(1998).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF031901; AAC29023.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 46 AA; 5288 MW; 08D56FA236813246 CRC64;

Query Match      28.8%; Score 38; DB 1; Length 46;
Best Local Similarity 38.9%; Pred. No. 7.8e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 VLEFTFKSCPPDAIKVFP 22
   | : | | | : | | | : |
Db 2 VIKTYTKTQTPVKEMF 19

RESULT 10
Q55H21_BACLD
ID Q65H21_BACLD PRELIMINARY; PRT; 45 AA.
AC Q65H21;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BL102772;
OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 13 / ATCC 14580 [Goettingen];
RX PubMed=15383718; DOI=10.1159/000079829;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The complete genome sequence of Bacillus licheniformis DSM13, an
RT organism with great industrial potential."
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
DR EMBL; AE017333; AAU41643.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 45 AA; 5027 MW; 44993075A5049368 CRC64;

Query Match      28.0%; Score 37; DB 2; Length 45;
Best Local Similarity 28.6%; Pred. No. 1.1e+03;
Matches 6; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSCPPDAIKVFP 23
   | | : | | : | : | : |
Db 8 EDVIDTIQLRHPRPKVKYND 28

RESULT 11
Q91G73_IRV6
ID Q91G73_IRV6 PRELIMINARY; PRT; 41 AA.
AC Q91G73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 023L.
GN Name=NTP1;
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
RA Muller K., Tidona C.A., Bahr U., Darai G.;
RT "Identification of a thymidylate synthase gene within the genome of
RT Chilo iridescent virus."
RL Virus Genes 17:243-258(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93118242; PubMed=1475907;
RA Sonntag K.C., Darai G.;
RT "Characterization of the third origin of DNA replication of the genome
RT of insect iridescent virus type 6."
RL Virus Genes 6:333-342(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94353641; PubMed=8073636;
RA Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
RT "Chilo iridescent virus encodes a putative helicase belonging to a
RT distinct family within the 'DEAD/H' superfamily: implications for the
RT evolution of large DNA viruses."
RL Virus Genes 8:151-158(1994).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94292906; PubMed=8021587;
RA Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
RA Koonin E.V., Darai G.;
RT "Insect iridescent virus type 6 encodes a polypeptide related to the
RT largest subunit of eukaryotic RNA polymerase II."
RL J. Gen. Virol. 75:1557-1567(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95213160; PubMed=7698884;
RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
RT "Identification of the primary structure and the coding capacity of
RT the genome of insect iridescent virus type 6 between the genome
RT coordinates 0.310 and 0.347 (7990 bp)."
RL Intervirology 37:287-297(1994).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
RA Bahr U., Tidona C.A., Darai G.;
RT "The DNA sequence of Chilo iridescent virus between the genome
RT coordinates 0.101 and 0.391; similarities in coding strategy between
RT insect and vertebrate iridoviruses."
RL Virus Genes 15:235-245(1997).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Delius H., Darai G., Fluegel R.M.;
RT "DNA analysis of insect iridescent virus 6: evidence for circular
RT permutation and terminal redundancy."
RL J. Virol. 49:609-614(1984).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
RT in mice."
RL Med. Microbiol. Immunol. 175:43-53(1986).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87321126; PubMed=2820141;
```

RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,
 RA Delius H., Darai G.;
 RT "Molecular cloning and physical mapping of the genome of insect
 RT iridescent virus type 6: further evidence for circular permutation of
 RT the viral genome.";
 RL Virology 160:66-74 (1987).
 RN [10]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89073752; PubMed=3201750;
 RA Fischer M., Schnitzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in
 RT the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496 (1988).
 RN [11]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92196996; PubMed=1549908;
 RA Handermann M., Schnitzler P., Roesen-Wolff A.P., Raab K.,
 RA Sonntag K.C., Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32 (1992).
 RN [12]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93260401; PubMed=8492091;
 RA Schwaesser R., Raab K., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 RT insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879 (1993).
 RN [13]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94167241; PubMed=8121799;
 RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 RT chromosomal HMG protein homologues, and a putative GTP phosphohydrolase
 RT in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166 (1994).
 RN [14]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
 RA Muller K., Tidona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 RT iridescent virus encoding enzymes involved in viral DNA replication
 RT and processing.";
 RL Virus Genes 18:243-264 (1999).
 RN [15]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
 RA Jakob N.J., Mueller K., Bahr U., Darai G.;
 RT "Analysis of the first complete DNA sequence of an invertebrate
 RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";
 RL Virology 286:182-196 (2001).
 DR EMBL; AF303741; AAK81959.1; -; Genomic DNA.
 SQ SEQUENCE 41 AA; 4692 MW; BCC7EC950BC6FB09 CRC64;
 Query Match 27.3%; Score 36; DB 2; Length 41;
 Best Local Similarity 52.6%; Pred. No. 1.4e+03;
 Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 1;
 QY 4 DVLETFVKSCPDIAKEVF 22
 :||| |||
 Db 14 EILETKQVKK----IKEVF 28
 RESULT 12
 Q87JQ4 VIBPA
 ID Q87JQ4 VIBPA PRELIMINARY; PRT; 43 AA.
 AC Q87JQ4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein VPA0194.
 GN OrderedLocusNames=VPA0194;

OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=670;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae.";
 RL Lancet 361:743-749 (2003).
 DR EMBL; BA000032; BAC61537.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 43 AA; 4813 MW; B65EBB8D43C1E79A CRC64;
 Query Match 27.3%; Score 36; DB 2; Length 43;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 5 VLETFVKSCPDIAI 18
 :||| |||
 Db 21 VFDLFTIKRPNAL 34
 RESULT 13
 Q570A7 ARATH
 ID Q570A7 ARATH PRELIMINARY; PRT; 45 AA.
 AC Q570A7;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein At5g55120.
 GN Name=At5g55120;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs.";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK220803; BAD94066.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 45 AA; 5017 MW; 479C66D474235F2D CRC64;
 Query Match 27.3%; Score 36; DB 2; Length 45;
 Best Local Similarity 35.3%; Pred. No. 1.5e+03;
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 8 TPTVKSCPDIAKEVFDN 24
 :||| |||
 Db 29 SFTIVHCPSVKEAVSN 45
 RESULT 14
 Q86B24 9CAEN
 ID Q86B24 9CAEN PRELIMINARY; PRT; 37 AA.
 AC Q86B24;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nuclear Receptor g (Fragment).
 GN Name=tNRg;
 OS Reishia clavigera.

```
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Muricoidea; Muricidae; Relishia.
OX NCBI_TaxID=128433;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=ganglion;
RC Takahashi Y., Kuroku S., Kato K., Kurokawa T., Takahashi S., Sato M.,
RA Horiguchi T., Iguchi T., Miyata T., Miura T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB077035; BAC66483.1; -; mRNA.
DR HSSP; P22829; ICIT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0046872; F:receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00105; zf-C4; 1.
DR ProDom; PD000035; Znf_C4; 1.
DR SMART; SM00399; Znf_C4; 1.
KW DNA-binding; Metal-Binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT TER 37
SQ SEQUENCE 37 AA; 4447 MW; 5D33991EB159B073 CRC64;

Query Match 26.5%; Score 35; DB 2; Length 37;
Best Local Similarity 41.2%; Pred. No. 1.7e+03;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 9 FTVKSCPDAIKEVFNK 25
Db 1 FTCECKGPFKRTVQNK 17

RESULT 15
QSFJ93 LACAC
ID QSFJ93 LACAC PRELIMINARY; PRT; 41 AA.
AC QSFJ93;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LBA1406;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=NCFM;
RX Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
DR EMBL; CP000033; AAV43231.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4883 MW; 1344C5BBI43B64F1 CRC64;

Query Match 26.5%; Score 35; DB 2; Length 41;
Best Local Similarity 55.6%; Pred. No. 1.9e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 PDAIKEVFD 23
Db 24 PSLKELFD 32
```

```
RESULT 16
Q8G001 BRUSU
ID Q8G001 BRUSU PRELIMINARY; PRT; 44 AA.
AC Q8G001;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BR1316;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Helling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014291; AAN30233.1; -; Genomic DNA.
DR TIGR; BR1316; -.
SQ SEQUENCE 44 AA; 4670 MW; A38180FD364DB2FB CRC64;

Query Match 26.5%; Score 35; DB 2; Length 44;
Best Local Similarity 41.2%; Pred. No. 2.1e+03;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 VLETFVKSQPDIAKEV 21
Db 12 VLCAFTLASCANTVRGV 28

RESULT 17
QSC039 SCHJA
ID QSC039 SCHJA PRELIMINARY; PRT; 49 AA.
AC QSC039;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV811097; AAX26986.1; -; mRNA.
DR InterPro; IPR011986; LigA.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5542 MW; 4818667A695E7AFF CRC64;

Query Match 26.5%; Score 35; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 14 CPDAIKEY 21
Db 41 CPDCVKDI 48
```



```
RESULT 18
Q8U2U2 PYRFU PRELIMINARY; PRT; 44 AA.
AC Q8U2U2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0737.
GN OrderedLocusNames=PF0737;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010192; AAL80861.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5284 MW; 479C3074528E272E CRC64;

Query Match 26.1%; Score 34.5; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 10; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

QY 1 PKQVLETFVTK--SCPDAIKEYVFNK 25
DB 2 PKQVLETFVTK--RALEILDEK 23

RESULT 19
Q7S6Q7 NEUCR PRELIMINARY; PRT; 44 AA.
AC Q7S6Q7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Names=NCU05533.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Silitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kyrstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plannann M., Sailer S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000322; EAA31259.1; -; Genomic DNA.
SQ SEQUENCE 44 AA; 5283 MW; 5D58B345C3059404 CRC64;

Query Match 26.1%; Score 34.5; DB 2; Length 44;
Best Local Similarity 39.3%; Pred. No. 2.4e+03;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 2;
```

```
QY 1 PKQVLETFVTK--SCPDAIKEYVFNK 25
DB 2 PEKLTFFNFTVRMTAPDPNKKKDEDNK 29

RESULT 20
PLAS MICAE STANDARD; PRT; 15 AA.
AC P10625;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-JUN-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Plastocyanin (Fragment).
GN Name=petE;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89134784; PubMed=2537099;
RA Tan S., Ho K.-K.;
RT "Purification of an acidic plastocyanin from Microcystis aeruginosa."
RL Biochim. Biophys. Acta 973:111-117(1989).
CC -1- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -1- SIMILARITY: Contains 1 plastocyanin-like domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; S03353; S03353.
DR HAMAP; MF_00566; -; 1.
DR InterPro; IPR000923; BlueCu 1.
DR PROSITE; PS00196; COPPER BLUE; PARTIAL.
KW Copper; Direct protein sequencing; Electron transport; Metal-binding;
KW Transport.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1555 MW; 32B6D4662F44F969 CRC64;

Query Match 25.8%; Score 34; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 9.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 17
DB 1 ETFTVKMGDA 11

RESULT 21
Q9XJQ5 9CAUD PRELIMINARY; PRT; 18 AA.
AC Q9XJQ5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NihN protein.
GN Name=nihN;
OS Bacteriophage 21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=10743;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20092464; PubMed=10628842; DOI=10.1007/s004380051122;
RA Karch H., Schmidt H., Janetzki-Mittmann C., Scheef J., Kroeger M.;
RT "Shiga toxins even when different are encoded at identical positions
RT in the genomes of related temperate bacteriophages."
RL Mol. Gen. Genet. 262:600-607(1999).
DR EMBL; AJ237660; CAB39992.1; -; Genomic DNA.
SQ SEQUENCE 18 AA; 1975 MW; 2A8A46857FDBBB8 CRC64;
```

```
Query Match      25.8%; Score 34; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TFTVKSCPD 16
   |||: ||
Db 2 TFSVKTIPT 10

RESULT 22
Q83B13 COXBU
ID Q83B13 COXBU PRELIMINARY; PRT; 30 AA.
AC Q83B13
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CBU1707;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.P.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
   burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR EMBL; AB016965; AA091202.1; -; Genomic_DNA.
DR TIGR; CBU1707; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 30 AA; 3223 MW; 79F932AF90F0F2A CRC64;

Query Match      25.8%; Score 34; DB 2; Length 30;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 10 TVKSC--PDAIKEVP 22
   :|: | |||: |
Db 6 SVRGCLLPDAIQIF 20

RESULT 23
Q5V7J5 HALMA
ID Q5V7J5 HALMA PRELIMINARY; PRT; 42 AA.
AC Q5V7J5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=pNG5041;
OS Haloarcula marismortui (Halo bacterium marismortui).
OG Plasmid pNG500.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
   the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).

DR EMBL; AY596294; AAV44462.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 42 AA; 5161 MW; 105FD4C99987D57C CRC64;

Query Match      25.8%; Score 34; DB 2; Length 42;
Best Local Similarity 26.1%; Pred. No. 2.7e+03;
Matches 6; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSCPDPAIKYVFNK 25
   ::::|: | | | | |
Db 14 RELIESQRENTVVDDIHDLFENK 36

RESULT 24
Q9NYL8 HUMAN
ID Q9NYL8 HUMAN PRELIMINARY; PRT; 46 AA.
AC Q9NYL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Ran binding protein 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McCarthy N.F., Lindeman R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237700; AAF64155.1; -; mRNA.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5051 MW; 5CF49EED493DDEBB CRC64;

Query Match      25.8%; Score 34; DB 2; Length 46;
Best Local Similarity 63.6%; Pred. No. 3e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKFS 13
   |::| | |
Db 17 KEVVFANKS 27

RESULT 25
Q7OUJ3 9BASI
ID Q7OUJ3 9BASI PRELIMINARY; PRT; 47 AA.
AC Q7OUJ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Laccase (EC 1.10.3.2) (Fragment).
GN Name=lac;
OS uncultured basidiomycete.
OC Eukaryota; Fungi; Basidiomycota; environmental samples.
OX NCBI_TaxID=175244;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Luis P., Walther G., Kellner H., Martin F., Buscot F.;
RT "Diversity of laccase genes from basidiomycetes in a forest soil.";
RL Soil Biol. Biochem. 36:1025-1036(2004).
DR EMBL; AJ540270; CAD62533.1; -; Genomic_DNA.
DR HSSP; Q9Y780; 1A65.
DR GO; GO:0008471; F:laccase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR011707; Cu-oxidase_3.
DR Pfam; PF07732; Cu-oxidase_3; 1.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 47
SQ SEQUENCE 47 AA; 5506 MW; ACFB3289EF50FAB1 CRC64;

Query Match      25.8%; Score 34; DB 2; Length 47;
```

Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 10 TVKSCPDPAIKEVFD 23
|:|:|:|:|:|
Db 18 SVTQCPIVQKESFD 31

RESULT 26
Q63506 RAT PRELIMINARY; PRT; 18 AA.
AC Q63506
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rat asialoglycoprotein receptor RHL1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87257885; PubMed=3600647;
RA McPhaul M., Berg P.;
RT Identification and characterization of cDNA clones encoding two
RT homologous proteins that are part of the asialoglycoprotein
RT receptor.";
RL Mol. Cell. Biol. 7:1841-1847(1987).
DR EMBL; M16349; AAA42039.1; -; mRNA.
GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 18 AA; 18 MW; 43474B8AB145735C CRC64;

Query Match 25.0%; Score 33; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDPAI 18
|:|:|:|:|:|
Db 6 VQSCPSAI 13

RESULT 27
Q9K5Y2 BACHD PRELIMINARY; PRT; 29 AA.
AC Q9K5Y2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BH3954 protein.
GN OrderedLocusNames=BH3954;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; BA000004; BAB07673.1; -; Genomic_DNA.
DR FIR; B84144; B84144.
KW Complete proteome.
SQ SEQUENCE 29 AA; 3647 MW; 8C1526D4AF5FB264 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 29;
Best Local Similarity 42.9%; Pred. No. 2.6e+03;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 9 FTVKSCPDPAIKEVF 22
|:|:|:|:|:|
Db 3 FVLKGPFDYFEKVF 16

RESULT 28
Q14579 HUMAN PRELIMINARY; PRT; 30 AA.
AC Q14579
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Humer (Fragment).
GN Name=mer5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oberbaumer I.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85129; CAA59443.1; -; mRNA.
DR FIR; S55462; S55462.
DR HSSP; R32119; IQMV.
FT NON_TER
SQ SEQUENCE 30 AA; 3334 MW; 5713AF472692E46E CRC64;

Query Match 25.0%; Score 33; DB 2; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 10 TVKSCPDPAIKEVF 22
|:|:|:|:|:|
Db 13 TIKPSPAASKEYF 25

RESULT 29
Q4XWD9 PLACH PRELIMINARY; PRT; 32 AA.
AC Q4XWD9
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC105305.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.B., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01002657; CAH78772.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 32 AA; 4013 MW; 2906341BFEBFB6E CRC64;

Query Match 25.0%; Score 33; DB 2; Length 32;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;

```
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 FTVKSCP 15
Db 15 FFKVSCP 21

RESULT 30
Q8DWB4 STRMU
ID Q8DWB4_STRMU PRELIMINARY; PRT; 33 AA.
AC Q8DWB4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SMU.153.
GN OrderedLocustNames=SMU.153;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UAI59 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., Meshan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carlson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL; A5014867; AAN57929.1; -; Genomic DNA.
KW Complete proteome.
SQ SEQUENCE 33 AA; 3793 MW; DF72C5448FADBAE0 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 33;
Best Local Similarity 30.4%; Pred. No. 3e+03;
Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAKEVFD 23
Db 3 PEKELDTNTLMKVVNKALSIFD 25

RESULT 31
Q4XE03 PLACH
ID Q4XE03_PLACH PRELIMINARY; PRT; 34 AA.
AC Q4XE03;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC402738.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.B., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAJ01007114; CAH04866.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON_TER 1

SQ SEQUENCE 34 AA; 4209 MW; 2ED6CD1870FF6FD7 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 34;
Best Local Similarity 62.5%; Pred. No. 3.1e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 18 IKEVFDNK 25
Db 27 LKEIFDDK 34

RESULT 32
Q84TL9 BRARP
ID Q84TL9_BRARP PRELIMINARY; PRT; 37 AA.
AC Q84TL9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor CRC (Fragment).
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Magnoliophyta; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Jang H., Hur Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY220357; AAO63101.1; -; mRNA.
DR InterPro; IPR006780; YABBY.
DR Pfam; PF04690; YABBY; 1.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 3937 MW; D87BDE9C33BA34CB CRC64;

Query Match 25.0%; Score 33; DB 2; Length 37;
Best Local Similarity 58.3%; Pred. No. 3.4e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTVK 12
Db 3 PLKRLMDTVTVK 14

RESULT 33
Q8E8X0 SHEON
ID Q8E8X0_SHEON PRELIMINARY; PRT; 41 AA.
AC Q8E8X0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO4531.
GN OrderedLocustNames=SO4531;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.P., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Uitterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealeon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
```

```
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015885; AAN57494.1; -; Genomic_DNA.
DR TIGR; SO4531; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4596 MW; 3F6E72512E9CA13 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 41;
Best Local Similarity 35.3%; Pred. No. 3.8e+03;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSCPDAL 18
| : | : | : | : |
Db 8 KYTIFEGISAIYCPDAV 24

RESULT 34
QX065_THEME PRELIMINARY; PRT; 41 AA.
AC QX065;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TW0970;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001759; AAU36049.1; -; Genomic_DNA.
DR PIR; G72312; G72312.
DR TIGR; TW0970; -.
DR InterPro; IPR010095; TepsaeT_teng_C.
DR Pfam; PF07282; Transposase_35; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4586 MW; 7E52C021810E2023 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 41;
Best Local Similarity 54.5%; Pred. No. 3.8e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 DVLETFVTVKSC 14
| : | : | : | : |
Db 23 EVLETHTSQTC 33

RESULT 35
Q4XGQ9_PLACH PRELIMINARY; PRT; 43 AA.
ID Q4XGQ9;
AC Q4XGQ9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC401678.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
" A comprehensive survey of the plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01006357; CAH83908.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4914 MW; 6A0EBAB7BC302A1E CRC64;

Query Match 25.0%; Score 33; DB 2; Length 43;
Best Local Similarity 35.0%; Pred. No. 3.9e+03;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSCPDALKEV 21
| : | : | : | : |
Db 8 KKIIKEFHLCFCFDQICSV 27

RESULT 36
Q4W2C5_MYZAU PRELIMINARY; PRT; 44 AA.
ID Q4W2C5;
AC Q4W2C5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative thyrotropin beta chain (Fragment).
GN Name=stbh;
OS Myzopoda aurita (old world sucker-footed bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
OC Myzopodidae; Myzopoda.
OX NCBI_TaxID=155038;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hick G.N., Jacobs D.S., Matthee C.R.;
RT "A phylogenetic perspective of the evolution of echolocation and
RT historical biogeography of extant bats (Chiroptera).";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ865655; CAI28439.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 44
SQ SEQUENCE 44 AA; 5045 MW; C7EC3B2E3B2B7520 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 44;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 6; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 5 VLETFVTVKSCPDALKEVF 22
| : | : | : | : |
Db 24 VYETVEIPGCGHVSPVF 41

RESULT 37
Q928G6_LISIN PRELIMINARY; PRT; 44 AA.
ID Q928G6;
AC Q928G6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lin2569 protein.
GN OrderedLocusNames=lin2569;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
```

```
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madiueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordfiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:845-852(2001).
DR EMBL; AL596172; CAC97796.1; -; Genomic_DNA.
DR FIR; AD1753; AD1753.
DR List181; LIN2569; -.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5094 MW; BB580562E5D52418 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 44;
Best Local Similarity 47.1%; Pred. No. 4e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDIAKE 20
Db 4 DLEMMTLGSLDYFAE 20

RESULT 38
Q5XDQ6 STRP6
ID Q5XDQ6_STRP6 PRELIMINARY; PRT; 47 AA.
AC Q5XDQ6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Transposase.
GN OrderedLocusNames=M6_Spy0322;
OS Streptococcus pyogenes (serotype M6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301450;
RN [1]
RC STRAIN=NCAS10394;
RX PubMed=15272401; DOI=10.1086/422697;
RA Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Phillips L.E.,
RA Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.;
RT "Progress toward characterization of the group A Streptococcus
RT metagenome: complete genome sequence of a macrolide-resistant serotype
RT M6 strain.";
RL J. Infect. Dis. 190:727-738(2004).
DR EMBL; CP000003; AAT86457.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 47 AA; 5473 MW; B3250A8EACB8BC95 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 47;
Best Local Similarity 26.1%; Pred. No. 4.3e+03;
Matches 6; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 KKDVLFTFKSCPDIAKEVFVN 24
Db 7 RKETQYTSFKIQEILNKVLQN 29

RESULT 39
Q4XVJ5 PLACH
ID Q4XVJ5_PLACH PRELIMINARY; PRT; 48 AA.
AC Q4XVJ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
```

```
GN ORFName=PC105662.00.0;
OS Plasmodium Chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01002813; CAH79066.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 48 AA; 5772 MW; 2A8986E4D2149C55 CRC64;

Query Match 25.0%; Score 33; DB 2; Length 48;
Best Local Similarity 33.3%; Pred. No. 4.4e+03;
Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLFTFKSCPDIAK 19
Db 7 KKKKKKTLIPFPNSLK 24

RESULT 40
Q45960 CLOBU
ID Q45960_CLOBU PRELIMINARY; PRT; 49 AA.
AC Q45960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RepC'.
GN Name=repC';
OS Clostridium butyricum.
OG Plasmid pCB101.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1492;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCIB 7423;
RA Brehm J.K., Pennock A., Young M., Oultram J.D., Minton N.P.;
RT "Physical characterisation of the replication origin of the cryptic
RT plasmid pCB101 isolated from Clostridium butyricum NCIB 7423.";
RL Plasmid 0:0-0(0).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCIB 7423;
RA Minton N.P.;
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1518909;
RA Brehm J.K., Pennock A., Bullman H.M., Young M., Oultram J.D.,
RA Minton N.P.;
RT "Physical characterization of the replication origin of the cryptic
RT plasmid pCB101 isolated from Clostridium butyricum NCIB 7423.";
RL Plasmid 28:1-13(1992).
DR EMBL; X62684; CAA44560.1; -; Genomic_DNA.
DR PIR; J01600; J01600.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002145; CopG_DNA_bd.
DR Pfam; PF01402; RH1_1; 1.
KW Plasmid.
SQ SEQUENCE 49 AA; 5637 MW; D0C4CB6F2DE130D CRC64;
```

Query Match 25.0%; Score 33; DB 2; Length 49;
 Best Local Similarity 41.7%; Pred. No. 4.5e+03;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 13 SCPDAIKKVFQDN 24
 Db |||:|:|:
 6 SIPDEVKQFFED 17

Search completed: January 20, 2006, 17:33:48
 Job time : 56.321 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:21:43 ; Search time 44.8889 Seconds
(without alignments)
176.187 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKXDVLETFVTKSPDAI 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	8	Adj57563 Human CD9
2	95	100.0	25	8	Adj57562 Human CD9
3	61	64.2	30	6	ABU05051 Human exp
4	49	51.6	10	6	ABU03385 Human exp
5	46	48.4	44	4	AAU03385 Human imm
6	36	37.9	34	3	AAY92549 Human
7	36	37.9	34	3	AAB02778 Human TGF
8	36	37.9	36	2	AAW30357 Fragment
9	36	37.9	36	3	AAU09511 Human TGF
10	36	37.9	46	8	ADS06580 Staphyloc
11	35	36.8	41	4	AAU20329 Human nov
12	34	35.8	15	5	ABP58897 Human DNA
13	34	35.8	17	9	ADV59436 G protein
14	34	35.8	17	9	ADV57877 G protein
15	34	35.8	17	9	ADV58632 G protein
16	34	35.8	18	9	ADV59442 G protein
17	34	35.8	18	9	ADV57883 G protein
18	34	35.8	18	9	ADV58638 G protein
19	34	35.8	20	9	ADV59441 G protein
20	34	35.8	20	9	ADV58637 G protein
21	34	35.8	20	9	ADV57882 G protein
22	34	35.8	34	3	AAY92548 Finger 2
23	34	35.8	34	3	AAU02777 Human TGF
24	34	35.8	36	2	AAW30356 Fragment

25	34	35.8	36	3	AAU09510 Human TGF
26	34	35.8	38	4	ABU33942 Peptide #
27	34	35.8	38	4	AAU33561 Peptide #
28	34	35.8	38	4	AAU73359 Human bon
29	34	35.8	38	4	AAU60687 Human liv
30	34	35.8	38	4	ABG55075 Human liv
31	34	35.8	38	5	ABG43212 Human pep
32	34	35.8	42	3	AAU55485 Arabidops
33	33	34.7	24	7	ADI32847 Peptide 1
34	33	34.7	40	4	ABU41573 Peptide #
35	33	34.7	40	4	AAU35365 Peptide #
36	33	34.7	40	4	AAU75253 Human bon
37	33	34.7	40	4	AAU62444 Human bra
38	33	34.7	40	4	ABG57015 Human liv
39	33	34.7	40	5	ABU44901 Human pep
40	33	34.7	49	2	AAU11424 Human 5'
41	32	33.7	18	9	ADU63982 Human MCS
42	32	33.7	21	4	AAU08273 Human com
43	32	33.7	23	8	ADH35039 Glycopept
44	32	33.7	27	4	AAU08250 Human com
45	32	33.7	28	4	AAU07404 Synthetic
46	32	33.7	28	5	AAU15758 Pda8d pep
47	32	33.7	28	5	ABU76766 Pda8d pep
48	32	33.7	28	5	ABG75545 Optimised
49	32	33.7	32	2	AAU38439 Human tra
50	32	33.7	33	3	AAU16941 Bacteriop

ALIGNMENTS

RESULT 1

ADJ57563

ID ADJ57563 standard; peptide; 18 AA.

XX AC ADJ57563;

XX DT 06-MAY-2004 (first entry)

XX DE Human CD9 fibronectin-binding domain peptide fragment.

XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;

XX KW haemostatic; antiangiogenic; cytostatic.

XX OS Homo sapiens.

XX FN WO2004007685-A2.

XX PD 22-JAN-2004.

XX PF 14-JUL-2003; 2003WO-US022050.

XX PR 12-JUL-2002; 2002US-0395864P.

XX PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;

XX PI Crossno JT, Lu Y;

XX WPI; 2004-122924/12.

XX DR Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

XX PT Claim 7; SEQ ID NO 6; 126pp; English.

XX CC The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57563. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of

CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix
 CC ; and modifying cell-to-cell interaction. The methods are based on the
 CC finding that increased CD9 expression is implicated in (i) decreased
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1
 CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 95; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
 |||||
 Db 1 PKKDVLETFVKSCPDAI 18

RESULT 2
 ADJ57562
 ID ADJ57562 standard; peptide; 25 AA.
 XX
 AC ADJ57562;

DT 06-MAY-2004 (first entry)
 DE Human CD9 fibronectin-binding domain peptide fragment.
 XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
 KW haemostatic; antiangiogenic; cytostatic.
 KW Homo sapiens.

OS

XX

PN WO2004007685-A2.

XX

PD 22-JAN-2004.

XX

PF 14-JUL-2003; 2003WO-US022050.

XX

PR 12-JUL-2002; 2002US-0395864P.

XX

PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;

XX Crosano JT, Lu Y;

XX WPI; 2004-122924/12.

XX

PT Interfering with CD9 binding to fibronectin by binding a fibronectin-

XX binding domain of the CD9 protein or polypeptide, useful in treating

XX thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis

XX and cancers.

XX

PS Claim 7; SEQ ID NO 5; 126pp; English.

CC The present sequence is that of a peptide fragment from the fibronectin-
 CC binding domain of human CD9 ADJ57562. The peptide, or an antibody that
 CC binds to it, is used in claimed methods for: interfering with CD9 binding
 CC to fibronectin; modifying adhesion, motility or spreading of a CD9-
 CC expressing cell on fibronectin; inhibiting proliferation or survival of
 CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix
 CC ; and modifying cell-to-cell interaction. The methods are based on the
 CC finding that increased CD9 expression is implicated in (i) decreased
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1
 CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 95; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
 |||||
 Db 1 PKKDVLETFVKSCPDAI 18

RESULT 2
 ADJ57562
 ID ADJ57562 standard; peptide; 25 AA.
 XX
 AC ADJ57562;

DT 06-MAY-2004 (first entry)
 DE Human CD9 fibronectin-binding domain peptide fragment.
 XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
 KW haemostatic; antiangiogenic; cytostatic.
 KW Homo sapiens.

OS

XX

PN WO2004007685-A2.

XX

PD 22-JAN-2004.

XX

PF 14-JUL-2003; 2003WO-US022050.

XX

PR 12-JUL-2002; 2002US-0395864P.

XX

PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;

XX Crosano JT, Lu Y;

XX WPI; 2004-122924/12.

XX

PT Interfering with CD9 binding to fibronectin by binding a fibronectin-

XX binding domain of the CD9 protein or polypeptide, useful in treating

XX thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis

XX and cancers.

XX

PS Claim 7; SEQ ID NO 5; 126pp; English.

CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 25 AA;

Query Match 100.0%; Score 95; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
 |||||
 Db 1 PKKDVLETFVKSCPDAI 18

RESULT 3
 ABU05051
 ID ABU05051 standard; protein; 30 AA.
 XX
 AC ABU05051;

XX

DT 29-JAN-2003 (first entry)

XX

DE Human expressed protein tag (EPT) #1717.

XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX protease; protease inhibitor; transporter; cytoskeletal protein;

XX receptor; transcription factor; cancer; MHC;

XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;

XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200278524-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-US009671.

XX

PR 28-MAR-2001; 2001US-0279495P.

XX

PR 21-MAY-2001; 2001US-0292544P.

XX

PR 08-AUG-2001; 2001US-0310801P.

XX

PR 01-OCT-2001; 2001US-0326370P.

XX

PR 04-DEC-2001; 2001US-0336780P.

CC (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.
 XX
 PS Example 2; SEQ ID NO 1717; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 30 AA;

Query Match 64.2%; Score 61; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVK 12
 |||||
 Db 19 PKKDVLFTTVK 30

RESULT 4
 ABU03385
 ID ABU03385 standard; protein; 10 AA.
 XX
 AC ABU03385;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #165.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 KW cytoskeletal proteins, receptors or transcription factors), useful for
 KW treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 KW leukemia.

XX Claim 10; SEQ ID NO 165; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 10 AA;

Query Match 51.6%; Score 49; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDVLFTTVK 12
 |||||
 Db 1 KDVLFTTVK 10

RESULT 5
 AAM83184
 ID AAM83184 standard; protein; 44 AA.
 XX
 AC AAM83184;

XX 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen SEQ ID NO:10777.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 11-JUL-2000; 2000US-0217487P.

XX 14-JUL-2000; 2000US-0217496P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 14-AUG-2000; 2000US-0225758P.

XX 14-AUG-2000; 2000US-0225759P.

XX 18-AUG-2000; 2000US-0226279P.

KW amytrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopenia;
 KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;
 KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta3;
 KW growth factor; hybrid protein.
 XX
 OS Homo sapiens.
 XX
 FN WO9708196-A1.
 XX
 PD 06-MAR-1997.
 XX
 XX 27-AUG-1996; 96WO-US014065.
 PF
 XX 28-AUG-1995; 95US-00519777.
 PR
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;
 PI WPI; 1997-179176/16.
 XX
 DR A novel growth factor Neurturin - used to treat neuro-degenerative and
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and
 PT eosinopenia.
 PT
 XX Claim 92; Fig 18; 206pp; English.
 PS
 XX AAW30355-W30377 represent growth factor fragments that are used in a
 CC hybrid polypeptide of the invention. These sequences form a hybrid with
 CC the human neurturin (NT) fragment shown in AAW30354. NT promotes the
 CC growth and differentiation of haematopoietic and neuronal cells, and
 CC their stem cells. The NT gene and protein are used to prevent or treat
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,
 CC nervous system tumours, multiple sclerosis and infection; and
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopenia,
 CC lymphopenia, monocytopenia, neutropenia, anaemia, thrombocytopenia
 CC and stem cell insufficiencies. The NT protein and gene are also useful to
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or
 CC flanking a target sequence) can be used for detecting NT in a sample or
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene
 CC are used to treat diseases promoted by NT expression e.g. obesity
 XX
 SQ Sequence 36 AA;
 Query Match 37.9%; Score 36; DB 2; Length 36;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 PKKQVLETFVKSC 14
 || : | ||||
 Db 20 PKVEQLSNMVKSC 33
 RESULT 9
 AAB09511
 ID AAB09511 standard; peptide; 36 AA.
 XX
 AC AAB09511;
 XX
 XX 11-SEP-2000 (first entry)
 DT Human TGF-beta 3 finger 2 subdomain.
 DE
 XX TGF-beta superfamily; transforming growth factor-beta;
 KW developmental regulation; finger 2 subdomain; basic region;
 KW protein refolding; stability; solubility; osteogenic protein; OP;
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
 KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;

KW connective tissue; cartilage; vulnary.
 XX
 OS Homo sapiens.
 XX
 FN WO200020607-A2.
 XX
 PD 13-APR-2000.
 XX
 XX 07-OCT-1999; 99WO-US023371.
 PF
 XX 07-OCT-1998; 98US-0103418P.
 PR
 XX 16-AUG-1999; 99US-00374958.
 PR
 XX (STYC) STRYKER CORP.
 PA
 XX Oppermann H, Tai M, McCartney J;
 PI WPI; 2000-303787/26.
 XX
 DR Transforming growth factor-beta superfamily member mutant induces tissue
 XX morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
 PT tissue and connective tissue and comprises a substitution in a region of
 PT the finger 2 domain.
 PT
 XX Disclosure; Fig 1; 162pp; English.
 PS
 XX The invention relates to mutant TGF-beta (transforming growth factor-
 CC beta) superfamily members. These mutants comprise one or more amino acid
 CC substitutions in the base region of the finger 2 subdomain, and a C-
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
 CC beta superfamily proteins regulate developmental processes and include
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.
 CC Specific examples of TGF-beta superfamily mutants encompassed by the
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
 CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
 CC cartilage and/or other mineralised skeletal or connective tissues e.g.,
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
 CC damaged mammalian tissue and to prevent or substantially inhibit
 CC immune/inflammatory response-mediated tissue damage and scar tissue
 CC formation following an injury. Compared to the wild-type TGF-beta
 CC superfamily members, the mutant proteins have improved in vitro refolding
 CC properties in a pH range of 6-9, increased solubility in aqueous solution
 CC and improved stability and/or activity. Sequences AAB09481-B09516
 CC represent wild-type finger 2 subdomains from a variety of TGF-beta
 CC superfamily proteins referred to in the specification
 XX
 SQ Sequence 36 AA;
 Query Match 37.9%; Score 36; DB 3; Length 36;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 PKKQVLETFVKSC 14
 || : | ||||
 Db 20 PKVEQLSNMVKSC 33
 RESULT 10
 ADS06580
 ID ADS06580 standard; protein; 46 AA.
 XX
 AC ADS06580;
 XX
 XX 04-NOV-2004 (first entry)
 DT

XX		Staphylococcus epidermis polypeptide seqid 5875.
DE		
KW		antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
KW		recombinant expression vector; infection; computer readable medium;
KW		computer based system.
XX		
OS		Staphylococcus epidermidis.
XX		
FN		US2004147734-A1.
XX		
PD		29-JUL-2004.
XX		
PF		01-DEC-2003; 2003US-00724972.
XX		
PR		08-NOV-1997; 97US-0064964P.
PR		13-AUG-1998; 98US-00134001.
PR		29-NOV-1999; 99US-00450969.
XX		
FA	(DOUC/)	DOUCETTE-STAMM L.
FA	(BUSH/)	BUSH D.
XX		
PI	Doucette-Stamm L,	Bush D;
XX		
DR	WPI; 2004-580138/56.	
XX	N-PSDB; ADS02808.	
XX		
PT	New isolated polypeptide and encoding nucleic acid derived from	
PT	Staphylococcus epidermidis, useful for diagnosing, preventing and/or	
PT	treating an S. epidermidis bacterial infection.	
XX		
PS	Claim 17; SEQ ID NO 5875; 741pp; English.	
XX		
CC	The invention describes an isolated nucleic acid comprising a nucleotide	
CC	sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:	
CC	1-3772) and encoding an Staphylococcus epidermidis polypeptide with any	
CC	of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as	
CC	given in the specification. Also described are: a recombinant expression	
CC	vector; a cell comprising a recombinant expression vector of (1);	
CC	producing an S. epidermidis polypeptide; an isolated nucleic acid	
CC	comprising a nucleotide sequence of at least 8 nucleotides in length; a	
CC	vaccine composition for prevention or treatment of an S. epidermidis	
CC	infection, comprising a nucleic acid cited above and a carrier; treating	
CC	a subject for S. epidermidis infection; a recombinant or substantially	
CC	pure preparation of an S. epidermidis polypeptide or its fragment; a	
CC	vaccine composition for prevention or treatment of an S. epidermidis	
CC	infection; detecting the presence of a Staphylococcus nucleic acid in a	
CC	sample; a computer readable medium having recorded in it the nucleotide	
CC	sequences with SEQ ID NO: 1-3772 or its fragments; a computer based	
CC	system for identifying fragments of the Staphylococcus genome of	
CC	commercial importance; a computer based system for identifying fragments	
CC	of the Staphylococcus plasmids of commercial importance; identifying	
CC	commercially important nucleic acid fragments of the Staphylococcus	
CC	genome and/or plasmids; and identifying an expression modulating fragment	
CC	of the Staphylococcus genome and/or plasmids. The methods and	
CC	compositions of the present invention are useful for the diagnosis,	
CC	prevention and/or treatment of an Staphylococcal epidermidis bacterial	
CC	infection. This is the amino acid sequence of a S. epidermis protein of	
CC	the invention.	
XX		
SQ	Sequence 46 AA;	
	Query Match	37.9%; Score 36; DB 8; Length 46;
	Best Local Similarity	35.3%; Pred No. 3.1e+02;
	Matches	6; Conservative 5; Mismatches 6; Indels 0; Gaps 0
OY	2 KDVLETFVKSCPDAI 18	
	: : : :	
Db	4 KEDMWTYRLKECGDIL 20	
RESULT 11		
AAU20329		

```
PR 08-SEP-2000; 2000US-02332081P.
PR 12-SEP-2000; 2000US-02331968P.
PR 14-SEP-2000; 2000US-02332397P.
PR 14-SEP-2000; 2000US-02332398P.
PR 14-SEP-2000; 2000US-02332399P.
PR 14-SEP-2000; 2000US-02332400P.
PR 14-SEP-2000; 2000US-02332401P.
PR 14-SEP-2000; 2000US-02332401P.
PR 14-SEP-2000; 2000US-02332633P.
PR 14-SEP-2000; 2000US-02332634P.
PR 14-SEP-2000; 2000US-02332635P.
PR 21-SEP-2000; 2000US-02342233P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234397P.
PR 25-SEP-2000; 2000US-0234398P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.

PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI. 2001-457726/49.
XX N-PSDB; AAS32432.
XX
XX Isolated polypeptide for treating, preventing and prognosing disorders
XX related to the endocrine system including endocrine disorders,
XX reproductive disorders, and gastrointestinal disorders and also for
XX testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 386; 558pp; English.
XX
XX The invention relates to cDNAs encoding novel human endocrine antigens or
XX a fragment having biological activity, a domain, an epitope, full length
XX protein, variant, allelic variant or a species homologue of the
XX cDNA/antigen. The DNAs and polypeptides are useful for preventing,
XX treating or ameliorating a medical condition when administered (e.g. by
XX gene therapy or antisense-therapy). Identifying mutations in the genes
XX coding for the antigens is useful for diagnosing a pathological condition
XX or a susceptibility to a pathological condition. The DNAs, antigens and
XX antibodies raised against the antigens useful for treating, preventing
XX and/or prognosing disorders related to the endocrine system or hormone
XX imbalance or reproductive disorders, cancers of endocrine tissues,
XX disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands
XX (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
XX hypothalamus and testes (e.g. vanishing testes syndrome), many examples
XX of diseases and disorders are given in the specification. The present
XX sequence represents an endocrine antigen of the invention. Note: the
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 41 AA;
XX
XX Query Match 36.8%; Score 35; DB 4; Length 41;
XX Best Local Similarity 31.2%; Pred. NO. 3.9e+02;
XX Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 PKQDVLETFYVKSCPD 16
XX |:::|::|
XX Db 5 PHREIFYFTLRPADP 20
XX
XX RESULT 12
XX ABP58897
XX ID ABP58897 standard; peptide; 15 AA.
XX
XX AC ABP58897;
XX
XX XX 10-APR-2003 (first entry)
XX
XX DT Human DNA binding protein 28.27 N-terminal peptide.
XX
XX DE Human; DNA binding protein 28.27; recombinant production; gene therapy;
XX malignant tumour; cancer; blood disease; human immunodeficiency virus;
XX HIV infection; immune disorder; inflammatory condition; cytostatic;
XX antinflammatory; immunomodulator; N-terminal peptide;
```


KW enzyme linked immunosorbent assay; ELISA.
XX Homo sapiens.
XX CNL361152-A.
XX 31-JUL-2002.
XX 26-DEC-2000; 2000CN-00135944.
XX 26-DEC-2000; 2000CN-00135944.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX Mao Y, Xie Y;
XX WPI; 2002-751571/82.
XX New polypeptide human DNA binding 28.27 and polynucleotides encoding this
PT polypeptide.
XX Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX The invention relates to human DNA binding protein 28.27 (ABP8896) and
CC nucleic acids encoding it (AB257649). The protein has a molecular weight
CC of 28.27 kD. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. DNA binding
CC protein 28.27 can be used in the treatment of a variety of diseases such
CC as malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders and inflammatory conditions. The present
CC sequence represents the 15 N-terminal amino acids of human DNA binding
CC protein 28.27 used in ELISA (enzyme linked immunosorbent assay) in an
CC exemplification of the invention
XX
XX SQ Sequence 15 AA;
Query Match 35.8%; Score 34; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 7 EFTVKSQCPD 16
DB 6 ETLSLNKCPCD 15
RESULT 13
ADV59436
ID ADV59436 standard; peptide; 17 AA.
XX
XX ADV59436;
XX DT 10-MAR-2005 (first entry)
XX G protein coupled receptor peptide SEQ ID NO 6941.
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX Unidentified.
XX WO2004111636-A2.
XX 23-DEC-2004.
XX 17-JUN-2004; 2004WO-EP051158.
XX 17-JUN-2003; 2003EP-00101775.
XX 17-JUN-2003; 2003US-0479061P.
XX (VIBV-) VIB VZW.
XX (UYGE-) UNIV GENT.
XX Kas K, Vandekerckhove J, Krols L;
PI

PI Kas K, Vandekerckhove J, Krols L;
XX WPI; 2005-057893/06.
XX Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX Example; SEQ ID NO 6941; 265pp; English.
XX The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
XX SQ Sequence 17 AA;
Query Match 35.8%; Score 34; DB 9; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 EFTVKSQCPD 16
DB 7 ETGEVQACPD 16
RESULT 14
ADV57877
ID ADV57877 standard; peptide; 17 AA.
XX
XX ADV57877;
XX DT 10-MAR-2005 (first entry)
XX G protein coupled receptor peptide SEQ ID NO 5381.
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX Unidentified.
XX WO2004111636-A2.
XX 23-DEC-2004.
XX 17-JUN-2004; 2004WO-EP051158.
XX 17-JUN-2003; 2003EP-00101775.
XX 17-JUN-2003; 2003US-0479061P.
XX (VIBV-) VIB VZW.
XX (UYGE-) UNIV GENT.
XX Kas K, Vandekerckhove J, Krols L;
PI

XX WPI; 2005-057893/06.
DR
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
XX
PS Example; SEQ ID NO 5381; 265pp; English.
XX
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers, preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
XX
SQ Sequence 17 AA;
Query Match 35.8%; Score 34; DB 9; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 EFTFTVKSCPD 16
||| :|||
Db 7 ETGEVQACPD 16
RESULT 15
ADV58632
ID ADV58632 standard; peptide; 17 AA.
XX
AC ADV58632;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 6137.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX WPI; 2005-057893/06.

DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
XX
PS Example; SEQ ID NO 6137; 265pp; English.
XX
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers, preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
XX
SQ Sequence 17 AA;
Query Match 35.8%; Score 34; DB 9; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 EFTFTVKSCPD 16
||| :|||
Db 7 ETGEVQACPD 16
RESULT 16
ADV59442
ID ADV59442 standard; peptide; 18 AA.
XX
AC ADV59442;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 6947.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 XX Example; SEQ ID NO 6947; 265pp; English.

PS The invention relates to a method of identifying a peptide combo which
 XX corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a G-protein coupled receptor peptide
 CC combo.

XX SQ Sequence 18 AA;

Query Match 35.8%; Score 34; DB 9; Length 18;
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 16
 |||:|:
 Db 7 ETGEVQACPD 16

RESULT 17

ADV57883
 ID ADV57883 standard; peptide; 18 AA.

AC ADV57883;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 5387.

DE diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

OS Unidentified.

PN WC2004111636-A2.

PD 23-DEC-2004.

PF 17-JUN-2004; 2004WO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

PA (UYGE-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX

PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 XX Example; SEQ ID NO 5387; 265pp; English.

PS The invention relates to a method of identifying a peptide combo which
 XX corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a G-protein coupled receptor peptide
 CC combo.

XX SQ Sequence 18 AA;

Query Match 35.8%; Score 34; DB 9; Length 18;
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 16
 |||:|:
 Db 7 ETGEVQACPD 16

RESULT 18

ADV58638

ID ADV58638 standard; peptide; 18 AA.

AC ADV58638;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 6143.

DE diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

OS Unidentified.

PN WC2004111636-A2.

PD 23-DEC-2004.

PF 17-JUN-2004; 2004WO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

PA (UYGE-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,

PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.

XX Example; SEQ ID NO 6143; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.

XX SQ Sequence 18 AA;

Query Match 35.8%; Score 34; DB 9; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 16
||| |::|||
Db 7 ETGEVQACPD 16

RESULT 19

ADV59441
ID ADV59441 standard; peptide; 20 AA.

XX AC ADV59441;

XX DT 10-MAR-2005 (first entry)

XX DE G protein coupled receptor peptide SEQ ID NO 6946.

XX KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX OS Unidentified.

XX PN WO2004111636-A2.

XX PD 23-DEC-2004.

XX PF 17-JUN-2004; 2004WO-EP051158.

XX PR 17-JUN-2003; 2003EP-00101775.

XX PR 17-JUN-2003; 2003US-0479061P.

XX PA (VIBV-) VIB VZW.

XX PA (UYGE-) UNIV GENT.

XX PI Kas K, Vandekerckhove J, Krols L;

XX DR WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the

PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.

XX Example; SEQ ID NO 6946; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.

XX SQ Sequence 20 AA;

Query Match 35.8%; Score 34; DB 9; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETFTVKSCPD 16
||| |::|||
Db 10 ETGEVQACPD 19

RESULT 20

ADV58637

ID ADV58637 standard; peptide; 20 AA.

XX AC ADV58637;

XX DT 10-MAR-2005 (first entry)

XX DE G protein coupled receptor peptide SEQ ID NO 6142.

XX KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX OS Unidentified.

XX PN WO2004111636-A2.

XX PD 23-DEC-2004.

XX PF 17-JUN-2004; 2004WO-EP051158.

XX PR 17-JUN-2003; 2003EP-00101775.

XX PR 17-JUN-2003; 2003US-0479061P.

XX PA (VIBV-) VIB VZW.

XX PA (UYGE-) UNIV GENT.

XX PI Kas K, Vandekerckhove J, Krols L;

XX DR WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the

PT family of protein.
XX Example; SEQ ID NO 6142; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
XX SQ Sequence 20 AA;
Query Match 35.8%; Score 34; DB 9; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 ETFTVKSCPD 16
||| |::|||
Db 10 ETGEVQACPD 19
RESULT 21
ADV57882
ID ADV57882 standard; peptide; 20 AA.
XX
AC ADV57882;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 5386.
XX
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX Unidentified.
XX WO2004111636-A2.
XX
XX 23-DEC-2004.
XX
XX 17-JUN-2004; 2004WO-EP051158.
XX
XX 17-JUN-2003; 2003EP-00101775.
XX
XX 17-JUN-2003; 2003US-0479061P.
XX
XX (VIBV-) VIB VZW
XX (UYGE-) UNIV GENT.
XX
XX Kas K, Vandekerckhove J, Kroels L;
XX
XX WPI; 2005-057893/06.
XX
XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.

XX
PS Example; SEQ ID NO 5386; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
XX SQ Sequence 20 AA;
Query Match 35.8%; Score 34; DB 9; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 ETFTVKSCPD 16
||| |::|||
Db 10 ETGEVQACPD 19
RESULT 22
AAY92548
ID AAY92548 standard; peptide; 34 AA.
XX
AC AAY92548;
XX
DT 10-AUG-2000 (first entry)
XX
DE Finger 2 subdomain of TGF-beta2.
XX
XX finger 2 subdomain; BMP; TGF-beta family; protein refolding;
XX fusion protein; osteopathic; antibacterial; cytostatic.
XX Homo sapiens.
XX WO200020449-A2.
XX
XX 13-APR-2000.
XX
XX 07-OCT-1999; 99WO-US023372.
XX
XX 07-OCT-1998; 98US-0103418P.
XX
XX 16-AUG-1999; 99US-00375333.
XX
XX (STYC) STRYKER CORP.
XX
XX Oppermann H, Tai M, McCartney J;
XX
XX WPI; 2000-303743/26.
XX
XX A biologically active TGF-beta family member fusion protein competent to
XX refold, comprising a C-terminal linked TGF-beta family protein.
XX Disclosure; Page 131; 160pp; English.
XX
XX AAY92519-53 are C-terminal residues of the finger 2 subdomain of various

CC known members of the BMP and TGF-beta families, starting with the first
 CC residue following the cysteine doublet. Novel proteins comprise
 CC biologically active TGF-beta family member fusion proteins competent to
 CC refold under suitable refolding conditions. The fusion proteins comprise:
 CC (1) a TGF-beta family protein C-terminal seven cysteine domain,
 CC comprising finger 1, finger 2 and heel subdomains; and (2) a heterologous
 CC leader sequence domain operatively linked to the C-terminal domain.
 CC Truncations, heterodimers and mutants of these fusion proteins and
 CC methods of purifying the heterodimers are also claimed. The TGF-beta
 CC family proteins can be used to induce the full cascade of morphogenic
 CC events which culminate in skeletal tissue formation, including cartilage
 CC and endochondral bone formation. They are useful in the binding of fibrin
 CC and fibronectin to the implanted matrix, chemotaxis of cells,
 CC proliferation of fibroblasts, differentiation into chondroblasts,
 CC cartilage formation, vascular invasion, bone formation, remodeling, and
 CC bone marrow differentiation. The proteins have improved physical
 CC properties such as solubility and stability, improved biological
 CC activity, including altered receptor binding and improved targeting
 CC capabilities

XX Sequence 34 AA;

Query Match 35.8%; Score 34; DB 3; Length 34;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFYKSC 14
 DB 18 PKIEQLSNMIVKSC 31

RESULT 23
 AAB02777
 ID AAB02777 standard; protein; 34 AA.

XX AAB02777;
 XX 22-AUG-2000 (first entry)
 XX Human TGF-beta2 finger 2 sub-domain sequence SEQ ID NO:30.
 XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
 KW bone morphogenic protein; osteogenic protein; mutant; modified;
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
 KW tissue repair; regeneration; proliferation; differentiation.

XX Homo sapiens.
 XX WO200020591-A2.
 XX 13-APR-2000.
 XX 07-OCT-1999; 99WO-US023370.
 XX 07-OCT-1998; 98US-0103418P.
 XX 16-AUG-1999; 99US-00374936.

XX (STYC) STRYKER CORP.
 XX Oppermann H, Tai M, McCartney J;
 XX WPI; 2000-303776/26.

XX Novel TGF-beta superfamily mutant chimeric protein, useful for inducing
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one
 PT monomer containing domains from two family members.

XX Disclosure; Page 120; 149pp; English.

XX The present invention describes a tumour growth factor beta (TGF-beta)
 CC superfamily chimeric protein (I) derived from at least 2 different
 CC members of the superfamily comprising a dimer with one monomer that

CC contains a finger 2 domain derived from a first family member and a
 CC finger 1 domain and heel domain, both derived from a second family
 CC member. The monomer further comprises a conserved C-terminal cysteine
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair
 CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised
 CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve
 CC and for inducing the proliferation and differentiation of uncommitted
 CC progenitor cells in a tissue-specific manner to support new tissue
 CC formation. AAB29897 to AAA29897 and AAB02748 to AAB02824 represent
 CC sequences used in the exemplification of the present invention

XX Sequence 34 AA;

Query Match 35.8%; Score 34; DB 3; Length 34;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFYKSC 14
 DB 18 PKIEQLSNMIVKSC 31

RESULT 24
 AAW30356
 ID AAW30356 standard; peptide; 36 AA.

XX AAW30356;
 XX 11-FEB-1998 (first entry)
 XX Fragment #2 of growth factor TGFbeta2.

XX Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopaenia;
 KW acute spinal cord injury; multiple sclerosis; eosinopaenia; lymphopaenia;
 KW monocytopenaia; neutropaenia; anaemia; thrombocytopaenia; neuroblastoma;
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta2;
 KW growth factor; hybrid protein.

XX Homo sapiens.
 XX WO9708196-A1.
 XX 06-MAR-1997.

XX 27-AUG-1996; 96WO-US014065.
 XX 28-AUG-1995; 95US-00519777.

XX (UNIW) UNIV WASHINGTON.

XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;

XX WPI; 1997-179176/16.

XX A novel growth factor Neurturin - used to treat neuro-degenerative and
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and
 PT eosinopenia.

XX Claim 92; Fig 18; 206pp; English.

XX AAW30355-W30377 represent growth factor fragments that are used in a
 CC hybrid polypeptide of the invention. These sequences form a hybrid with
 CC the human neurturin (NT) fragment shown in AAW30354. NT promotes the
 CC growth and differentiation of haematopoietic and neuronal cells, and
 CC their stem cells. The NT gene and protein are used to prevent or treat
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,

CC nervous system tumours, multiple sclerosis and infection; and
 CC haematopoietic cell degenerative diseases, e.g. eosinopaenia, basopaenia,
 CC lymphopaenia, monocytopenia, neutropaenia, anaemia, thrombocytopaenia,
 CC and stem cell insufficiencies. The NT protein and gene are also useful to
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or
 CC flanking a target sequence) can be used for detecting NT in a sample or
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene
 CC are used to treat diseases promoted by NT expression e.g. obesity
 XX
 XX SQ Sequence 36 AA;

Query Match 35.8%; Score 34; DB 2; Length 36;
 Best Local Similarity 50.0%; Pred. No. 5e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14
 || : |||||
 Db 20 PKIEQLSNMIVKSC 33

RESULT 25
 AAB09510
 ID AAB09510 standard; peptide; 36 AA.

XX AAB09510;

XX 11-SEP-2000 (first entry)

XX Human TGF-beta 2 finger 2 subdomain.

XX TGF-beta superfamily; transforming growth factor-beta;
 KW developmental regulation; finger 2 subdomain; basic region;
 KW protein refolding; stability; solubility; osteogenic protein; OP;
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
 KW inhibitor; tissue morphogenesis; regeneration; bone; dental tissue;
 KW connective tissue; cartilage; vulvular;

XX Homo sapiens.

XX WO200020607-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US023371.

XX 07-OCT-1998; 98US-0103418P.

XX 16-AUG-1999; 99US-00374958.

XX (STYC) STRYKER CORP.

XX Oppermann H, Tai M, McCartney J;

XX WPI; 2000-303787/26.

XX Transforming growth factor-beta superfamily member mutant induces tissue
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
 PT tissue and connective tissue and comprises a substitution in a region of
 PT the finger 2 domain.

XX Disclosure; Fig 1; 162pp; English.

XX The invention relates to mutant TGF-beta (transforming growth factor-
 CC beta) superfamily members. These mutants comprise one or more amino acid
 CC substitutions in the base region of the finger 2 subdomain, and a C-
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
 CC beta superfamily proteins regulate developmental processes and include
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibitors.
 CC Specific examples of TGF-beta superfamily mutants encompassed by the

CC invention are the finger 2 subdomain mutants of human osteogenic protein-
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
 CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
 CC cartilage and/or other mineralised skeletal or connective tissues e.g.,
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
 CC damaged mammalian tissue and to prevent or substantially inhibit
 CC immune/inflammatory response-mediated tissue damage and scar tissue
 CC formation following an injury. Compared to the wild-type TGF-beta
 CC superfamily members, the mutant proteins have improved in vitro refolding
 CC properties in a pH range of 6-9, increased solubility in aqueous solution
 CC and improved stability and/or activity. Sequences AAB09481-B09516
 CC represent wild-type finger 2 subdomains from a variety of TGF-beta
 CC superfamily proteins referred to in the specification
 XX
 XX SQ Sequence 36 AA;

Query Match 35.8%; Score 34; DB 3; Length 36;
 Best Local Similarity 50.0%; Pred. No. 5e+02;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14

|| : |||||
 Db 20 PKIEQLSNMIVKSC 33

RESULT 26

AAB39942

ID AAB39942 standard; peptide; 38 AA.

XX AAB39942;

XX 04-FEB-2002 (first entry)

XX Peptide #7448 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 21-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human foetal liver.

XX Claim 27; SEQ ID NO 32577; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 38 AA;

Query Match 35.8%; Score 34; DB 4; Length 38;

Best Local Similarity 60.0%; Pred. No. 5.3e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15

Db 15 LSSWTVASCP 24

RESULT 27

AAM33561

ID AAM33561 standard; protein; 38 AA.

XX AC AAM33561;

XX DT 17-OCT-2001 (first entry)

XX PEPTIDE #7598 encoded by probe for measuring placental gene expression.

XX DE Probe; microarray; human; placenta; antenatal diagnosis;

XX KW Genetic disorder.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX DR Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human placenta.

XX PS Claim 27; SEQ ID NO 33830; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP:

XX CC see AA1315-AA157546). The present sequence is a peptide encoded by one

XX CC such probe. The probes are useful for producing a microarray for

XX CC predicting, measuring and displaying gene expression in samples derived

XX CC from human placenta. The probes are useful for antenatal diagnosis of

XX CC human genetic disorders

XX SQ Sequence 38 AA;

Query Match 35.8%; Score 34; DB 4; Length 38;

Best Local Similarity 60.0%; Pred. No. 5.3e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15

Db 15 LSSWTVASCP 24

RESULT 28

AAM73359

ID AAM73359 standard; protein; 38 AA.

XX AC AAM73359;

XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33665.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;

XX KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PS gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 33665; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC bone marrow. They can be used to measure gene expression in bone marrow

XX CC samples, which may enable the improved diagnosis and treatment of cancers

XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a

XX CC protein encoded by one of the probes of the invention

XX SQ Sequence 38 AA;

Query Match 35.8%; Score 34; DB 4; Length 38;

Best Local Similarity 60.0%; Pred. No. 5.3e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15

Db 15 LSSWTVASCP 24

RESULT 29

AAM60687

ID AAM60687 standard; protein; 38 AA.

XX AC AAM60687;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32792.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;

XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX OS Homo sapiens.

PA	(MOLE-) MOLECULAR DYNAMICS INC.	
XX		
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	
XX		
DR	WPI; 2002-114183/15.	
XX		
PT	Spatially-addressable set of single exon nucleic acid probes, used to	
PT	measure gene expression in human lung samples.	
XX		
PS	Claim 27; SEQ ID NO 32877; 634bp; English.	
XX		
CC	The invention relates to a spatially-addressable set of single exon	
CC	nucleic acid probes for measuring gene expression in a sample derived	
CC	from human lung comprising single exon nucleic acid probes having one of	
CC	12614 nucleic acid sequences mentioned in the specification, or their	
CC	complements or the 12387 open reading frames derived from the 12614	
CC	probes. Also included are a microarray comprising the novel set of probes	
CC	; the novel set of probes which hybridise at high stringency to a nucleic	
CC	acid expressed in the human lung; measuring gene expression in a sample	
CC	derived from human lung, comprising (a) contacting the array with a	
CC	collection of detectably labeled nucleic acids derived from human lung	
CC	mRNA, and (b) measuring the label detectably bound to each probe of the	
CC	array; identifying exons in a eukaryotic genome, comprising (a)	
CC	algorithmically predicting at least one exon from genomic sequences of	
CC	the eukaryote; and (b) detecting specific hybridisation of detectably	
CC	labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,	
CC	having a fragment identical to the predicted exon, the probe is included	
CC	in the above mentioned microarray; assigning exons to a single gene,	
CC	comprising (a) identifying exons from genomic sequence by the method	
CC	above and (b) measuring the expression of each of the exons in several	
CC	tissues and/or cell types using hybridisation to a single exon	
CC	microarrays having a probe with the exon, where a common pattern of	
CC	expression of the exons in the tissues and/or cell types indicates that	
CC	the exons should be assigned to a single gene; a peptide comprising one	
CC	of 12011 sequences, mentioned in the specification, or encoded by the	
CC	probes/open reading frames (ORF). The probes are used for gene expression	
CC	analysis, and for identifying exons in a gene, particularly using human	
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung	
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung	
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,	
CC	tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-	
CC	Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary	
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,	
CC	Kargener syndrome, fibrocystic pulmonary dysplasia, primary ciliary	
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The	
CC	present sequence is a peptide/protein encoded by a single exon probe of	
CC	the invention. Note: The sequence data for this patent did not form part	
CC	of the printed specification, but was obtained in electronic format	
CC	directly from WIPO at ftp.wipo.int/pub/published_pt_sequences	
XX		
SQ	Sequence 38 AA;	
	Query Match 35.8%; Score 34; DB 5; Length 38;	
	Best Local Similarity 60.0%; Pred. No. 5.3e+02;	
	Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
QY	6 LETFTVKSCP 15	
	: : : :	
Db	15 LSSWTVASCP 24	
RESULT 32		
AAG55485		
ID	AAG55485 standard; protein; 42 AA.	
XX		
AC	AAG55485;	
XX		
DT	18-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 71153.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	

KW	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999; 99US-0121825P.	
PR	05-MAR-1999; 99US-0121180P.	
PR	09-MAR-1999; 99US-0123548P.	
PR	23-MAR-1999; 99US-0125788P.	
PR	25-MAR-1999; 99US-0126264P.	
PR	29-MAR-1999; 99US-0126785P.	
PR	01-APR-1999; 99US-0127462P.	
PR	06-APR-1999; 99US-0128234P.	
PR	08-APR-1999; 99US-0128714P.	
PR	16-APR-1999; 99US-0129845P.	
PR	19-APR-1999; 99US-0130077P.	
PR	21-APR-1999; 99US-0130449P.	
PR	23-APR-1999; 99US-0130510P.	
PR	23-APR-1999; 99US-0130891P.	
PR	28-APR-1999; 99US-0131444P.	
PR	30-APR-1999; 99US-0132048P.	
PR	30-APR-1999; 99US-0132407P.	
PR	04-MAY-1999; 99US-0132484P.	
PR	05-MAY-1999; 99US-0132485P.	
PR	06-MAY-1999; 99US-0132486P.	
PR	06-MAY-1999; 99US-0132487P.	
PR	07-MAY-1999; 99US-0132863P.	
PR	11-MAY-1999; 99US-0134256P.	
PR	14-MAY-1999; 99US-0134218P.	
PR	14-MAY-1999; 99US-0134219P.	
PR	14-MAY-1999; 99US-0134221P.	
PR	14-MAY-1999; 99US-0134370P.	
PR	18-MAY-1999; 99US-0134768P.	
PR	19-MAY-1999; 99US-0134941P.	
PR	20-MAY-1999; 99US-0135124P.	
PR	21-MAY-1999; 99US-0135353P.	
PR	24-MAY-1999; 99US-0135629P.	
PR	25-MAY-1999; 99US-0136021P.	
PR	27-MAY-1999; 99US-0136392P.	
PR	28-MAY-1999; 99US-0136782P.	
PR	01-JUN-1999; 99US-0137222P.	
PR	03-JUN-1999; 99US-0137528P.	
PR	04-JUN-1999; 99US-0137502P.	
PR	07-JUN-1999; 99US-0137724P.	
PR	08-JUN-1999; 99US-0138094P.	
PR	10-JUN-1999; 99US-0138540P.	
PR	10-JUN-1999; 99US-0138847P.	
PR	14-JUN-1999; 99US-0139119P.	
PR	16-JUN-1999; 99US-0139452P.	
PR	16-JUN-1999; 99US-0139453P.	
PR	17-JUN-1999; 99US-0139492P.	
PR	18-JUN-1999; 99US-0139454P.	
PR	18-JUN-1999; 99US-0139455P.	
PR	18-JUN-1999; 99US-0139456P.	
PR	18-JUN-1999; 99US-0139457P.	
PR	18-JUN-1999; 99US-0139458P.	
PR	18-JUN-1999; 99US-0139459P.	
PR	18-JUN-1999; 99US-0139460P.	
PR	18-JUN-1999; 99US-0139461P.	
PR	18-JUN-1999; 99US-0139462P.	
PR	18-JUN-1999; 99US-0139463P.	
PR	18-JUN-1999; 99US-0139750P.	
PR	18-JUN-1999; 99US-0139763P.	
PR	21-JUN-1999; 99US-0139817P.	
PR	22-JUN-1999; 99US-0139899P.	
PR	23-JUN-1999; 99US-0140353P.	
PR	23-JUN-1999; 99US-0140354P.	
PR	24-JUN-1999; 99US-0140695P.	

```
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.

PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 35.8%; Score 34; DB 3; Length 42;
Best Local Similarity 100.0%; Fred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TVKSCP 15
Db 28 TVKSCP 33

RESULT 33
ADI32847
ID ADI32847 standard; peptide; 24 AA.
XX AC ADI32847;
XX DT 22-APR-2004 (first entry)
XX DE Peptide 1 related to human betaine homocysteine methyl transferase BHMT.
XX KW human; betaine homocysteine methyl transferase; BHMT; homocysteinaemia;
XX KW cardiovascular disease.
XX OS Unidentified.
XX PN CN1408854-A.
XX PD 09-APR-2003.
XX
```

PF 24-SEP-2001; 2001CN-00142193.
 XX
 PR 24-SEP-2001; 2001CN-00142193.
 XX
 PA (HYGI-) INST HYGIENICS & ENVIRONMENTAL MEDICAL S.
 PI Qian L, Wu S;
 XX WPI; 2003-680504/65.
 DR
 XX Preparing and applying recombined human betaine homocysteine methyl transferase.
 PT
 PT
 XX Example 1; Page 5; 6pp; Chinese.
 PS
 XX The invention relates to a novel method for preparing and applying recombinant human betaine homocysteine methyl transferase (BHMT) to biological technology which relates to efficient expression technology of recombinant human BHMT. The recombinant human betaine homocysteine methyl transferase of the invention may be used as a biological preparation for treating homocysteinaemia and related cardiovascular diseases. The current sequence is that of the peptide fragment 1 of the invention which is related to human betaine homocysteine methyl transferase (BHMT).
 CC
 CC
 XX Sequence 24 AA;
 SQ
 Query Match 34.7%; Score 33; DB 7; Length 24;
 Best Local Similarity 85.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 DVLETF 10
 DB ||:|||||
 17 DVMEFT 23
 RESULT 34
 ABB41573
 ID ABB41573 standard; peptide; 40 AA.
 XX
 AC ABB41573;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #9079 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 CC Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human foetal liver.
 PT
 PT
 XX Claim 27; SEQ ID NO 34208; 639pp + Sequence Listing; English.

XX
 CC The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 40 AA;
 Query Match 34.7%; Score 33; DB 4; Length 40;
 Best Local Similarity 60.0%; Pred. No. 8.2e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LETFTVKSCP 15
 DB :|||||
 1 VSTFTVKQAP 10
 RESULT 35
 AAM35365
 ID AAM35365 standard; protein; 40 AA.
 XX
 AC AAM35365;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #9402 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488897/53.
 XX
 CC Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
 PT
 PT
 XX Claim 27; SEQ ID NO 35634; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SNP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
 CC
 XX Sequence 40 AA;
 Query Match 34.7%; Score 33; DB 4; Length 40;
 Best Local Similarity 60.0%; Pred. No. 8.2e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY      6 LETFTVKSCP 15
DB      : |||||
        1 VSTFTVKQAP 10

RESULT 36
AAM75253
ID      AAM75253 standard; protein; 40 AA.
XX
AC      AAM75253;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human bone marrow expressed probe encoded protein SEQ ID NO: 35559.
XX
KW      Human; bone marrow expressed exon; gene expression analysis; probe;
KW      microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS      Homo sapiens.
XX
PN      WO200157276-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US000668.
XX
PR      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
PR      30-JUN-2000; 2000US-00608408.
PR      03-AUG-2000; 2000US-00632366.
PR      21-SEP-2000; 2000US-0234687P.
PR      27-SEP-2000; 2000US-0236359P.
PR      04-OCT-2000; 2000GB-00024263.
XX
PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR      WPI; 2001-488900/53.
XX
PT      Human genome-derived single exon nucleic acid probes useful for analyzing
PT      gene expression in human bone marrow.
XX
PS      Example 4; SEQ ID NO 35559; 658pp + Sequence Listing; English.
XX
CC      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      bone marrow. They can be used to measure gene expression in bone marrow
CC      samples, which may enable the improved diagnosis and treatment of cancers
CC      such as lymphoma, leukaemia and myeloma. The present sequence is a
CC      protein encoded by one of the probes of the invention
XX
SQ      Sequence 40 AA;

Query Match      34.7%; Score 33; DB 4; Length 40;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches      6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LETFTVKSCP 15
DB      : |||||
        1 VSTFTVKQAP 10

RESULT 37
AAM62444
ID      AAM62444 standard; protein; 40 AA.
XX
AC      AAM62444;
XX
DT      05-NOV-2001 (first entry)
XX
DE      Human brain expressed single exon probe encoded protein SEQ ID NO: 34549.

XX
KW      Human; brain expressed exon; gene expression analysis; probe; microarray;
KW      Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS      Homo sapiens.
XX
PN      WO200157275-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US000667.
XX
PR      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
PR      30-JUN-2000; 2000US-00608408.
PR      03-AUG-2000; 2000US-00632366.
PR      21-SEP-2000; 2000US-0234687P.
PR      27-SEP-2000; 2000US-0236359P.
PR      04-OCT-2000; 2000GB-00024263.
XX
PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR      WPI; 2001-483446/52.
XX
PT      Single exon nucleic acid probes for analyzing gene expression in human
PT      brains.
XX
PS      Example 4; SEQ ID NO 34549; 650pp + Sequence Listing; English.
XX
CC      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      brain. They can be used to measure gene expression in brain cell samples,
CC      which may enable the diagnosis and improved treatment of nervous system
CC      diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC      epilepsy and cancers. The present sequence is a protein encoded by one of
CC      the probes of the invention
XX
SQ      Sequence 40 AA;

Query Match      34.7%; Score 33; DB 4; Length 40;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches      6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LETFTVKSCP 15
DB      : |||||
        1 VSTFTVKQAP 10

RESULT 38
ABG57015
ID      ABG57015 standard; peptide; 40 AA.
XX
AC      ABG57015;
XX
DT      25-FEB-2003 (first entry)
XX
DE      Human liver peptide, SEQ ID No 35663.
XX
KW      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW      hypercholesterolaemia; coronary heart disease.
XX
OS      Homo sapiens.
XX
PN      WO200157273-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US000664.
XX
PR      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT
XX
XX Claim 27; SEQ ID NO 35663; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 40 AA;
SQ
Query Match 34.7%; Score 33; DB 4; Length 40;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 LETFTVKSCP 15
: ||||| |
Db 1 VSTFTVKQAP 10
RESULT 39
ABG44901
ID ABG44901 standard; peptide; 40 AA.
XX
XX ABG44901;
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human peptide encoded by genome-derived single exon probe SEQ ID 34566.
DE
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
OS
XX WO200186003-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000665.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX
XX 26-MAY-2000; 2000US-0207456P.
PR

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
PT
XX
XX Claim 27; SEQ ID NO 34566; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 40 AA;
SQ
Query Match 34.7%; Score 33; DB 5; Length 40;
Best Local Similarity 60.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 LETFTVKSCP 15
: ||||| |
Db 1 VSTFTVKQAP 10
RESULT 40
AAV11424
ID AAV11424 standard; protein; 49 AA.
XX
XX AAV11424;
XX

DT 21-JUN-1999 (first entry)
 XX Human 5' EST secreted protein SEQ ID No 246.
 DE ,
 XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition.
 XX
 OS Homo sapiens.
 XX
 XX WO9906551-A2.
 XX
 XX 11-FEB-1999.
 XX
 XX 31-JUL-1998; 98WO-IB001235.
 PF
 XX 01-AUG-1997; 97US-00905133.
 PR
 XX (GEST) GENSET.
 PA
 XX Dumas Milne Edwards J, Duclert A, Lacroix B;
 PI
 XX WPI; 1999-153781/13.
 DR N-PSDB; AAX39490.
 DR
 XX New nucleic acids encoding human secreted - proteins obtained from cDNA
 PT libraries prepared from substantia nigra, cerebellum, surrenals and fetal
 PT brain tissue.
 PT
 XX Claim 34; Page 367; 434pp; English.
 PS
 XX AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY11374 to
 CC AAY11531, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell
 XX
 SQ Sequence 49 AA;

Query Match 34.7%; Score 33; DB 2; Length 49;
 Best Local Similarity 85.7%; Pred. No. 1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TFTVKSC 14
 |||||
 Db 6 TFTFKSC 12

Search completed: January 20, 2006, 17:30:43
 Job time : 46.8889 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:26:44 ; Search time 12.4444 Seconds
(without alignments)
119.584 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKKDVLETFVKSCPDAl 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	29	1	US-08-254-493-6
2	95	100.0	29	1	US-08-408-222B-6
3	36	37.9	31	1	US-08-486-057B-38
4	36	37.9	31	1	US-08-789-588-38
5	36	37.9	32	6	5262319-9
6	36	37.9	34	2	US-09-374-958C-31
7	36	37.9	34	2	US-09-374-936-31
8	36	37.9	42	2	US-09-848-664A-14
9	35	36.8	17	2	US-08-974-549A-100
10	35	36.8	17	2	US-08-912-951-100
11	35	36.8	17	2	US-09-402-181B-100
12	35	36.8	17	2	US-09-721-456-100
13	35	36.8	26	2	US-08-851-843A-140
14	35	36.8	26	2	US-08-974-549A-258
15	35	36.8	26	2	US-08-854-050-140
16	35	36.8	26	2	US-09-430-323-140
17	35	36.8	26	2	US-09-402-181B-258
18	35	36.8	26	2	US-09-721-456-258
19	35	36.8	26	2	US-09-766-253-140
20	35	36.8	26	2	US-10-054-295-140
21	35	36.8	26	2	US-09-438-486A-140
22	35	36.8	27	2	US-08-851-843A-162
23	35	36.8	27	2	US-08-974-549A-282
24	35	36.8	27	2	US-08-854-050-162
25	35	36.8	27	2	US-09-430-323-162
26	35	36.8	27	2	US-09-402-181B-282
27	35	36.8	27	2	US-09-721-456-282

28	35	36.8	27	2	US-09-766-253-162	Sequence 162, App
29	35	36.8	27	2	US-10-054-295-162	Sequence 162, App
30	35	36.8	27	2	US-09-438-486A-162	Sequence 162, App
31	35	36.8	32	2	US-09-082-358B-57	Sequence 57, Appl
32	35	36.8	34	2	US-08-974-549A-45	Sequence 45, Appl
33	35	36.8	34	2	US-08-912-951-45	Sequence 45, Appl
34	35	36.8	34	2	US-09-402-181B-45	Sequence 45, Appl
35	35	36.8	34	2	US-09-721-456-45	Sequence 45, Appl
36	35	36.8	34	2	US-09-042-460-46	Sequence 46, Appl
37	34	35.8	31	1	US-08-486-057B-20	Sequence 20, Appl
38	34	35.8	31	1	US-08-789-588-20	Sequence 20, Appl
39	34	35.8	34	2	US-09-374-958C-30	Sequence 30, Appl
40	34	35.8	34	2	US-09-374-936-30	Sequence 30, Appl
41	34	35.8	42	2	US-09-848-664A-13	Sequence 13, Appl
42	32	33.7	27	2	US-09-084-303B-240	Sequence 240, App
43	32	33.7	28	2	US-09-058-459-2	Sequence 2, Appli
44	32	33.7	28	2	US-09-127-926-2	Sequence 2, Appli
45	32	33.7	28	2	US-09-714-357-2	Sequence 2, Appli
46	32	33.7	28	2	US-10-057-552-2	Sequence 2, Appli
47	32	33.7	28	2	US-09-827-960-2	Sequence 2, Appli
48	32	33.7	28	2	US-09-837-886-2	Sequence 2, Appli
49	32	33.7	28	2	US-09-812-034-2	Sequence 2, Appli
50	32	33.7	34	2	US-09-374-958C-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKENAWA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0223321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200251 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-493-6

Query Match 100.0%; Score 95; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
Db 5 PKKDVLETFVKSCPDAI 22

RESULT 2
US-08-408-222B-6
Sequence 6, Application US/08408222B
Patent No. 5776727
GENERAL INFORMATION:
APPLICANT: Ikeyama, Shuichi
APPLICANT: Koyama, Masaru
APPLICANT: Miyake, Masauyuki
APPLICANT: Senoo, Masaharu
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,222B
FILING DATE: 22-MAR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,493
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-085396-1991
FILING DATE: 14-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-022321-1992
FILING DATE: 07-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reenick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41777-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-408-222B-6

Query Match 100.0%; Score 95; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
Db 5 PKKDVLETFVKSCPDAI 22

RESULT 3
US-08-486-057B-38
Sequence 38, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-057B-38

Query Match 37.9%; Score 36; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSC 14

Db 15 PKVEQLSNMVKSC 28
|| : | |||
RESULT 4
US-08-789-588-38
; Sequence 38, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; TITLE OF INVENTION: Process for Refolding Recombinantly
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-38
Query Match 37.9%; Score 36; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 PKKDVLFTFVKSC 14
|| : | |||
Db 15 PKVEQLSNMVKSC 28
|| : | |||
RESULT 5
US-08-789-588-38
; Sequence 38, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; TITLE OF INVENTION: Process for Refolding Recombinantly
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-38
Query Match 37.9%; Score 36; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 PKKDVLFTFVKSC 14
|| : | |||
Db 15 PKVEQLSNMVKSC 28
|| : | |||
RESULT 6
US-09-374-958C-31
; Sequence 31, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/374,958C
; FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-09-374-958C-31
Query Match 37.9%; Score 36; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 PKKDVLFTFVKSC 14
|| : | |||
Db 18 PKVEQLSNMVKSC 31
|| : | |||
RESULT 7
US-09-374-936-31
; Sequence 31, Application US/09374936
; Patent No. 6846906
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng

APPLICANT: McCartney, John
TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
FILE REFERENCE: STK-077
CURRENT APPLICATION NUMBER: US/09/374,936
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TGF-Beta3
US-09-374-936-31

Query Match 37.9%; Score 36; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSC 14
Db 18 PKVEQLSNMVKSC 31

RESULT 8

US-09-848-664A-14
Sequence 14, Application US/09848664A
Patent No. 6723344
GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.
TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth
TITLE OF INVENTION: Factors from Heparin Containing Matrices
FILE REFERENCE: ETH 108
CURRENT APPLICATION NUMBER: US/09/848,664A
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US/09/298,084A
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-848-664A-14

Query Match 37.9%; Score 36; DB 2; Length 42;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSC 14
Db 26 PKVEQLSNMVKSC 39

RESULT 9

US-08-974-549A-100
Sequence 100, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
OTHER INFORMATION: peptide from Saccharomyces
OTHER INFORMATION: cerevisiae EST2"
US-08-974-549A-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

```
RESULT 10
US-08-912-951-100
; Sequence 100, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; OTHER INFORMATION: peptide from Saccharomyces
; OTHER INFORMATION: cerevisiae EST2"
US-08-912-951-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
DB 8 FDKKSCYDSI 17

RESULT 11
US-09-402-181B-100
; Sequence 100, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
```

```
;
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE CHARACTERISTICS:
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-402-181B-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 12
US-09-721-456-100
; Sequence 100, Application US/09721456
; Patent No. 661710
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
```

```
;
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-721-456-100

Query Match 36.8%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKVSCYDSI 17

RESULT 13
US-08-851-843A-140
; Sequence 140, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
```

```
;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
;
US-08-851-843A-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db | | | | | | |
7 FDKVSCYDSI 16

RESULT 14
US-08-974-549A-258
; Sequence 258, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
;
US-08-974-549A-258

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db | | | | | | |
7 FDKVSCYDSI 16

RESULT 15
US-08-854-050-140
; Sequence 140, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
```

```

; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
; US-08-854-050-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0;

QY 9 FTVKSCPDAI 18
| | | | | |
Db 7 FDKSCYDSI 16

RESULT 16
US-09-430-323-140
; Sequence 140, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
; US-08-854-050-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0;

QY 9 FTVKSCPDAI 18
| | | | | |
Db 7 FDKSCYDSI 16

RESULT 17
US-09-402-181B-258
; Sequence 258, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```


Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 680880e1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-766-253-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | |
Db 7 FDKSCYDSI 16

RESULT 20
US-10-054-295-140
; Sequence 140, Application US/10054295
; Patent No. 6921664
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. 6921664e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-054-295-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | |
Db 7 FDKSCYDSI 16

RESULT 21
US-09-438-486A-140
; Sequence 140, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/851,843

;
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/844,419
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 08/724,643
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 223
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 140
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: amino acid sequence
US-09-438-486A-140

Query Match 36.8%; Score 35; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAL 18
| | | | | | | |
Db 7 FDKVSCYDSI 16

RESULT 22
US-08-851-843A-162
; Sequence 162, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-851-843A-162

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAL 18
| | | | | | | |
Db 8 FDKVSCYDSI 17

RESULT 23
US-08-974-549A-282
; Sequence 282, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312

```
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: WO PCT/US97/17618
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA: WO PCT/US97/17885
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-974-549A-282

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
DB 8 FDKSCYDSI 17

RESULT 24
US-08-854-050-162
; Sequence 162, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; OTHER INFORMATION: Saccharomyces cerevisiae EST2"
US-08-854-050-162

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
DB 8 FDKSCYDSI 17

RESULT 25
US-09-430-323-162
; Sequence 162, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
```

APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-430-323-162

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17

RESULT 26
US-09-402-181B-282
Sequence 282, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-09-402-181B-282

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17

RESULT 27
US-09-721-456-282
Sequence 282, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/721,456
  FILING DATE: 22-NOV-1997
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/974,549A
  FILING DATE: 19-NOV-1997
  APPLICATION NUMBER: US/08/724,643
  FILING DATE: 01-OCT-1996
  APPLICATION NUMBER: US/08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US/08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US/08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US/08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US/08/911,312
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US/08/912,951
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US/08/915,503
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph Ted
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 282:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 27 amino acids
    TYPE: amino acid
    STRANDEDNESS: <Unknown>
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
  FEATURE:
    NAME/KEY: Peptide
    LOCATION: 1..27
    OTHER INFORMATION: /note= "motif A peptide from
    Saccharomyces cerevisiae EST2"
  SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-09-721-456-282
Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 28
US-09-766-253-162
Sequence 162, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
  Lingner, Joachim
  Nakamura, Toru
  Chapman, Karen B.
  Morin, Gregg B.
  Andrews, William H.
  TITLE OF INVENTION: No. 6921664e1 Telomerase
  NUMBER OF SEQUENCES: 225
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend and Crew LLP
  STREET: Two Embarcadero Center, 8th Floor

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/721,456
  FILING DATE: 22-NOV-1997
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/974,549A
  FILING DATE: 19-NOV-1997
  APPLICATION NUMBER: US/08/724,643
  FILING DATE: 01-OCT-1996
  APPLICATION NUMBER: US/08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US/08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US/08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US/08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US/08/911,312
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US/08/912,951
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US/08/915,503
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph Ted
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 282:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 27 amino acids
    TYPE: amino acid
    STRANDEDNESS: <Unknown>
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
  FEATURE:
    NAME/KEY: Peptide
    LOCATION: 1..27
    OTHER INFORMATION: /note= "motif A peptide from
    Saccharomyces cerevisiae EST2"
  SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-09-721-456-282
Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17

RESULT 29
US-10-054-295-162
Sequence 162, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
  Lingner, Joachim
  Nakamura, Toru
  Chapman, Karen B.
  Morin, Gregg B.
  Harley, Calvin
  Andrews, William H.
  TITLE OF INVENTION: No. 6921664e1 Telomerase
  NUMBER OF SEQUENCES: 225
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend and Crew LLP
  STREET: Two Embarcadero Center, 8th Floor
```

;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/054,295
;; FILING DATE: 18-Jan-2002
;; CLASSIFICATION: 536
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/854,050
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 162:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..27
;; OTHER INFORMATION: /note= "motif A peptide from
;; Saccharomyces cerevisiae EST2"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-10-054-295-162

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | |
Db 8 FDKVSCVDSI 17

RESULT 30
US-09-438-486A-162
; Sequence 162, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
; APPLICANT: CECH, THOMAS R.
; APPLICANT: LINGNER, JOACHIM
; APPLICANT: NAKAMURA, TORU
; APPLICANT: CHAPMAN, KAREN B.
; APPLICANT: MORIN, GREGG B.
; APPLICANT: HARLEY, CALVIN
; APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
; TITLE OF INVENTION: TELOMERASE VARIANTS
; FILE REFERENCE: 018/062
; CURRENT APPLICATION NUMBER: US/09/438,486A
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 08/851,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017

;; PRIOR FILING DATE: 1997-04-25
;; PRIOR APPLICATION NUMBER: 08/844,419
;; PRIOR FILING DATE: 1997-04-18
;; PRIOR APPLICATION NUMBER: 08/724,643
;; PRIOR FILING DATE: 1996-10-01
;; NUMBER OF SEQ ID NOS: 223
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 162
;; LENGTH: 27
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
;; OTHER INFORMATION: amino acid sequence
US-09-438-486A-162

Query Match 36.8%; Score 35; DB 2; Length 27;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | |
Db 8 FDKVSCVDSI 17

RESULT 31
US-09-082-358B-57
; Sequence 57, Application US/09082358B
; Patent No. 6469153
; GENERAL INFORMATION:
; APPLICANT: Goff, Stephen P.
; APPLICANT: Li, Xingquiang
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
; TITLE OF INVENTION: EIP-1, and EIP-3
; FILE REFERENCE: 0575/54804
; CURRENT APPLICATION NUMBER: US/09/082,358B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 32
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-57

Query Match 36.8%; Score 35; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 VLETFVKSCPD 16
| | | | | | | |
Db 4 VLASFQQACPD 15

RESULT 32
US-08-974-549A-45
; Sequence 45, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: HARLEY, CALVIN B.
; APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

1 COUNTRY: USA
2 ZIP: 94111-3834
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6 SOFTWARE: Patent In Release #1.0, Version #1.30
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/974,549A
9 FILING DATE: 19-NOV-1997
10 CLASSIFICATION: 536
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/724,643
13 FILING DATE: 01-OCT-1996
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/844,419
16 FILING DATE: 18-APR-1997
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/846,017
19 FILING DATE: 25-APR-1997
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/851,843
22 FILING DATE: 06-MAY-1997
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/854,050
25 FILING DATE: 09-MAY-1997
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/911,312
28 FILING DATE: 14-AUG-1997
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 08/912,951
31 FILING DATE: 14-AUG-1997
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 08/915,503
34 FILING DATE: 14-AUG-1997
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: WO PCT/US97/17618
37 FILING DATE: 01-OCT-1997
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: WO PCT/US97/17885
40 FILING DATE: 01-OCT-1997
41 ATTORNEY/AGENT INFORMATION:
42 NAME: Apple, Randolph Ted
43 REGISTRATION NUMBER: 36,429
44 REFERENCE/DOCKET NUMBER: 015389-002610US
45 TELEPHONE: (415) 576-0200
46 TELEFAX: (415) 576-0300
47 INFORMATION FOR SEQ ID NO: 45:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 34 amino acids
50 TYPE: amino acid
51 STRANDEDNESS:
52 TOPOLOGY: linear
53 MOLECULE TYPE: peptide
54 FEATURE:
55 NAME/KEY: Peptide
56 LOCATION: 1..34
57 OTHER INFORMATION: /note= "motif A peptide from
58 OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
59 US-08-974-549A-45

Query Match 36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 10 FDKSCYDSI 19

RESULT 33
US-08-912-951-45

1 Sequence 45, Application US/08912951
2 Patent No. 6475789
3 GENERAL INFORMATION:
4 APPLICANT: Cech, Thomas R.
5 APPLICANT: Lingner, Joachim
6 APPLICANT: Nakamura, Toru
7 APPLICANT: Chapman, Karen B.
8 APPLICANT: Morin, Gregg B.
9 APPLICANT: Harley, Calvin
10 APPLICANT: Andrews, William H.
11 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
12 TITLE OF INVENTION: THERAPEUTIC METHODS
13 NUMBER OF SEQUENCES: 335
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: Townsend and Townsend and Crew LLP
16 STREET: Two Embarcadero Center, 8th Floor
17 CITY: San Francisco
18 STATE: California
19 COUNTRY: United States of America
20 ZIP: 94111
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: Floppy disk
23 COMPUTER: IBM PC compatible
24 OPERATING SYSTEM: PC-DOS/MS-DOS
25 SOFTWARE: Patent In Release #1.0, Version #1.30
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/08/912,951
28 FILING DATE: 14-AUG-1997
29 CLASSIFICATION: 435
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/854,050
32 FILING DATE: 09-MAY-1997
33 CLASSIFICATION: 435
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 08/851,843
36 FILING DATE: 06-MAY-1997
37 CLASSIFICATION: 435
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 08/844,419
40 FILING DATE: 18-APR-1997
41 CLASSIFICATION: 435
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 08/724,643
44 FILING DATE: 01-OCT-1996
45 CLASSIFICATION: 435
46 ATTORNEY/AGENT INFORMATION:
47 NAME: Apple, Randolph T.
48 REGISTRATION NUMBER: 36,429
49 REFERENCE/DOCKET NUMBER: 015389-002600US
50 TELECOMMUNICATION INFORMATION:
51 TELEPHONE: (415) 576-0200
52 TELEFAX: (415) 576-0300
53 INFORMATION FOR SEQ ID NO: 45:
54 SEQUENCE CHARACTERISTICS:
55 LENGTH: 34 amino acids
56 TYPE: amino acid
57 STRANDEDNESS:
58 TOPOLOGY: linear
59 MOLECULE TYPE: peptide
60 FEATURE:
61 NAME/KEY: Peptide
62 LOCATION: 1..34
63 OTHER INFORMATION: /note= "motif A peptide from
64 OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
65 US-08-912-951-45
66 Query Match 36.8%; Score 35; DB 2; Length 34;
67 Best Local Similarity 70.0%; Pred. No. 53;
68 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;


```
Qy 9 FTVKSCPD1 18
Db 10 FDKVSCYDSI 19

RESULT 34
US-09-402-181B-45
; Sequence 45, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "motif A peptide from

Qy 9 FTVKSCPD1 18
Db 10 FDKVSCYDSI 19

Query Match 36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPD1 18
Db 10 FDKVSCYDSI 19

RESULT 35
US-09-721-456-45
; Sequence 45, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
```

;
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-721-456-45

Query Match 36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 10 FDKKSCYDSI 19

RESULT 36
US-09-042-460-46
; Sequence 46, Application US/09042460
; Patent No. 6767719
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Allsopp, Richard
; APPLICANT: Definno, Ronald
; APPLICANT: Greenberg, Roger
; TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,460
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/979,742
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 015389-0031100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-042-460-46

Query Match 36.8%; Score 35; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 10 FDKKSCYDSI 19

RESULT 37
US-08-486-057B-20
; Sequence 20, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGP-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703

; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-057B-20

Query Match 35.8%; Score 34; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14
||:|
Db 15 PKIEQLSNMIVKSC 28
||||

RESULT 38
US-08-789-588-20
; Sequence 20, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Process for Refolding Recombinantly
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-789-588-20

Query Match 35.8%; Score 34; DB 1; Length 31;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14
||:|
Db 15 PKIEQLSNMIVKSC 28
||||

RESULT 39
US-09-374-958C-30
; Sequence 30, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Morphogenic Proteins
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-09-374-958C-30

Query Match 35.8%; Score 34; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14
||:|
Db 18 PKIEQLSNMIVKSC 31
||||

RESULT 40
US-09-374-936-30
; Sequence 30, Application US/09374936
; Patent No. 6846906
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-077
; CURRENT APPLICATION NUMBER: US/09/374,936
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 88

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-09-374-936-30
```

```
Query Match      35.8%; Score 34; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      1 PKKDVLETFVVKSC 14
          |||:|
Db      18 PKIEQLSNMIVKSC 31
```

```
Search completed: January 20, 2006, 17:35:33
Job time : 12.4444 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:27:09 ; Search time 34.4444 Seconds
(without alignments)
218.350 Million cell updates/sec

Title: US-10-619-323-6
Perfect score: 95
Sequence: 1 PKKDVLETFVKSCPDAl 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	4	US-10-619-323-6
2	95	100.0	25	4	US-10-619-323-5
3	61	64.2	30	5	US-10-473-127-1717
4	49	51.6	10	5	US-10-473-127-1717
5	39	41.1	49	4	US-10-424-599-278211
6	39	41.1	50	4	US-10-424-599-165124
7	37	38.9	46	4	US-10-437-963-170639
8	36	37.9	42	3	US-09-848-664-14
9	36	37.9	46	4	US-10-724-972A-5875
10	35	36.8	17	4	US-10-044-692-100
11	35	36.8	17	4	US-10-044-539-100
12	35	36.8	17	4	US-10-325-810-100
13	35	36.8	17	5	US-10-877-124-100
14	35	36.8	17	5	US-10-877-022-100
15	35	36.8	17	5	US-10-877-146-100
16	35	36.8	26	3	US-09-843-676-140
17	35	36.8	26	3	US-09-766-253-140
18	35	36.8	26	3	US-09-438-486-140
19	35	36.8	26	4	US-10-053-758-140
20	35	36.8	26	4	US-10-054-295-140
21	35	36.8	26	4	US-10-054-611-140
22	35	36.8	26	4	US-10-325-810-258
23	35	36.8	26	5	US-10-877-124-258
24	35	36.8	26	5	US-10-877-022-258
25	35	36.8	26	5	US-10-877-146-258
26	35	36.8	27	3	US-09-843-676-162
27	35	36.8	27	3	US-09-766-253-162

28	35	36.8	27	3	US-09-438-486-162	Sequence 162, App
29	35	36.8	27	4	US-10-053-758-162	Sequence 162, App
30	35	36.8	27	4	US-10-054-295-162	Sequence 162, App
31	35	36.8	27	4	US-10-054-611-162	Sequence 162, App
32	35	36.8	27	4	US-10-325-810-282	Sequence 282, App
33	35	36.8	27	5	US-10-877-022-282	Sequence 282, App
34	35	36.8	27	5	US-10-877-124-282	Sequence 282, App
35	35	36.8	27	5	US-10-877-146-282	Sequence 282, App
36	35	36.8	34	4	US-10-044-692-45	Sequence 45, Appl
37	35	36.8	34	4	US-10-044-539-45	Sequence 45, Appl
38	35	36.8	34	4	US-10-325-810-45	Sequence 45, Appl
39	35	36.8	34	5	US-10-877-124-45	Sequence 45, Appl
40	35	36.8	34	5	US-10-877-022-45	Sequence 45, Appl
41	35	36.8	34	5	US-10-862-698-46	Sequence 46, Appl
42	35	36.8	34	5	US-10-877-146-45	Sequence 45, Appl
43	35	36.8	41	4	US-10-074-024-386	Sequence 386, App
44	34	35.8	18	4	US-10-430-685-121	Sequence 121, App
45	34	35.8	38	3	US-09-864-761-44222	Sequence 44222, A
46	34	35.8	42	3	US-09-848-664-13	Sequence 13, Appl
47	34	35.8	45	4	US-10-425-115-207847	Sequence 207847
48	33	34.7	33	4	US-10-437-963-118353	Sequence 118353
49	33	34.7	36	4	US-10-425-115-286889	Sequence 286889
50	33	34.7	40	3	US-09-864-761-45049	Sequence 45049, A

ALIGNMENTS

RESULT 1

US-10-619-323-6
; Sequence 6, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide

US-10-619-323-6

Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18

Db 1 PKKDVLETFVKSCPDAl 18

RESULT 2

US-10-619-323-5
; Sequence 5, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.

```
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-5

Query Match 100.0%; Score 95; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLTTFTVKSCPDAI 18
Db 1 PKDVLTTFTVKSCPDAI 18
|||||

RESULT 3
US-10-473-127-1717
; Sequence 1717, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1717
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1717

Query Match 64.2%; Score 61; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLTTFTVK 12
Db 19 PKDVLTTFTVK 30
|||||

RESULT 4
US-10-473-127-165
; Sequence 165, Application US/10473127
```

```
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-165

Query Match 51.6%; Score 49; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDVLETTFTVK 12
Db 1 KDVLETTFTVK 10
|||||

RESULT 5
US-10-424-599-278211
; Sequence 278211, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278211
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(49)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93248C.1.pep
US-10-424-599-278211

Query Match 41.1%; Score 39; DB 4; Length 49;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 ETFTVKSCPDA 17
Db 9 ETFDVEGCPTA 19
|||||

RESULT 6
```



```

;
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
;
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-692-100
Query Match 36.8%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKSCYDSI 17

RESULT 11
US-10-044-539-100
; Sequence 100, Application US/10044539
; Publication No. US2003010009A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.

;
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
;
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-044-539-100
Query Match 36.8%; Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
Db 8 FDKSCYDSI 17

RESULT 12
US-10-325-810-100
; Sequence 100, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;
;

```


Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-325-810-100

Query Match 36.8% Score 35; DB 4; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18

Db 8 FDVKSVDISI 17
RESULT 13
US-10-877-124-100
; Sequence 100, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Peptide

```
;
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-124-100

Query Match          36.8%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
   | | | | | | |
Db 8 FDKVSCYDSI 17

RESULT 14
US-10-877-022-100
; Sequence 100, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /note= "telomerase RT finger motif A
; peptide from Saccharomyces
; cerevisiae EST2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-022-100

Query Match          36.8%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
   | | | | | | |
Db 8 FDKVSCYDSI 17

RESULT 15
US-10-877-146-100
; Sequence 100, Application US/10877146
; Publication No. US20050013825A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
```

APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-877-146-100
Query Match 36.8%; Score 35; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 9 FTVKSCPDAl 18
Db 8 FDKVSCYDSI 17
RESULT 16
US-09-843-676-140
Sequence 140, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-843-676-140
Query Match 36.8%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 9 FTVKSCPDAl 18
Db 7 FDKVSCYDSI 16
RESULT 17
US-09-766-253-140
Sequence 140, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-766-253-140

Query Match 36.8%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | |
Db 7 FDKVSCYDSI 16

RESULT 18
US-09-438-486-140
; Sequence 140, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
US-09-438-486-140
Query Match 36.8%; Score 35; DB 3; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAl 18
| | | | | | | |
Db 7 FDKVSCYDSI 16

RESULT 19
US-10-053-758-140
; Sequence 140, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-053-758-140

Query Match 36.8%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | | | |
Db 7 FDVKSICYDSI 16

RESULT 20
US-10-054-295-140
; Sequence 140, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-054-295-140

Query Match 36.8%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | | | |
Db 7 FDVKSICYDSI 16

RESULT 21
US-10-054-611-140
; Sequence 140, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-054-611-140

Query Match 36.8%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18
Db 7 FDKSCYDSI 16

RESULT 22
US-10-325-810-258
; Sequence 258, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Aussenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note= "motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-325-810-258

Query Match 36.8%; Score 35; DB 4; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAI 18
Db 7 FDKSCYDSI 16

RESULT 23
US-10-877-124-258
; Sequence 258, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 14-AUG-1997

```

; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..26
; OTHER INFORMATION: /note="motif 3(A) peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-877-124-258

Query Match 36.8%; Score 35; DB 5; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0

Qy 9 FTVKSCPDAL 18
Db 7 FDKVSCYDSI 16

RESULT 24
US-10-877-022-258
; Sequence 258, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lirngner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

1 APPLICATION NUMBER: US/10/877,022
2 FILING DATE: 24-Jun-2004
3 CLASSIFICATION: <Unknown>
4
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US/09/432,503
7 FILING DATE: 02-Nov-1999
8 APPLICATION NUMBER: 08/974,549
9 FILING DATE: <Unknown>
10 APPLICATION NUMBER: US 08/844,419
11 FILING DATE: 18-Apr-1997
12 APPLICATION NUMBER: US 08/846,017
13 FILING DATE: 25-Apr-1997
14 APPLICATION NUMBER: US 08/851,843
15 FILING DATE: 06-May-1997
16 APPLICATION NUMBER: US 08/854,050
17 FILING DATE: 09-May-1997
18 APPLICATION NUMBER: US 08/911,312
19 FILING DATE: 14-Aug-1997
20 APPLICATION NUMBER: US 08/912,951
21 FILING DATE: 14-Aug-1997
22 APPLICATION NUMBER: US 08/915,503
23 FILING DATE: 14-Aug-1997
24 APPLICATION NUMBER: WO PCT/US97/17618
25 FILING DATE: 01-Oct-1997
26 APPLICATION NUMBER: WO PCT/US97/17885
27 FILING DATE: 01-Oct-1997
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Apple, Randolph Ted
30 REGISTRATION NUMBER: 36,429
31 REFERENCE/DOCKET NUMBER: 015389-002610US
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (415) 576-0200
34 TELEFAX: (415) 576-0300
35 INFORMATION FOR SEQ ID NO: 258:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 26 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: <Unknown>
40 TOPOLOGY: linear
41 MOLECULE TYPE: peptide
42 FEATURE:
43 NAME/KEY: Peptide
44 LOCATION: 1..26
45 OTHER INFORMATION: /note="motif 3(A) peptide from
46 Saccharomyces cerevisiae EST2p"
47 SEQUENCE DESCRIPTION: SEQ ID NO: 258:
48
49 US-10-877-022-258
50
51 Query Match 36.8%; Score 35; DB 5; Length 26;
52 Best Local Similarity 70.0%; Pred.No. 1.5e+02;
53 Matches 7; Conservative 1; Mismatches 2; Indels
54
55 Qy 9 FTVKSCPDAI 18
56 Db 7 FDKSCYDSI 16
57
58 RESULT 25
59 US-10-877-146-258
60 Sequence 258, Application US/10877146
61 Publication No. US20050013825A1
62 GENERAL INFORMATION:
63 APPLICANT: Cech, Thomas R.
64 Lirngner, Joachim
65 Nakamura, Toru
66 Chapman, Karen B.
67 Morin, Gregg B.
68 Harley, Calvin B.
69 Andrews, William H.
70
71 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
72 NUMBER OF SEQUENCES: 727
73 CORRESPONDENCE ADDRESS:
74 ADDRESSER: Townsend and Townsend and Crew LLP

```

STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..26
OTHER INFORMATION: /note= "motif 3(A) peptide from Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-877-146-258
Query Match 36.8%; Score 35; DB 5; Length 26;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
DB 7 FDVKSICYDSI 16
RESULT 26
US-09-843-676-162
; Sequence 162, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: NO. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-843-676-162
Query Match 36.8%; Score 35; DB 3; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
DB 8 FDVKSICYDSI 17
RESULT 27
US-09-766-253-162
; Sequence 162, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-843-676-162
Query Match 36.8%; Score 35; DB 3; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
DB 8 FDVKSICYDSI 17
RESULT 27
US-09-766-253-162
; Sequence 162, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-766-253-162
Query Match 36.8%; Score 35; DB 3; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17
RESULT 28
US-09-438-486-162
Sequence 162, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"
US-09-438-486-162
Query Match 36.8%; Score 35; DB 3; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAL 18
Db 8 FDKSCYDSI 17
RESULT 29
US-10-053-758-162
Sequence 162, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.

;/ TITLE OF INVENTION: No. US20030032075A1el Telomerase
;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION NUMBER: US/10/053,758
;/ FILING DATE: 18-Jan-2002
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/854,050
;/ FILING DATE: 09-MAY-1997
;/ APPLICATION NUMBER: US/08/851,843
;/ FILING DATE: 06-MAY-1997
;/ APPLICATION NUMBER: US/08/846,017
;/ FILING DATE: 25-APR-1997
;/ APPLICATION NUMBER: US/08/844,419
;/ FILING DATE: 18-APR-1997
;/ APPLICATION NUMBER: US/08/724,643
;/ FILING DATE: 01-OCT-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 162:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 27 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FEATURE:
;/ NAME/KEY: Peptide
;/ LOCATION: 1..27
;/ OTHER INFORMATION: /note= "motif A peptide from
;/ Saccharomyces cerevisiae EST2"
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 162:
;/ US-10-053-758-162
;/
;/ Query Match 36.8%; Score 35; DB 4; Length 27;
;/ Best Local Similarity 70.0%; Pred. No. 1.6e+02;
;/ Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;/
;/ QY 9 FTVKSCPDAl 18
;/ Db 8 FDVKSCYDSI 17
;/
;/ RESULT 30
;/ US-10-054-295-162
;/ Sequence 162, Application US/10054295
;/ Publication No. US20030044953A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cech, Thomas R.
;/ Lingner, Joachim
;/ Nakamura, Toru
;/ Chapman, Karen B.
;/ Morin, Gregg B.
;/ Harley, Calvin
;/ Andrews, William H.
;/ TITLE OF INVENTION: No. US20030044953A1el Telomerase

;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION NUMBER: US/10/054,295
;/ FILING DATE: 18-Jan-2002
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/854,050
;/ FILING DATE: <Unknown>
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 162:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 27 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FEATURE:
;/ NAME/KEY: Peptide
;/ LOCATION: 1..27
;/ OTHER INFORMATION: /note= "motif A peptide from
;/ Saccharomyces cerevisiae EST2"
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 162:
;/ US-10-054-295-162
;/
;/ Query Match 36.8%; Score 35; DB 4; Length 27;
;/ Best Local Similarity 70.0%; Pred. No. 1.6e+02;
;/ Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;/
;/ QY 9 FTVKSCPDAl 18
;/ Db 8 FDVKSCYDSI 17
;/
;/ RESULT 31
;/ US-10-054-611-162
;/ Sequence 162, Application US/10054611
;/ Publication No. US20030059787A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cech, Thomas R.
;/ Lingner, Joachim
;/ Nakamura, Toru
;/ Chapman, Karen B.
;/ Morin, Gregg B.
;/ Harley, Calvin
;/ Andrews, William H.
;/ TITLE OF INVENTION: No. US20030059787A1el Telomerase
;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-10-054-611-162
Query Match 36.8%; Score 35; DB 4; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAI 18
Db 8 FDKVSCYDSI 17
RESULT 32
US-10-325-810-282
Sequence 282, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 282:
US-10-325-810-282
Query Match 36.8%; Score 35; DB 4; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 FTVKSCPDAI 18
Db 8 FDKVSCYDSI 17
RESULT 33
US-10-877-124-282
Sequence 282, Application US/10877124
Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.

Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..27
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"
SEQUENCE DESCRIPTION: SEQ ID NO: 282:

Query Match 36.8%; Score 35; DB 5; Length 27;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0;

QY 9 FTVKSCPDAI 18
| | | | | | | |
Db 8 FDKVSKYDSI 17

RESULT 34
US-10-877-022-282
; Sequence 282, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..27
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2"

```
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 282;
/ US-10-877-022-282
/
/ Query Match          36.8%; Score 35; DB 5; Length 27;
/ Best Local Similarity 70.0%; Pred. No. 1.6e+02;
/ Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 9 FTVKSCPDAl 18
/      | | | | | | |
/ Db 8 FDVKSVCDSI 17
/
/ RESULT 35
/ US-10-877-146-282
/ Sequence 282, Application US/10877146
/ Publication No. US20050013825A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/      Lingner, Joachim
/      Nakamura, Toru
/      Chapman, Karen B.
/      Morin, Gregg B.
/      Harley, Calvin B.
/      Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/877,146
/ FILING DATE: 24-Jun-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,503
/ FILING DATE: 02-Nov-1999
/ APPLICATION NUMBER: 08/974,549
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 282:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..27
/ OTHER INFORMATION: /note= "motif A peptide from
/      Saccharomyces cerevisiae EST2"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 282:
/ US-10-877-146-282
/
/ Query Match          36.8%; Score 35; DB 5; Length 27;
/ Best Local Similarity 70.0%; Pred. No. 1.6e+02;
/ Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 9 FTVKSCPDAl 18
/      | | | | | | |
/ Db 8 FDVKSVCDSI 17
/
/ RESULT 36
/ US-10-044-692-45
/ Sequence 45, Application US/10044692
/ Publication No. US20030096344A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/      Lingner, Joachim
/      Nakamura, Toru
/      Chapman, Karen B.
/      Morin, Gregg B.
/      Harley, Calvin
/      Andrews, William H.
/ TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
/      THERAPEUTIC METHODS
/ NUMBER OF SEQUENCES: 335
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/044,692
/ FILING DATE: 11-Jan-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/912,951
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002600US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
```

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..34
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-044-692-45

Query Match 36.8%; Score 35; DB 4; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | |
Db 10 FDKSCYDSI 19

RESULT 37

US-10-044-539-45
Sequence 45, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..34
OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2p"
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-044-539-45

Query Match 36.8%; Score 35; DB 4; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
| | | | | | | |
Db 10 FDKSCYDSI 19

RESULT 38

US-10-325-810-45
Sequence 45, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951

;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Aussenhus, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-002620US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..34
;; OTHER INFORMATION: /note= "motif A peptide from
;; Saccharomyces cerevisiae EST2p"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-325-810-45

Query Match 36.8%; Score 35; DB 4; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18
| | | | | | | |
Db 10 FDKKSCYDSI 19
| | | | | | | |

RESULT 39
US-10-877-124-45
; Sequence 45, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..34
;; OTHER INFORMATION: /note= "motif A peptide from
;; Saccharomyces cerevisiae EST2p"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-877-124-45

Query Match 36.8%; Score 35; DB 5; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAl 18
| | | | | | | |
Db 10 FDKKSCYDSI 19
| | | | | | | |

RESULT 40
US-10-877-022-45
; Sequence 45, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "motif A peptide from
; Saccharomyces cerevisiae EST2p"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-877-022-45

Query Match 36.8%; Score 35; DB 5; Length 34;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
Db 10 FDKSCYDSI 19

```

Search completed: January 20, 2006, 17:38:20
Job time : 35.4444 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:30:50 ; Search time 3.11111 Seconds
(without alignments)
58.632 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKKDVLFTTVKSCPDAl 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 41278

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Published Applications AA_New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	37.9	34	6	US-10-816-768-31
2	34	35.8	34	6	US-10-816-768-30
3	32	33.7	34	6	US-10-816-768-29
4	31	32.6	37	6	US-10-957-351-6
5	30	31.6	35	6	US-10-957-351-34
6	29.5	31.1	33	7	US-11-121-301-50
7	29	30.5	44	6	US-10-986-501-356
8	28	29.5	32	6	US-10-957-351-196
9	28	29.5	35	6	US-10-957-351-112
10	28	29.5	38	6	US-10-957-351-183
11	28	29.5	44	6	US-10-467-657-1118
12	28	29.5	44	6	US-10-957-887B-278
13	27	28.4	9	6	US-10-859-643-2
14	27	28.4	9	6	US-10-859-643-254
15	27	28.4	9	6	US-10-859-643-690
16	27	28.4	9	7	US-11-097-864-2
17	27	28.4	9	7	US-11-097-864-250
18	27	28.4	9	7	US-11-097-864-690
19	27	28.4	9	7	US-11-097-912-2
20	27	28.4	9	7	US-11-097-912-254
21	27	28.4	9	7	US-11-097-912-690
22	27	28.4	10	6	US-10-859-643-350
23	27	28.4	10	7	US-11-097-864-350
24	27	28.4	10	7	US-11-097-912-350
25	27	28.4	15	7	US-11-019-894A-28

26 27 28.4 17 6 US-10-723-207-72 Sequence 72, Appl
27 27 28.4 19 6 US-10-503-575-192 Sequence 192, Appl
28 27 28.4 21 6 US-10-467-657-3848 Sequence 3848, Ap
29 27 28.4 30 6 US-10-467-657-5752 Sequence 5752, Ap
30 27 28.4 35 6 US-10-467-657-7362 Sequence 7362, Ap
31 27 28.4 35 6 US-10-467-657-8218 Sequence 8218, Ap
32 27 28.4 35 6 US-10-957-351-195 Sequence 195, Appl
33 27 28.4 35 7 US-11-121-301-23 Sequence 23, Appl
34 27 28.4 38 6 US-10-957-351-155 Sequence 155, Appl
35 27 28.4 47 7 US-11-123-896-453 Sequence 453, Appl
36 26.5 27.9 33 7 US-11-121-301-49 Sequence 49, Appl
37 26.5 27.9 43 6 US-10-467-657-2778 Sequence 2778, Ap
38 26 27.4 16 6 US-10-723-207-50 Sequence 50, Appl
39 26 27.4 16 7 US-11-054-515-2313 Sequence 2313, Ap
40 26 27.4 20 6 US-10-623-155-407 Sequence 407, Appl
41 26 27.4 20 6 US-10-623-155-518 Sequence 518, Appl
42 26 27.4 30 6 US-10-467-657-6636 Sequence 6636, Ap
43 26 27.4 30 6 US-10-467-657-8160 Sequence 8160, Ap
44 26 27.4 34 6 US-10-816-768-33 Sequence 33, Appl
45 26 27.4 43 6 US-10-957-887B-91 Sequence 91, Appl
46 26 27.4 44 6 US-10-957-887B-4 Sequence 4, Appl
47 26 27.4 44 6 US-10-957-887B-4 Sequence 4, Appl
48 25.5 26.8 13 6 US-10-511-559-223 Sequence 223, Appl
49 25.5 26.8 35 6 US-10-816-768-3 Sequence 3, Appl
50 25.5 26.8 37 7 US-11-033-039-169 Sequence 169, Appl

ALIGNMENTS

RESULT 1
US-10-816-768-31
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-10-816-768-31
Query Match 37.9%; Score 36; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 PKKDVLFTTVKSC 14
|||:|
DB 18 PKVEQLSNMVKSC 31
RESULT 2
US-10-816-768-30
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 30
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta2
US-10-816-768-30

Query Match 35.8%; Score 34; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 6; Indels 6; Gaps 0;

QY 1 PKKDVLFTTVKSC 14
|| : |||||
Db 18 PKIEQLSNMIVKSC 31

RESULT 3

US-10-816-768-29
; Sequence 29, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 29
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta1
US-10-816-768-29

Query Match 33.7%; Score 32; DB 6; Length 34;
Best Local Similarity 42.9%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 1 PKKDVLFTTVKSC 14
|| : |||||
Db 18 PKVEQLSNMIVKSC 31

RESULT 4

US-10-957-351-6
; Sequence 6, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlrath, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain

US-10-957-351-6

Query Match 32.6%; Score 31; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KSCPD 16
|||||
Db 26 KSCPD 30

RESULT 5

US-10-957-351-34
; Sequence 34, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlrath, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-34

Query Match 31.6%; Score 30; DB 6; Length 35;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 LETFTVKSCPD 17
|| : |||||
Db 18 LECDDTFNCPDA 29

RESULT 6

US-11-121-301-50
; Sequence 50, Application US/11121301
; Publication No. US20050277176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USDI
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-121-301-50

Query Match 31.1%; Score 29.5; DB 7; Length 33;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

```

QY 7 ETFTVKSCPD 17
    ||| : |||
Db 18 ETF-MHLCPD 27

RESULT 7
US-10-986-501-356
; Sequence 356, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 356
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-356

Query Match 30.5%; Score 29; DB 6; Length 44;
Best Local Similarity 38.5%; Pred. No. 95;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 6 LETFTVKSCPD 18
    :||| : |||
Db 28 IQETAVSCVDGV 40

RESULT 8
US-10-957-351-196
; Sequence 196, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-183

Query Match 29.5%; Score 28; DB 6; Length 35;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
    ||| : |||
Db 23 VRDCPD 28

RESULT 9
US-10-957-351-112
; Sequence 112, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-112

Query Match 29.5%; Score 28; DB 6; Length 35;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
    ||| : |||
Db 23 VRDCPD 28

RESULT 10
US-10-957-351-183
; Sequence 183, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perliroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 183
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-183

```


RESULT 15
US-10-859-643-690
; Sequence 690, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-690

Query Match 28.4%; Score 27; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 16
US-11-097-864-2
; Sequence 2, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-2

Query Match 28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 17
US-11-097-864-254
; Sequence 254, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-254

Query Match 28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

RESULT 18
US-11-097-864-690
; Sequence 690, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-690

Query Match 28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 2 VESCP 7

```
Db          2 VESCP 7

RESULT 19
US-11-097-912-2
; Sequence 2, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-2

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
|:|:|:|:
Db          2 VESCP 7

RESULT 20
US-11-097-912-254
; Sequence 254, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-254

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
|:|:|:|:
Db          2 VESCP 7

RESULT 21
US-11-097-912-690
; Sequence 690, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-690

Query Match      28.4%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
|:|:|:|:
Db          2 VESCP 7

RESULT 22
US-10-859-643-350
; Sequence 350, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-350

Query Match      28.4%; Score 27; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKSCPD 16
```

Db 11 VKSCPD 16
|:|:|:
3 VESCFE 8

RESULT 23

US-11-097-864-350
; Sequence 350, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-350

Query Match 28.4%; Score 27; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 3 VESCFE 8

RESULT 24

US-11-097-912-350
; Sequence 350, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-350

Query Match 28.4%; Score 27; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|:|:
Db 3 VESCFE 8

RESULT 25

US-11-019-894A-28
; Sequence 28, Application US/11019894A
; Publication No. US20050245451A1
; GENERAL INFORMATION:
; APPLICANT: Pincus, Matthew R.
; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED
; FILE REFERENCE: 1181-17 CIP A
; CURRENT APPLICATION NUMBER: US/11/019,894A
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 10/386,737
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/827,683
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,102
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/363,785
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide; retro-inverso peptide analog of SEQ ID NO:1;
; OTHER INFORMATION: all D-amino acids
US-11-019-894A-28

Query Match 28.4%; Score 27; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
|:|:|:|:
Db 5 LDSFTEQSLP 14

RESULT 26

US-10-723-207-72
; Sequence 72, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: synthesized from amino acids with no genetic
; OTHER INFORMATION: material as source
US-10-723-207-72

```
Query Match      28.4%; Score 27; DB 6; Length 17;
Best Local Similarity 36.4%; Pred. No. 73;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 KDVLFTFKVS 13
   :|::||:|
Db 3 RDIIDFTNES 13

RESULT 27
US-10-503-575-192
; Sequence 192, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-192

Query Match      28.4%; Score 27; DB 6; Length 19;
Best Local Similarity 62.5%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 EFTFKVSC 14
   :|::|||
Db 1 DDFTKGSC 8

RESULT 28
US-10-467-657-3848
; Sequence 3848, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3848
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3848

Query Match      28.4%; Score 27; DB 6; Length 21;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
   :|::|||
```

```
Db 9 LKPCPD 14
   :|::|||

RESULT 29
US-10-467-657-5752
; Sequence 5752, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5752
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5752

Query Match      28.4%; Score 27; DB 6; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 TVKSCP 15
   :|::|||
Db 10 SVKACP 15

RESULT 30
US-10-467-657-7362
; Sequence 7362, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7362
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7362

Query Match      28.4%; Score 27; DB 6; Length 35;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 5 VLETFVKVS--CPD 16
   ||::|||
Db 6 VLSVLSVASSPCPD 19
   ||::|||

RESULT 31
US-10-467-657-8218
; Sequence 8218, Application US/10467657
```


; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8218
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8218

Query Match 28.4%; Score 27; DB 6; Length 35;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 5 VLETFVTKS--CPD 16
|||:|:|
Db 6 VLSVLSVASSPCPD 19

RESULT 32
US-10-957-351-195
; Sequence 195, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-195

Query Match 28.4%; Score 27; DB 6; Length 35;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
|:|
Db 23 VQCCPD 28

RESULT 33
US-11-121-301-23
; Sequence 23, Application US/11121301
; Publication No. US20050277176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.

; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USD1
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-121-301-23

Query Match 28.4%; Score 27; DB 7; Length 35;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 ETEFVKSCP 15
:|:|:|
Db 8 DTCRLKNCP 16

RESULT 34
US-10-957-351-155
; Sequence 155, Application US/10957351
; Publication No. US20060008844A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001400US
; CURRENT APPLICATION NUMBER: US/10/957,351
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 155
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human LDL-receptor class A domain
US-10-957-351-155

Query Match 28.4%; Score 27; DB 6; Length 38;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 KSCPD 16
|:|
Db 26 KDCPD 30

RESULT 35
US-11-123-896-453
; Sequence 453, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of

; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 453
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-11-123-896-453

Query Match 28.4%; Score 27; DB 7; Length 47;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 FTVKSCPD 16
||| |||
Db 15 FTTGSCDD 22

RESULT 36
US-11-121-301-49
; Sequence 49, Application US/11121301
; Publication No. US20050277176A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOWA:041USD1
; CURRENT APPLICATION NUMBER: US/11/121,301
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/252,734
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-121-301-49

Query Match 27.9%; Score 26.5; DB 7; Length 33;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 7 EFTVKSCPD 17
||| : |||
Db 18 ETY-MHLCPD 27

RESULT 37
US-10-467-657-2778
; Sequence 2778, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2778
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2778

Query Match 27.9%; Score 26.5; DB 6; Length 43;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 2 KKDVLFTFKSC 14
||| |||
Db 20 KKDFL--SVQSC 29

RESULT 38
US-10-723-207-50
; Sequence 50, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: synthesized from amino acids with no genetic
; OTHER INFORMATION: material as source
US-10-723-207-50

Query Match 27.4%; Score 26; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TFTVKSC 14
||| |||
Db 10 TLTVTSC 16

RESULT 39
US-11-054-515-2313
; Sequence 2313, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418

```
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2313
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2313

Query Match      27.4%; Score 26; DB 7; Length 16;
Best Local Similarity 31.2%; Pred. No. 1e+02;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      1 PKKDVLETFVTKSCPD 16
Db      1 PFYDTLTSVLEFFPD 16

RESULT 40
US-10-623-155-407
; Sequence 407, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 407
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-407

Query Match      27.4%; Score 26; DB 6; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 LETFTVK 12
Db      5 LENFTLK 11

Search completed: January 20, 2006, 17:38:44
Job time : 4.11111 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:23:49 ; Search time 6.66667 Seconds
(without alignments)
259.785 Million cell updates/sec

Title: US-10-619-323-6
Perfect score: 95
Sequence: 1 PKNDVLETFVTKSCPDAL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.8	15	2 S03353	plastocyanin - Mic
2	33	34.7	41	2 G72312	hypothetical prote
3	32	33.7	49	2 S72793	cysteine synthase
4	31	32.6	38	2 S12409	ribosomal protein
5	31	32.6	44	2 AD1753	Lactococcus lactis
6	31	32.6	50	2 AB0925	hypothetical prote
7	30	31.6	50	2 AB1546	hypothetical prote
8	29	30.5	12	2 A61309	glycoprotein hormo
9	29	30.5	32	2 S11610	ribosomal protein
10	29	30.5	34	2 F95187	hypothetical prote
11	28	29.5	33	2 A60601	keratin, 55k, nucl
12	28	29.5	38	2 I70022	kallikrein - mouse
13	28	29.5	42	2 T07581	hypothetical prote
14	28	29.5	43	2 A34071	gag polyprotein -
15	28	29.5	45	2 T07537	hypothetical prote
16	28	29.5	45	2 S36709	B7 protein - equin
17	28	29.5	46	2 H71262	hypothetical prote
18	28	29.5	48	2 A32457	myeloperoxidase [E
19	27.5	28.9	36	1 WISWAA	alpha-amylase inh
20	27.5	28.9	41	2 C39558	matricoxin A - el
21	27	28.4	21	2 A60225	pyruvate dehydroge
22	27	28.4	33	2 S22603	ribosomal protein
23	27	28.4	37	2 T29808	hypothetical prote
24	27	28.4	39	2 T03344	gene e23 protein -
25	27	28.4	45	1 HPBO	haptoglobin precur
26	27	28.4	45	2 JS0655	hypothetical 5K pr
27	27	28.4	48	2 T07305	hypothetical prote
28	27	28.4	48	2 AB1181	hypothetical prote
29	26.5	27.9	30	2 D70253	conserved hypothet

30	26.5	27.9	34	2 S65371	tRNA-guanine trans
31	26	27.4	19	2 PA0012	superoxide dismuta
32	26	27.4	23	2 D60583	glycoprotein hormo
33	26	27.4	27	2 C85939	hypothetical prote
34	26	27.4	30	2 A60914	pheromone-binding
35	26	27.4	33	2 C82312	hypothetical prote
36	26	27.4	35	2 S29726	lignin peroxidase
37	26	27.4	35	2 S29728	lignin peroxidase
38	26	27.4	35	2 S29729	manganese(II) pero
39	26	27.4	35	2 S29731	manganese(II) pero
40	26	27.4	36	2 S70092	hypothetical prote
41	26	27.4	38	2 I70018	kallikrein - mouse
42	26	27.4	45	2 S43149	Ig upsilon chain -
43	26	27.4	48	2 C70864	hypothetical prote
44	26	27.4	48	2 AC1538	hypothetical prote
45	26	27.4	49	2 D70091	hypothetical prote
46	26	27.4	50	2 G97151	hypothetical prote
47	25.5	26.8	26	2 A44036	collagen alpha 1(X
48	25	26.3	21	2 D42762	proteasome endopep
49	25	26.3	23	2 S72535	probable acr-2 reg
50	25	26.3	33	2 H72332	hypothetical prote

ALIGNMENTS

RESULT 1
S03353
plastocyanin - Microcystis aeruginosa (fragment)
C:Species: Microcystis aeruginosa
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03353
R:Tan, S.; Ho, K.K.
Biochim. Biophys. Acta 973, 111-117, 1989
A:Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.
A:Reference number: S03353; MUID:89134784; PMID:2537099
A:Accession: S03353
A:Molecule type: protein
A:Residues: 1-15 <TAN>
A:Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match 35.8%; Score 34; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTTVKSCDPA 17
|||||
DB 1 EFTTVKMGDA 11

RESULT 2
G72312
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: G72312
R:Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72312
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-41 <ARN>
A:Cross-references: UNIPROT:Q9X065; UNIPARC:UPI00000C1340; GB:AE001759; GB:AE000512; NT
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0970

Query Match 34.7%; Score 33; DB 2; Length 41;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;

A;Gene: CP0727

Query Match 31.6%; Score 30; DB 2; Length 50;
Best Local Similarity 37.5%; Pred. No. 6.7e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSPDA 17
||| |
Db 23 RKDYELWFVYGSCPES 38

RESULT 8

A61309
glycoprotein hormones alpha chain - hamster (fragment)
N;Alternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; lut

C;Species: Cricetinae gen. sp. (hamster)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004

C;Accession: A61309

R;Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.

Endocrinology 111, 1263-1269, 1982

A;Title: Isolation and characterization of hamster luteinizing hormone.

A;Reference number: A61309; MUID:63003498; PMID:6889489

A;Accession: A61309

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <GLE>

A;Cross-references: UNIPROT:Q7M0A7; UNIPARC:UPI00001765C7

C;Superfamily: glycoprotein hormones alpha chain

C;Keywords: glycoprotein

Query Match 30.5%; Score 29; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 FTVKSCP 15
||| |
Db 6 FTVQGGCP 12

RESULT 9

S11610
ribosomal protein S4.eR [validated] - Halobacterium salinarum (fragment)
N;Alternate names: ribosomal protein HS5

C;Species: Halobacterium salinarum

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004

C;Accession: S11610

R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.

Zbl. Bakt. Hyg. 1. Abt. Orig. C 3, 200-208, 1982

A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea

A;Reference number: S11609

A;Accession: S11610

A;Molecule type: protein

A;Residues: 1-32 <YAG>

A;Cross-references: UNIPROT:Q7M553; UNIPARC:UPI000017725F

A;Note: the protein is designated as ribosomal protein HS5

A;Note: the source is designated as Halobacterium cutirubrum

C;Superfamily: ribosomal protein S4

C;Keywords: protein biosynthesis; ribosome

Query Match 30.5%; Score 29; DB 2; Length 32;
Best Local Similarity 53.8%; Pred. No. 6.4e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKS 13
||| |
Db 14 FVZKTKTFTFSKS 26

RESULT 10

P95187
hypothetical protein SP1611 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: F95187
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Helon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-34 <KUR>
A;Cross-references: UNIPROT:Q97PJ8; UNIPARC:UPI00000518PB; GB:AE005672; PIDN:AAK75695.1
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1611

Query Match 30.5%; Score 29; DB 2; Length 34;
Best Local Similarity 35.7%; Pred. No. 6.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKS 14
||| |
Db 12 PBEDIIVTGLPKYC 25

RESULT 11

A60601
keratin, 55k, nuclear matrix - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A60601

R;Alique, R.; Bastos, R.; Serratos, J.; Enrich, C.; James, P.; Pujades, C.; Bachs, O.

Exp. Cell Res. 186, 346-353, 1990

A;Title: Increase in a 55-kDa keratin-like protein in the nuclear matrix of rat liver c

A;Reference number: A60601; MUID:90127112; PMID:1688805

A;Accession: A60601

A;Molecule type: protein

A;Residues: 1-33 <ALI>

A;Cross-references: UNIPROT:Q7M056; UNIPARC:UPI00001774C5

C;Superfamily: cytoskeletal keratin

C;Keywords: nuclear matrix; nucleus

Query Match 29.5%; Score 28; DB 2; Length 33;
Best Local Similarity 54.5%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVK 12
||| |
Db 8 KKDVDVDEAYXXK 18

RESULT 12

I70022
kallikrein - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I70022

R;Evans, B.A.; Drinkwater, C.C.; Richards, R.I.

J. Biol. Chem. 262, 8027-8034, 1987

A;Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of t

A;Reference number: I55260; MUID:87250386; PMID:3036794

A;Accession: I70022

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-38 <RES>

A;Cross-references: UNIPARC:UPI000016CE68; GB:M18590; NID:g198528; PIDN:AAA39352.1; PID

C;Genetics:

A;Gene: KAL

Query Match 29.5%; Score 28; DB 2; Length 38;
Best Local Similarity 38.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 DVLETFVTKSCPD 16
Db 9 ELLEDLTVRRIPN 21

RESULT 13

T07581

hypothetical protein 42g - Japanese black pine chloroplast
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07581
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; PMID:95024047; PMID:7937893
A:Accession: T07581
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <WAK>
A:Cross-references: UNIPROT:Q33005; UNIPARC:UPI00000939B4; EMBL:D17510; NID:G529643; PII
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 29.5%; Score 28; DB 2; Length 42;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKS 13
Db 24 KSCILHIYIKS 35

RESULT 14

A34071

gag polyprotein - avian retrovirus NK24 (fragment)
C:Species: avian retrovirus NK24
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 07-Feb-1997
C:Accession: A34071
R:Nishizawa, M.; Goto, N.; Kawai, S.
J. Virol. 61, 3733-3740, 1987
A:Title: An avian transforming retrovirus isolated from a nephroblastoma that carries the
A:Reference number: A34071; PMID:88062920; PMID:2824811
A:Accession: A34071
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-43 <NIS>
A:Cross-references: UNIPARC:UPI000017857A
A:Note: the authors translated the codon AAC for residue 43 as Thr
C:Superfamily: avian retrovirus gag polyprotein
C:Keywords: polyprotein

Query Match 29.5%; Score 28; DB 2; Length 43;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 VLETFVTKSCPD 16
Db 12 IIDCFRQKSQPD 23

RESULT 15

T07537

hypothetical protein 44c - Japanese black pine chloroplast
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07537
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; PMID:95024047; PMID:7937893
A:Accession: T07537

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-44 <WAK>
A:Cross-references: UNIPROT:Q32976; UNIPARC:UPI000009538A; EMBL:D17510; NID:G529643; PII
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 29.5%; Score 28; DB 2; Length 44;
Best Local Similarity 46.2%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVTKS 13
Db 6 PKKDBERTFTFTSS 18

RESULT 16

S36709

B7 protein - equine herpesvirus 4 (fragment)
C:Species: equine herpesvirus 4
C>Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S36709
R:Riggio, P.
submitted to the EMBL Data Library, November 1989
A:Reference number: S36709
A:Accession: S36709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-45 <RIG>
A:Cross-references: UNIPROT:Q00041; UNIPARC:UPI0000126247; EMBL:X17684; NID:G312459; PII
C:Superfamily: herpesvirus 77k alpha trans-inducing protein
C:Keywords: transcription regulation

Query Match 29.5%; Score 28; DB 2; Length 45;
Best Local Similarity 41.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 KDVLETFVTKSC 14
Db 14 KNLIERRAVKGC 25

RESULT 17

H71262

hypothetical protein TP0940 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: H71262
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rean, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDe
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; PMID:98332770; PMID:9665876
A:Accession: H71262
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-46 <COL>
A:Cross-references: UNIPROT:O83910; UNIPARC:UPI00000139B45; GB:AE001262; NID:AE000520; NID

A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0940

Query Match 29.5%; Score 28; DB 2; Length 46;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 FTVKSCPD 18
Db 37 FPAPGCPD 46

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29808
 R:Latreille, P.; Stellyes, L.
 submitted to the EMBL Data Library, June 1996
 A:Description: The sequence of C. elegans cosmid C25A8.
 A:Reference number: Z20689
 A:Accession: T29808
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <LAT>
 A:Cross-references: UNIPROT:Q18145; UNIPARC:UPI0000081748; EMBL:U61958; PIDN:AB03181.1;
 A:Experimental source: strain Bristol N2; clone C25A8
 C:Genetics:
 A:Gene: CESP:C25A8.1
 A:Map position: 4

Query Match 28.4%; Score 27; DB 2; Length 37;
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVL 6
 ||:|:|
 Db 28 PKEDVL 33

RESULT 24
 T03344
 gene e23 protein - Lactococcus phage b1L170
 C:Species: Lactococcus phage b1L170
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T03344
 R:Cruciz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, M.
 submitted to the EMBL Data Library, June 1997
 A:Description: Sequence and organization of the lactococcal isometric b1L170 phage genome
 A:Reference number: Z14903
 A:Accession: T03344
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-39 <CRU>
 A:Cross-references: UNIPROT:O80137; UNIPARC:UPI000009BB13; EMBL:AF009630; NID:G3282260;
 C:Genetics:
 A:Gene: e23

Query Match 28.4%; Score 27; DB 2; Length 39;
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;
 Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSC 14
 ||:|:|:|
 Db 2 KDTVKTLMIAC 13

RESULT 25
 HPB0
 haptoglobin precursor - bovine (fragments)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Feb-1992 #sequence_revision 31-May-1996 #text_change 31-Oct-1997
 C:Accession: A40430; B40430
 R:Morimatsu, M.; Syuto, B.; Shimada, N.; Fujinaga, T.; Yamamoto, S.; Saito, M.; Naiki, M.
 J. Biol. Chem. 266, 11833-11837, 1991
 A:Title: Isolation and characterization of bovine haptoglobin from acute phase sera.
 A:Reference number: A40430; MUID:91268055; PMID:1904872
 A:Accession: A40430
 A:Molecule type: protein
 A:Residues: 1-25 <MOR>
 A:Cross-references: UNIPROT:Q7M365; UNIPARC:UPI0000172B09
 A:Accession: B40430
 A:Molecule type: protein
 A:Residues: 26-45 <MO2>
 A:Cross-references: UNIPARC:UPI0000172B0A
 C:Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two chains of
 C:Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with hemogl

C:Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology
 C:Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron transpo
 F:1-25/Product: haptoglobin alpha chain (fragment) #status experimental <ALP>
 F:26-45/Product: haptoglobin beta chain (fragment) #status experimental <BET>

Query Match 28.4%; Score 27; DB 1; Length 45;
 Best Local Similarity 62.5%; Pred. No. 1.9e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TVKSCPD 17
 ||:|:|
 Db 8 TADSCPKA 15

RESULT 26
 JS0655
 hypothetical 5K protein (kan region) - Streptomyces griseus (strain SS-1198PR)
 C:Species: Streptomyces griseus
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JS0655
 R:Ishikawa, J.; Hotta, K.
 Gene 108, 127-132, 1991
 A:Title: Nucleotide sequence and transcriptional start point of the kan gene encoding a
 A:Reference number: JS0652; MUID:92104494; PMID:1761222
 A:Accession: JS0655
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-45 <ISH>
 A:Cross-references: UNIPROT:Q7M0K4; UNIPARC:UPI000017AB1A

Query Match 28.4%; Score 27; DB 2; Length 45;
 Best Local Similarity 45.5%; Pred. No. 1.9e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 EFTVKSCPD 17
 ||:|:|:|
 Db 31 EAWTRNCDA 41

RESULT 27
 T07305
 hypothetical protein 48d - Chlorella vulgaris chloroplast
 C:Species: chloroplast Chlorella vulgaris
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
 C:Accession: T07305
 R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
 Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
 A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chl
 A:Reference number: Z15985; MUID:97303241; PMID:9159184
 A:Accession: T07305
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-48 <WAK>
 A:Cross-references: UNIPARC:UPI000011E47A; EMBL:AB001684; NID:G2224352; PIDN:BAA57953.1;
 C:Genetics:
 A:Keywords: chloroplast

Query Match 28.4%; Score 27; DB 2; Length 48;
 Best Local Similarity 36.4%; Pred. No. 2e+03;
 Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKS 13
 ||:|:|:|
 Db 27 KPILKTFPSLEN 37

RESULT 28
 AB1181
 hypothetical protein lmo0850 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AB1181

A;Reference number: S29724; MUID:93143365; PMID:8424691
A;Accession: S29729
A;Molecule type: protein
A;Residues: 1-35 <JOH>
A;Cross-references: UNIPROT:Q9URAI; UNIPARC:UPI0000065C1D
A;Experimental source: strain PRL 572
C;Superfamily: peroxidase
C;Keywords: extracellular protein; heme; manganese; oxidoreductase

Query Match 27.4%; Score 26; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SCPDAI 18
: : :
Db 2 ACPDGV 7

RESULT 39

S29731
manganese(II) peroxidase (BC 1.11.1.-) 5 - white-rot fungus (Trametes versicolor) (fragment)
C;Species: Trametes versicolor (white-rot fungus)
C;Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 12-Jul-2004
C;Accession: S29731
R;Johansson, T.; Welinder, K.G.; Nyman, P.O.
Arch. Biochem. Biophys. 300, 57-62, 1993
A;Title: Isozymes of lignin peroxidase and manganese(II) peroxidase from the white-rot fungus.

A;Reference number: S29724; MUID:93143365; PMID:8424691
A;Accession: S29731
A;Molecule type: protein
A;Residues: 1-35 <JOH>
A;Cross-references: UNIPROT:Q9UR99; UNIPARC:UPI000006ADBA
A;Experimental source: strain PRL 572
C;Superfamily: peroxidase
C;Keywords: extracellular protein; heme; manganese; oxidoreductase

Query Match 27.4%; Score 26; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 SCPDAI 18
: : :
Db 2 ACPDGV 7

RESULT 40

S70092
hypothetical protein (orf36) - Amycolatopsis methanolica
C;Species: Amycolatopsis methanolica
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S70092
R;Vrijbloed, J.W.; Jelinkova, M.; Hessels, G.I.; Dijkhuizen, L.
Mol. Microbiol. 18, 21-31, 1995
A;Title: Identification of the minimal replicon of plasmid pMEA300 of the methylotrophic bacterium Amycolatopsis methanolica.
A;Reference number: S70087; MUID:96154938; PMID:8596458
A;Accession: S70092
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <VRI>
A;Cross-references: UNIPARC:UPI000017AD65; EMBL:L36679

Query Match 27.4%; Score 26; DB 2; Length 36;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPD 16
: : :
Db 13 VATCPD 18

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:22:44 ; Search time 39.1111 Seconds
(without alignments)
324.703 Million cell updates/sec

Title: US-10-619-323-6
Perfect score: 95
Sequence: 1 PKXVLETTVKSCPDAL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	38.9	39	Q4RAQ9_TETNG	Q4ra99 tetraodon n
2	36	37.9	43	Q87JQ4_VIBPA	Q87j04 vibrio para
3	34	35.8	15	PLAS MICA	P10625 microcystis
4	34	35.8	18	Q9XJ05_9CAUD	Q9xj05 bacterioph
5	34	35.8	46	Q9NYL8_HUMAN	Q9nyl8 homo sapien
6	33	34.7	18	Q63506_RAT	Q63506 rattus norv
7	33	34.7	32	Q4XWD9_PLACH	Q4xwd9 plasmodium
8	33	34.7	37	Q84TL9_BRARP	Q84tl9 brassica ra
9	33	34.7	41	Q8BX0_SHEON	Q8bx0 shewanella
10	33	34.7	41	Q9X065_THEMEA	Q9x065 thermotoga
11	32.5	34.2	22	Q6VQ25_9NEOP	Q6vq25 heliconius
12	32	33.7	38	Q4LQW8_9PICO	Q4lq08 hepatitis a
13	32	33.7	43	Q4XQ9_PLACH	Q4xq9 plasmodium
14	32	33.7	49	Q59529_MYCIE	Q59529 mycobacteri
15	31.5	33.2	35	Q8ZXW8_PYRAE	Q8zxw8 pyrobaculum
16	31	32.6	16	Q9PRV2_PETWA	Q9prv2 petromyzon
17	31	32.6	29	Q71992_9RETR	Q71992 human endog
18	31	32.6	33	Q65817_MANSAM	Q65817 manheimia
19	31	32.6	35	Q8LXA8_MUSAC	Q8lxa8 musa acumin
20	31	32.6	41	Q8VVR6_STAAU	Q8vvr6 staphylococ
21	31	32.6	44	Q8U2U2_PYRUF	Q8u2u2 pyrococcus
22	31	32.6	44	Q7S6Q7_NEUCR	Q7s6q7 neurospora
23	31	32.6	44	Q928G6_LISIN	Q928g6 listeria in
24	31	32.6	44	Q8G001_BRUSU	Q8g001 brucella su
25	31	32.6	48	Q81213_BACAN	Q81213 bacillus an
26	31	32.6	48	Q4RC18_TETNG	Q4rc18 tetraodon n
27	31	32.6	48	Q4RNV7_TETNG	Q4rny7 tetraodon n
28	31	32.6	50	Q82374_SALTI	Q82374 salmonella
29	30.5	32.1	40	Q4YRD6_PLABE	Q4yrd6 plasmodium
30	30	31.6	16	Q47605_ECOLI	Q47605 escherichia
31	30	31.6	20	Q62435_MOUSE	Q62435 mus musculus

32	30	31.6	30	2	Q86487_RVVF	Q86487 rift valley
33	30	31.6	30	2	Q86488_RVVF	Q86488 rift valley
34	30	31.6	30	2	Q86489_RVVF	Q86489 rift valley
35	30	31.6	30	2	Q86490_RVVF	Q86490 rift valley
36	30	31.6	30	2	Q86491_RVVF	Q86491 rift valley
37	30	31.6	30	2	Q86492_RVVF	Q86492 rift valley
38	30	31.6	30	2	Q86493_RVVF	Q86493 rift valley
39	30	31.6	30	2	Q04247_RVVF	Q04247 rift valley
40	30	31.6	30	2	Q4JFJ3_RVVF	Q4jfj3 rift valley
41	30	31.6	30	2	Q4JFJ4_RVVF	Q4jfj4 rift valley
42	30	31.6	30	2	Q4JFJ5_RVVF	Q4jfj5 rift valley
43	30	31.6	30	2	Q4JFJ6_RVVF	Q4jfj6 rift valley
44	30	31.6	30	2	Q4JFJ7_RVVF	Q4jfj7 rift valley
45	30	31.6	30	2	Q4JFJ8_RVVF	Q4jfj8 rift valley
46	30	31.6	30	2	Q4JFJ9_RVVF	Q4jfj9 rift valley
47	30	31.6	30	2	Q4JFK0_RVVF	Q4jfk0 rift valley
48	30	31.6	30	2	Q4JFK1_RVVF	Q4jfk1 rift valley
49	30	31.6	30	2	Q4JFK2_RVVF	Q4jfk2 rift valley
50	30	31.6	30	2	Q4JFK3_RVVF	Q4jfk3 rift valley

ALIGNMENTS

RESULT 1
Q4RAQ9_TETNG
ID Q4RAQ9_TETNG PRELIMINARY; PRT; 39 AA.
AC Q4RAQ9_TETNG PRELIMINARY; PRT; 39 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome undetermined SCAF23077, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037463001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasiava C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet F., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAE01023077; 1
FT NON TER 1
SQ SEQUENCE 39 AA; 4099 MW; 897972726CB0CCFE CRC64;

Query Match 38.9%; Score 37; DB 2; Length 39;
Best Local Similarity 66.7%; Pred.No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 TVKSCPDAL 18

```

Db          30 TVKNCPTAV 38      |||:||| :| :|
Q87JQ4_VIBPA
ID   Q87JQ4_VIBPA PRELIMINARY;          PRT;           43 AA.
AC   Q87JQ4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DI   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DR   Hypothetical protein VPA0194.
DS   OrderedLocusNames=VPA0194;
GN   Vibrio parahaemolyticus.
OS   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxId=670;
RN   [1]
RC   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP   STRAIN=RMD 2210633 / Serotype O3:KG;
RX   MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RJ   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RL   distinct from that of V. cholerae.";
RR   Lancet 361:743-749(2003).
RW   EMBL; BA000032; BAG61537.1; -; Genomic DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE 43 AA, 4813 MW, B65EBB8D43C1E79A CRC64;

Query Match       37.9%; Score 36; DB 2; Length 43;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches        6; Conservative    5; Mismatches    3; Indels    0; Gaps    0;

QY   5 VLETFTVKSCPDAI 18
      | : ||: ||:
DB   21 VFOLFTRKPNAL 34

RESULT 3
PLAS_MICAE STANDARD;          PRT;           15 AA.
ID   PLAS_MICAE
AC   P10625;
DT   01-JUL-1989 (Rel. 11, Created)
DI   01-JUL-1989 (Rel. 11, Last sequence update)
DE   10-MAY-2005 (Rel. 47, Last annotation update)
DD   Plastocyanin (Fragment).
GN   Name=pctc;
OC   Microcystis aeruginosa.
OC   Bacteria; Cyanobacteria; Chroococcales; Microcystis.
ON   NCBI_TaxId=1126;
RX   [1]
RP   PROTEIN SEQUENCE.
RM   MEDLINE=89134784; PubMed=2537099;
RA   Tan S., Ho K.-K.;
RT   "Purification of an acidic plastocyanin from Microcystis aeruginosa.";
RL   Biochim. Biophys. Acta 973:111-117(1989).
CC   -1- FUNCTION: Participates in electron transfer between P700 and the
CC   cytochrome b6-f complex in photosystem I.
CC   -1- SIMILARITY: Contains 1 plastocyanin-like domain.
-----
This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
PIR; S03353; S03353.
DR   HAMAP; MF 00566; -: 1.
DR   InterPro; IPRO00923; BlueGut_1.
DR   PROSITE; PS00196; COPPER_BLUE; PARTIAL.
KW   Copper; Direct protein sequencing; Electron transport; Metal-binding;

```



```
RESULT 6
Q63506 RAT PRELIMINARY; PRT; 18 AA.
AC Q63506;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rat asialoglycoprotein receptor RHL1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87257885; PubMed=3600647;
RA McPhaul M., Berg P.;
RT "Identification and characterization of cDNA clones encoding two
RT homologous proteins that are part of the asialoglycoprotein
RT receptor."
RL Mol. Cell. Biol. 7:1841-1847(1987).
DR EMBL; M16349; AAA42039.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 18
SQ SEQUENCE 18 AA; 1988 MW; 43474B8AB145735C CRC64;

Query Match 34.7%; Score 33; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VKSCPDAL 18
DB 6 VQSCPSAI 13

RESULT 7
Q4XWD9 PLACH
ID Q4XWD9 PLACH PRELIMINARY; PRT; 32 AA.
AC Q4XWD9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC105305.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01002657; CAH7872.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 32 AA; 4013 MW; 2906341BFEFPBB6E CRC64;

Query Match 34.7%; Score 33; DB 2; Length 32;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 9 FTVKSCP 15
DB 15 FFVKSCP 21

RESULT 8
Q84TL9 BRARP
ID Q84TL9 BRARP PRELIMINARY; PRT; 37 AA.
AC Q84TL9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor CRC (Fragment).
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Jang H., Huz Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY220357; AAO63101.1; -; mRNA.
DR InterPro; IPR006780; YABBY.
DR Pfam; PF04690; YABBY; 1.
FT NON TER 1
FT NON TER 37
SQ SEQUENCE 37 AA; 3937 MW; D87BDE9C33BA34CB CRC64;

Query Match 34.7%; Score 33; DB 2; Length 37;
Best Local Similarity 58.3%; Pred. No. 8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKQVLETFVK 12
DB 3 PLKRLDITVK 14

RESULT 9
Q8E8X0 SHEON
ID Q8E8X0 SHEON PRELIMINARY; PRT; 41 AA.
AC Q8E8X0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO4531.
GN OrderedLocustNames=SO4531;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.E., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feidblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RA "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AR015885; AAN57494.1; -; Genomic_DNA.
DR TIGR; SO4531; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4596 MW; 3F6B72512EE9CA13 CRC64;
```

Query Match 34.7%; Score 33; DB 2; Length 41;
Best Local Similarity 35.3%; Pred. No. 8.9e+02;
Matches 6; Conservative 3; Mismatches 8; Indels 0;
Gaps 0;

Qy 2 KKDVLFTTVKSCPAI 18
| : | : ||| :
Db 8 KYTIFEGISAIYCPDAV 24

RESULT 10	
Q9X065.THEMA	
ID Q9X065.THEMA PRELIMINARY;	PRT; 41 AA.
AC Q9X065;	
DT 01-NOV-1999 (TrEMBLrel. 12, Created)	
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE Hypothetical protein.	
GN OrderedLocusNames=TW0970;	
OS Thermotoga maritima.	
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga	
OX NCBI_TaxID=2336;	
RN [1]	

RP NUCLEOTIDE SEQUENCE
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RC MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of *Thermotoga maritima*.";
RL Nature 399:323-329(1999).
DR EMBL: AE001759; AAD36049.1; -; Genomic_DNA.
DR PIR: G72312; G72312.
DR TIGR: TW0970; -;
DR InterPro: IPR010095; TspaseT_teng_C.
DR Pfam: PR07282; Transposase_35; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 41 AA; 4586 MW; 7B52C021082023 CRC64;

```
Query Match          34.7%; Score 33; DB 2; Length 41;
Best Local Similarity 54.5%; Pred. NO. 8.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

Qy	4	DVLETFV	KSC	14
		:		::
Db	23	EVLETH	SOTC	33

RESULT	ID	Q6VQ25_9NEOP	PRELIMINARY;	PRT;	22 AA.
1	AC	Q6VQ25_			
2	DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
3	DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
4	DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
5	DE	Mannose phosphate isomerase (Fragment).			
6	OS	Heliconius melpomene plesseni.			
7	OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;			
8	OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;			
9	OC	Papilionoidea; Nymphalidae; Heliconiinae; Heliconius;			
10	NCBI	NCBI_TaxID=248314;			
11	PN	PN			

RX nucleotide sequence.
 RA PubMed=15210977; DOI=10.1073/pnas.0306243101;
 RA Flanagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
 RA Planas S., Linares M., Heckel D., McWilliam W.O.
 RT "Historical demography of Mullerian mimicry in the neotropical
 RT *Heliconius* butterflies.";
 RL *Proc. Natl. Acad. Sci. U.S.A.* 101:9704-9709 (2004)

DR	EMBL; AY332459; AAQ98782.1; -; Genomic DNA.
DR	GO; GO:0016853; F:isomerase activity; IEA.
KW	Isomerase.
FT	NON_TER 1 1
FT	NON_TER 22 22
SO	NON_TER 22 AA; 2501 MW; 2DRA189858262C
FO	SEQUENCE

Query Match 34.2%; Score 32.5; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels

Qy 1 PKQDVLETFVKSCPD 16
Db 7 PTKDHAELQH-KTSCPD 21

RESULT	12
Q4L0M8	9PICO PRELIMINARY; PRT; 38 AA.
ID	
Q4L0M8;	
AC	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DDT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	RNA polymerase (Fragment).
GN	Name=RNAP;
OS	Hepatitis A virus.
OC	Viruses; sgRNA positive-strand viruses, no DNA stage; Picornaviridae;
CC	Hepatocovirus.
OX	NCBI_TaxID=12092;
RN	[1]
NUCLEOTIDE SEQUENCE.	
RP	STRAIN=IND01-6_IIIA;
RC	Chitambar S.D.;
RA	"Genetic heterogeneity of hepatitis A virus isolates from Pune, western India,"
RT	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RL	ENBL; AF649642; AAV69913.1; -- Genomic_RNA.
DR	NON_TER 1 FT NON TER 1
FE	SEQUENCE 38 AA; 4487 MW; 9B353AB44CB6BD4B CRC64;
SQ	

Query Match 33.7%; Score 32; DB 2; Length 38;
Best Local Similarity 47.1%; Pred. No. 1.2e+03;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 PKKVLETF--VKSCP 15
| : ||| : | : |||
Db 2 PLEKVLEKTRAIDSCP 18

```

RESULT 13
Q4XG09 PLACH
ID Q4XG09_PLACH PRELIMINARY; PRT; 43 AA.
AC Q4XG09;
DT 13-SEP-2005 (TREMblrel. 31, Created)
DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
DE Hypothetical protein (Fragment) .
GN ORFNames=PC401678.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
[1]
RN NUCLEOTIDE SEQUENCE.
RP

```

RA Bertram M., Florentin L., Janssen C., S. Paisin A., Churcheides G.K.,
RA James K., Rutherford K., Harris B., Trueman H.E., Mendoza J.,
RA Cuadri M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Quail S.L., Rajandream M.A., Carucci D.J., Yates J.P., Kafatos F.C.,
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the plasmidome life cycle by genomic,
RT transcriptomic, and proteomic analyses."; Science 307:83-86(2005).
RL Science 307:83-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01006357; CAH83908.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 4914 MW; 6A0EBAB7BC302A1E CRC64;

Query Match 33.7%; Score 32; DB 2; Length 43;
Best Local Similarity 35.3%; Pred. No. 1.4e+03;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLFTFTVKSCPDAI 18
||::|::|
DB 8 KKIIKEFHLRCFCDOI 24

RESULT 14
Q59529 MYCLE
ID Q59529 MYCLE PRELIMINARY; PRT; 49 AA.
AC Q59529;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CysM (EC 4.2.99.8).
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00014; AAA50898.1; -; Genomic_DNA.
DR PIR; S72793; S72793.
DR GO; GO:0016829; F-lyase activity; IEA.
KW Lyase.
SQ SEQUENCE 49 AA; 5575 MW; 8B5B3B41CA813D5E CRC64;

Query Match 33.7%; Score 32; DB 2; Length 49;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 KDVLEFTFTVKSC 14
||::|::|
DB 38 KDLFPSTVTRTC 49

RESULT 15
Q82WX8 PYRAE
ID Q82WX8 PYRAE PRELIMINARY; PRT; 35 AA.
AC Q82WX8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PAREP2a.
GN OrderedLocusNames=PAE1570;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792899; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AB009828; AAL63571.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 35 AA; 4009 MW; 6E27A3D94168BF24 CRC64;

Query Match 33.2%; Score 31.5; DB 2; Length 35;
Best Local Similarity 41.2%; Pred. No. 1.3e+03;
Matches 7; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 6 LETFTVKSC-----PDA 17
:|::|::|
DB 1 METLSVKECRVKLFEA 17

RESULT 16
Q9PRY2 PETMA
ID Q9PRY2 PETMA PRELIMINARY; PRT; 16 AA.
AC Q9PRY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Lectin 30 kDa subunit (fragment).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94249896; PubMed=8192354;
RA Schluter S.F., Schroeder J., Wang B., Marchalonis J.J.;
RT "Recognition molecules and immunoglobulin domains in invertebrates.";
RT Ann. N. Y. Acad. Sci. 712:74-81(1994).
SQ SEQUENCE 16 AA; 1728 MW; 3BBF03DD4185F446 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 KSCPPDA 17
|::|::|
DB 5 KGCPDA 10

RESULT 17
O71992 9RETR
ID O71992 9RETR PRELIMINARY; PRT; 29 AA.
AC O71992;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Reverse transcriptase (fragment).
OS Human endogenous retrovirus.
OC Viruses; Retroviral viruses; Retroviridae.
OX NCBI_TaxID=11827;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rose T., Schultz E.R., Henikoff J.G., Pietrokovski S., McCallum C.M.,
RA Henikoff S.;
RT "Consensus-degenerate hybrid oligonucleotide primers for amplification
of distantly-related sequences.";
RL Nucleic Acids Res. 0:0-0(1998).
DR EMBL; AF050505; AAC05560.1; -; Genomic DNA.
DR GO; GO:0003964; F-RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 29
SQ SEQUENCE 29 AA; 3303 MW; CD65212FE4DB04AB CRC64;

Query Match 32.6%; Score 31; DB 2; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCP 15

```
Db 17 FTCKKCP 23

RESULT 18
Q65S17 MANSUM
ID Q65S17_MANSUM PRELIMINARY; PRT; 33 AA.
AC Q65S17;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1466;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB015827; AAU38073.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 33 AA; 3808 MW; 4CF423D666243384 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 33;
Best Local Similarity 46.7%; Pred. No. 1.5e+03;
Matches 7; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 2 KKDVLFTFTV--KSC 14
||:|:|:|
Db 17 KKPILKSYLVVEKSC 31

RESULT 19
Q8LKA8 MUSAC
ID Q8LKA8_MUSAC PRELIMINARY; PRT; 35 AA.
AC Q8LKA8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Osmotin-like protein (Fragment).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Regav I., Gepstein S., Khayat E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516691; AM69297.1; -; mRNA.
DR HSSP; PJ3679; IDUS.
DR InterPro; IPR001938; Thaumatin.
DR Pfam; PF0314; Thaumatin; 1.
DR ProDom; PD001321; Thaumatin; 1.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3964 MW; 414338178F1747B2 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 35;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPD 17
|:|:|:|
Db 15 FFKRNCPPD 23

RESULT 20
Q8VVR6 STAAU
ID Q8VVR6_STAAU PRELIMINARY; PRT; 41 AA.
AC Q8VVR6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF31.
OS Staphylococcus aureus.
OG Plasmid ETB plasmid.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21562640; PubMed=11705958;
RA DOI=10.1128/IAI.69.12.7760-7771.2001;
RA Yamaguchi T., Hayashi T., Takami H., Ohnisi M., Murata T.,
RA Nakayama K., Asakawa K., Ohara M., Komatsuzaawa H., Sugai M.;
RT "Complete nucleotide sequence of a Staphylococcus aureus exfoliative
RT toxin B plasmid and identification of a novel ADP-ribosyltransferase,
RT EDIN-C.";
RL Infect. Immun. 69:7760-7771(2001).
DR EMBL; AP003088; BAB78429.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 41 AA; 4558 MW; CFE1AAB2C0389744 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 41;
Best Local Similarity 31.2%; Pred. No. 1.9e+03;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 PKQVLETFVTVKSCP 16
|:|:|:|
Db 3 PHKNIVEALNCIALPD 18

RESULT 21
Q8U2U2 PYRFU
ID Q8U2U2_PYRFU PRELIMINARY; PRT; 44 AA.
AC Q8U2U2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0737.
GN OrderedLocusNames=PF0737;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010192; AAL80861.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5284 MW; 479C3074528E272E CRC64;

Query Match 32.6%; Score 31; DB 2; Length 44;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQVLETFVTVK 12
||:|:|:|
Db 2 PKSPSLVETLTK 13

RESULT 22
Q7S6Q7 NEUCR
ID Q7S6Q7_NEUCR PRELIMINARY; PRT; 44 AA.
AC Q7S6Q7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
```

01-MAR-2004 (TRENBLrel. 26, Last sequence update)
01-MAR-2004 (TRENBLrel. 26, Last annotation update)
Predicted protein.
GN Name=NCU05533.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxId=5141;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=OR74E;
RA Galagan J.E.; Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamnyavskis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzstofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Planann M., Sella S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboite D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
EMBL; AABX01000322; EAA31259.1; -; Genomic DNA.
SR SEQUENCE 44 AA; 5283 MW; 5D59B345C3059404 CRC64;

Query Match 32.6%; Score 31; DB 2; Length 44;
Best Local Similarity 38.9%; Pred. No. 2.le+03;
Matches 7; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 PKKDVLETFVK--SCPDP 16
| : | | | : | |
DB 2 PEKKLTPNFTVRMTAPD 19

RESULT 23
Q928G6 LISIN
ID ID Q928G6 LISIN PRELIMINARY; PRT; 44 AA.
AC AC Q928G6
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Lin2569 protein.
GN OrderedLocusNames=lin2569;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxId=1642;
[1]
RN RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537219; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Ruenliok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauguet O.,
RA Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kraft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Matournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordieck G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:1849-1852(2001).
DR EMBL; AJ596172; CAC97796.1; -; Genomic DNA.
DR PIR; AD1753; AD1753.

RA Holtzapfel E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzborg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS017025; AAP24489.1; -; Genomic DNA.
DR EMBL; AS017334; AAT29559.1; -; Genomic DNA.
DR TIGR; BA0463; -;
DR TIGR; GBAA0463; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 48 AA; 5591 MW; B3EECD3DCA388B609 CRC64;
Query Match 32.6%; Score 31; DB 2; Length 48;
Best Local Similarity 85.7%; Pred. No. 2.3e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PKKQVLE 7
Db 26 PSKQVLE 32
RESULT 26
Q4RC18 TETNG
ID Q4RC18 TETNG PRELIMINARY; PRT; 48 AA.
AC Q4RC18;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 5 SCAF18819, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0038457001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01018819; CAG13895.1; -; Genomic DNA.
FT NON_TER 1 48
FT NON_TER 48 48
SQ SEQUENCE 48 AA; 5561 MW; ABCB2CCE7B88813F CRC64;
Query Match 32.6%; Score 31; DB 2; Length 48;
Best Local Similarity 35.3%; Pred. No. 2.3e+03;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 PKKQVLETFYKSCPD 17
Db 13 PRASMVVXDCVKACSDS 29
RESULT 27
Q4RNY7 TETNG
ID Q4RNY7 TETNG PRELIMINARY; PRT; 48 AA.
AC Q4RNY7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 10 SCAF15009, whole genome shotgun sequence.
DE ORFNames=GSTENG00031353001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015009; CAG09895.1; -; Genomic DNA.
SQ SEQUENCE 48 AA; 5634 MW; F15FPD65C046C13B CRC64;
Query Match 32.6%; Score 31; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKKQVLE 6
Db 20 PKKQVLE 25
RESULT 28
Q8Z374 SALT
ID Q8Z374 SALT PRELIMINARY; PRT; 50 AA.
AC Q8Z374; Q7C6T9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein STY3659.
GN OrderedLocuNames=STY3659, t3401;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.P., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627279; CAD09420.1; -; Genomic_DNA.
DR EMBL; AE016845; AK070924.1; -; Genomic_DNA.
SQ Complete proteome; Hypothetical protein.
SQ SEQUENCE 50 AA; 5747 MW; F6BA26E5DFB21F6E CRC64;

Query Match 32.6%; Score 31; DB 2; Length 50;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PKKDVLET 8
||| |||
DB 33 PKKSVLKT 40

RESULT 29
Q4YRD6 PLABE PRELIMINARY; PRT; 40 AA.
AC Q4YRD6;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=P8107303.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; CAAI01002794; CAH99421.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 40 AA; 4792 MW; 8F9ED2034E69675F CRC64;

Query Match 32.1%; Score 30.5; DB 2; Length 40;
Best Local Similarity 46.7%; Pred. No. 2.3e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 KKVLETFVTKSPD 16
||| : |||
DB 17 KKHINKLFT---CPD 28

RESULT 30
Q47605 ECOLI PRELIMINARY; PRT; 16 AA.
ID Q47605 ECOLI PRELIMINARY;
AC Q47605;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63622; AAA24561.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1853 MW; E46774511496607C CRC64;

Query Match 31.6%; Score 30; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KDVLETFVTKSC 14
||| : |||
DB 1 KDLDFTTIGNC 12

RESULT 31
Q62435 MOUSE PRELIMINARY; PRT; 20 AA.
ID Q62435 MOUSE PRELIMINARY;
AC Q62435;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Mutant formin (Fragment).
GN Name=Fmnl; Synonyms=Fmn;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ldtgbri mutant;
RX MEDLINE=96394449; PubMed=8798555; DOI=10.1074/jbc.271.38.23472;
RA Chan D.C., Leder P.;
RT "Genetic evidence that formins function within the nucleus.";
RL J. Biol. Chem. 271:23472-23477(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ldtgbri mutant;
RA Chan D. C., Leder P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60966; AAC52807.1; -; mRNA.
DR MGI; MGI:101815; Fmn.

```
DR MGI; MGI:101815; Fmnl.
DR GO; GO:0005515; F:protein binding; IPI.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2297 MW; A548619EB899933A CRC64;

Query Match          31.6%; Score 30; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KDVLFTFTVKSCP 15
   |||||
Db 2 KDLLEFFFKGSP 14

RESULT 32
Q86487 RVFV
ID Q86487 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86487;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33073; AAA47428.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3295 MW; D0241F37F21A6AE CRC64;

Query Match          31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23

RESULT 33
Q86488 RVFV
ID Q86488 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86488;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33076; AAA47431.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3297 MW; 8017A1F36AFB96AC CRC64;

Query Match          31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23

RESULT 35
Q86490 RVFV
ID Q86490 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86490;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631 (1988).
DR EMBL; M33078; AAA47432.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3297 MW; 8017A1F36AFB96AC CRC64;

Query Match          31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23
```



```
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3269 MW; 933693F37F21A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23

RESULT 36
Q86491 RVFV
ID Q86491 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86491;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV);
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33080; AAA47435.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3304 MW; 8017B4137F21A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23

RESULT 37
Q86492 RVFV
ID Q86492 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86492;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV);
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33086; AAA47438.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3285 MW; 8017A1F37F21A6AC CRC64;
```

```
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3297 MW; 8017A1F36AFB96AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23

RESULT 38
Q86493 RVFV
ID Q86493 RVFV PRELIMINARY; PRT; 30 AA.
AC Q86493;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV);
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33095; AAA47447.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3297 MW; 8017BD2B221A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LETFTVKSCP 15
   |::|: ||
Db 14 LKSFDISQCP 23

RESULT 39
Q04247 RVFV
ID Q04247 RVFV PRELIMINARY; PRT; 30 AA.
AC Q04247;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV);
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89086601; PubMed=2462795;
RA Battles J.K., Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus.";
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33085; AAA47437.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3285 MW; 8017A1F37F21A6AC CRC64;
```

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Gaps 0;

QY 6 LETFTVKSCP 15
|::|:|
Db 14 LKSFDISQCP 23

RESULT 40
Q4JFJ3 RVFV
ID Q4JFJ3_RVFV PRELIMINARY; PRT; 30 AA.
AC Q4JFJ3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Nonstructural glycoprotein (Fragment).
GN Name=nonstructural glycoprotein;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Zimbabwean isolate ZIM34;
RX MEDLINE=89086601; PubMed=2462795;
RA Batties J.K.; Dalrymple J.M.;
RT "Genetic variation among geographic isolates of Rift Valley fever virus."
RL Am. J. Trop. Med. Hyg. 39:617-631(1988).
DR EMBL; M33096; AAA47448.1; -; Genomic_RNA.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3285 MW; 8017A1F37F21A6AC CRC64;

Query Match 31.6%; Score 30; DB 2; Length 30;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Gaps 0;

QY 6 LETFTVKSCP 15
|::|:|
Db 14 LKSFDISQCP 23

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: January 20, 2006, 17:38:51 ; Search time 85.3846 Seconds
(without alignments)
391.480 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192
Perfect score: 80
Sequence: 1 HKDEVIKVEQFYKDTYNKL.....LETFTVKSCPAIKEVFONK 80

Scoring table: OLIGO
Gapop 60.0 , Gapext 50.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pcp:
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pcp:
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pcp:
4: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pcp:
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pcp:
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	227	2	US-08-592-711-6
2	80	100.0	227	3	US-09-183-055-6
3	80	100.0	227	3	US-09-350-202-6
4	80	100.0	227	4	US-10-390-330-6
5	80	100.0	227	5	US-10-473-127-1723
6	80	100.0	227	5	US-10-473-127-1726
7	80	100.0	228	4	US-10-156-136-39
8	80	100.0	228	4	US-10-331-496A-41
9	80	100.0	228	4	US-10-619-323-1
10	80	100.0	228	4	US-10-794-899-97
11	80	100.0	228	5	US-10-473-127-1714
12	80	100.0	228	5	US-10-473-127-1715
13	80	100.0	228	5	US-10-473-127-1716
14	80	100.0	228	5	US-10-473-127-1718
15	80	100.0	228	5	US-10-473-127-1719
16	80	100.0	228	5	US-10-473-127-1722
17	80	100.0	228	5	US-10-473-127-1725
18	80	100.0	228	5	US-10-789-378-18
19	80	100.0	228	5	US-10-482-029-144
20	80	100.0	228	5	US-10-852-335A-187
21	80	100.0	228	6	US-11-041-419-39
22	80	100.0	275	3	US-09-925-301-1381
23	80	100.0	275	4	US-10-106-698-5930
24	80	100.0	275	5	US-10-473-127-1720
25	80	100.0	275	5	US-10-473-127-1721
26	47	58.8	79	5	US-10-473-127-1724
27	43	53.8	454	5	US-10-450-763-44426

28	40	50.0	209	4	US-10-106-698-6825	Sequence 6825, Ap
29	38	47.5	38	4	US-10-619-323-4	Sequence 4, Appli
30	32	40.0	74	4	US-10-425-115-240878	Sequence 240878, Ap
31	30	37.5	30	5	US-10-473-127-1717	Sequence 1717, Ap
32	25	31.2	25	4	US-10-619-323-5	Sequence 5, Appli
33	22	27.5	22	4	US-10-619-323-7	Sequence 7, Appli
34	22	27.5	22	4	US-10-619-323-21	Sequence 21, Appli
35	18	22.5	18	4	US-10-619-323-6	Sequence 6, Appli
36	15	18.8	226	4	US-10-205-194-162	Sequence 162, App
37	10	12.5	10	5	US-10-473-127-165	Sequence 165, App
38	8	10.0	33	4	US-10-264-049-4196	Sequence 4196, App
39	8	10.0	303	4	US-10-724-972A-4282	Sequence 4282, Ap
40	7	8.8	79	4	US-10-424-599-217223	Sequence 217223, Ap
41	7	8.8	100	5	US-10-732-923-4618	Sequence 4618, Ap
42	7	8.8	103	4	US-10-424-599-143977	Sequence 143977, Ap
43	7	8.8	103	5	US-10-947-973-32	Sequence 32, Appli
44	7	8.8	119	4	US-10-437-963-127318	Sequence 127318, Ap
45	7	8.8	119	4	US-10-425-115-285766	Sequence 285766, Ap
46	7	8.8	246	4	US-10-425-114-38255	Sequence 38255, A
47	7	8.8	343	4	US-10-425-115-269703	Sequence 269703, A
48	7	8.8	516	3	US-09-815-242-11309	Sequence 11309, A
49	7	8.8	516	4	US-10-282-122A-58663	Sequence 58663, A
50	7	8.8	608	4	US-10-183-687-204	Sequence 204, App
51	7	8.8	679	4	US-10-425-114-37268	Sequence 37268, A
52	7	8.8	698	4	US-10-424-599-146787	Sequence 146787, Ap
53	7	8.8	701	4	US-10-425-115-241473	Sequence 241473, Ap
54	7	8.8	827	4	US-10-156-761-8159	Sequence 8159, Ap
55	7	8.8	827	4	US-10-425-114-63377	Sequence 63377, A
56	7	8.8	855	4	US-10-369-493-10058	Sequence 10058, A
57	7	8.8	904	5	US-10-732-923-6733	Sequence 6733, Ap
58	7	8.8	1020	4	US-10-282-122A-58016	Sequence 58016, A
59	7	8.8	1104	4	US-10-171-319-8	Sequence 8, Appli
60	7	8.8	1104	4	US-10-352-724-1	Sequence 1, Appli
61	7	8.8	1140	6	US-11-097-143-20817	Sequence 20817, A
62	7	8.8	1663	4	US-10-425-115-291153	Sequence 291153, A
63	7	8.8	2444	9	US-11-097-143-42213	Sequence 42213, A
64	6	7.5	9	4	US-10-210-148-52	Sequence 52, Appli
65	6	7.5	25	4	US-10-601-656-79	Sequence 79, Appli
66	6	7.5	25	4	US-10-601-656-80	Sequence 80, Appli
67	6	7.5	25	5	US-10-873-015-92	Sequence 92, Appli
68	6	7.5	25	5	US-10-873-015-93	Sequence 93, Appli
69	6	7.5	31	4	US-10-400-083-9	Sequence 9, Appli
70	6	7.5	31	6	US-11-066-566-1	Sequence 1, Appli
71	6	7.5	32	6	US-11-066-566-2	Sequence 2, Appli
72	6	7.5	32	6	US-11-066-566-3	Sequence 3, Appli
73	6	7.5	33	4	US-10-092-750-14	Sequence 14, Appli
74	6	7.5	33	5	US-10-499-353A-553	Sequence 553, App
75	6	7.5	39	4	US-10-425-115-238107	Sequence 238107, Ap
76	6	7.5	51	4	US-10-424-599-184894	Sequence 184894, A
77	6	7.5	55	4	US-10-424-599-148371	Sequence 148371, Ap
78	6	7.5	55	4	US-10-425-115-357476	Sequence 357476, Ap
79	6	7.5	56	4	US-10-425-115-363355	Sequence 363355, Ap
80	6	7.5	57	4	US-10-767-701-48817	Sequence 48817, A
81	6	7.5	62	4	US-10-029-386-31642	Sequence 31642, A
82	6	7.5	66	5	US-10-732-923-4548	Sequence 4548, Ap
83	6	7.5	68	3	US-09-895-913A-272	Sequence 272, App
84	6	7.5	71	5	US-10-499-353A-662	Sequence 662, App
85	6	7.5	72	4	US-10-424-599-219751	Sequence 219751, Ap
86	6	7.5	72	4	US-10-425-115-212639	Sequence 212639, Ap
87	6	7.5	72	5	US-10-450-763-37584	Sequence 37584, A
88	6	7.5	75	4	US-10-424-599-167765	Sequence 167765, A
89	6	7.5	78	4	US-10-425-114-43932	Sequence 43932, A
90	6	7.5	78	4	US-10-425-114-44073	Sequence 44073, A
91	6	7.5	79	4	US-10-425-115-308011	Sequence 308011, Ap
92	6	7.5	81	4	US-10-437-963-142691	Sequence 142691, Ap
93	6	7.5	81	4	US-10-400-083-1	Sequence 1, Appli
94	6	7.5	83	4	US-10-424-599-216031	Sequence 216031, Ap
95	6	7.5	88	4	US-10-400-083-5	Sequence 5, Appli
96	6	7.5	90	3	US-09-876-889-17	Sequence 17, Appli
97	6	7.5	90	4	US-10-693-999-4	Sequence 4, Appli
98	6	7.5	90	4	US-10-693-999-5	Sequence 5, Appli
99	6	7.5	90	4	US-10-400-083-6	Sequence 6, Appli
100	6	7.5	90	5	US-10-450-763-57152	Sequence 57152, A

101	6	7.5	91	4	US-10-282-122A-48985	Sequence 48985, A	174	6	7.5	169	4	US-10-424-599-160487	Sequence 160487,
102	6	7.5	92	4	US-10-437-963-138750	Sequence 138750,	175	6	7.5	171	4	US-10-767-701-41615	Sequence 41615, A
103	6	7.5	93	4	US-10-437-963-161910	Sequence 161910,	176	6	7.5	173	4	US-10-097-111-314	Sequence 314, App
104	6	7.5	92	4	US-10-425-115-243779	Sequence 243779,	177	6	7.5	173	4	US-10-425-115-295975	Sequence 295975,
105	6	7.5	92	5	US-10-732-923-4616	Sequence 4616, App	178	6	7.5	175	5	US-10-128-558-386	Sequence 386, App
106	6	7.5	93	4	US-10-415-478A-56	Sequence 56, App1	179	6	7.5	175	5	US-10-450-763-54071	Sequence 54071, A
107	6	7.5	93	5	US-10-472-928-2080	Sequence 2080, App	180	6	7.5	179	4	US-10-425-115-211486	Sequence 211486,
108	6	7.5	95	4	US-10-424-599-183489	Sequence 183489,	181	6	7.5	181	4	US-10-149-819-14	Sequence 14, App1
109	6	7.5	96	4	US-10-425-114-44440	Sequence 44440, A	182	6	7.5	183	4	US-10-369-493-21469	Sequence 21469, A
110	6	7.5	96	4	US-10-437-963-176947	Sequence 176947,	183	6	7.5	186	5	US-10-472-928-2884	Sequence 2884, Ap
111	6	7.5	97	4	US-10-424-599-137678	Sequence 137678,	184	6	7.5	186	4	US-10-104-047-2159	Sequence 2159, Ap
112	6	7.5	97	5	US-10-947-979-30	Sequence 30, App1	185	6	7.5	188	4	US-10-767-701-36311	Sequence 36311, A
113	6	7.5	97	5	US-10-732-923-4612	Sequence 4612, App	186	6	7.5	192	4	US-10-112-944-778	Sequence 778, App
114	6	7.5	97	5	US-10-732-923-4613	Sequence 4613, App	187	6	7.5	192	4	US-10-425-115-329363	Sequence 329363,
115	6	7.5	97	5	US-10-732-923-4614	Sequence 4614, App	188	6	7.5	194	4	US-10-437-963-117350	Sequence 117350,
116	6	7.5	97	5	US-10-732-923-4615	Sequence 4615, App	189	6	7.5	197	4	US-10-424-599-176820	Sequence 176820,
117	6	7.5	97	5	US-10-425-114-42963	Sequence 42963, A	190	6	7.5	202	4	US-10-087-192-1308	Sequence 1308, Ap
118	6	7.5	98	4	US-10-425-114-53363	Sequence 53363, A	191	6	7.5	205	4	US-10-424-599-194704	Sequence 194704,
119	6	7.5	98	4	US-10-425-114-71946	Sequence 71946, A	192	6	7.5	205	4	US-10-437-963-117602	Sequence 117602,
120	6	7.5	98	4	US-10-425-114-71946	Sequence 71946, A	193	6	7.5	207	4	US-10-724-972A-5001	Sequence 5001, Ap
121	6	7.5	98	4	US-10-425-115-336280	Sequence 336280,	194	6	7.5	208	4	US-10-767-701-42923	Sequence 42923, A
122	6	7.5	99	4	US-10-425-114-44643	Sequence 44643, A	195	6	7.5	210	4	US-10-148-641A-8	Sequence 8, App1
123	6	7.5	100	4	US-10-425-115-212744	Sequence 212744,	196	6	7.5	210	4	US-10-767-701-62449	Sequence 62449, A
124	6	7.5	101	4	US-10-425-114-43845	Sequence 43845, A	197	6	7.5	211	4	US-10-425-114-44997	Sequence 44997, A
125	6	7.5	101	4	US-10-425-115-358309	Sequence 358309,	198	6	7.5	212	4	US-10-425-115-348394	Sequence 348394,
126	6	7.5	101	5	US-10-732-923-4620	Sequence 4620, App	199	6	7.5	217	4	US-10-334-143-64	Sequence 64, App1
127	6	7.5	102	5	US-10-732-923-4840	Sequence 4840, App	200	6	7.5	222	3	US-09-925-301-1244	Sequence 1244, Ap
128	6	7.5	102	5	US-10-450-763-57153	Sequence 57153, A	201	6	7.5	222	4	US-10-437-963-169287	Sequence 169287,
129	6	7.5	103	4	US-10-425-114-42976	Sequence 42976, A	202	6	7.5	225	5	US-10-491-467-40	Sequence 40, App1
130	6	7.5	103	4	US-10-425-114-46649	Sequence 46649, A	203	6	7.5	225	4	US-10-425-115-333593	Sequence 333593,
131	6	7.5	103	5	US-10-450-763-41575	Sequence 41575, A	204	6	7.5	227	4	US-10-424-599-249946	Sequence 249946,
132	6	7.5	104	4	US-10-425-114-41168	Sequence 41168, A	205	6	7.5	230	4	US-10-282-122A-61111	Sequence 61111, A
133	6	7.5	104	5	US-10-450-763-41882	Sequence 41882, A	206	6	7.5	233	4	US-10-767-701-43040	Sequence 43040, A
134	6	7.5	105	4	US-10-425-114-54962	Sequence 54962, A	207	6	7.5	235	4	US-10-282-122A-57689	Sequence 57689, A
135	6	7.5	106	4	US-10-425-115-337484	Sequence 337484,	208	6	7.5	235	5	US-10-732-923-7021	Sequence 7021, Ap
136	6	7.5	106	5	US-10-450-763-54070	Sequence 54070, A	209	6	7.5	236	4	US-10-425-115-333687	Sequence 333687,
137	6	7.5	107	4	US-10-437-963-171807	Sequence 171807,	210	6	7.5	236	4	US-10-425-115-360181	Sequence 360181,
138	6	7.5	109	4	US-10-264-049-2663	Sequence 2663, App	211	6	7.5	241	4	US-10-425-115-216864	Sequence 216864,
139	6	7.5	110	4	US-10-338-740-200	Sequence 200, App	212	6	7.5	241	6	US-11-097-143-42351	Sequence 42351, A
140	6	7.5	111	4	US-10-425-115-257857	Sequence 257857,	213	6	7.5	244	4	US-10-437-963-189035	Sequence 189035,
141	6	7.5	112	4	US-10-425-114-45629	Sequence 45629, A	214	6	7.5	245	5	US-10-732-923-4604	Sequence 4604, Ap
142	6	7.5	112	4	US-10-425-114-55059	Sequence 55059, A	215	6	7.5	246	5	US-10-501-282-5602	Sequence 5602, Ap
143	6	7.5	113	5	US-10-450-763-41571	Sequence 41571, A	216	6	7.5	247	5	US-10-437-963-114542	Sequence 114542,
144	6	7.5	116	4	US-10-437-963-110411	Sequence 110411,	217	6	7.5	250	4	US-10-408-765A-1534	Sequence 1534, Ap
145	6	7.5	118	4	US-10-282-122A-71025	Sequence 71025, A	218	6	7.5	255	4	US-10-408-765A-1843	Sequence 1843, Ap
146	6	7.5	120	5	US-10-450-763-37587	Sequence 37587, A	219	6	7.5	258	4	US-10-106-698-6371	Sequence 6371, Ap
147	6	7.5	122	4	US-10-437-963-194885	Sequence 194885,	220	6	7.5	259	4	US-10-424-599-153842	Sequence 153842,
148	6	7.5	122	4	US-10-724-972A-5099	Sequence 5099, App	221	6	7.5	259	5	US-10-501-282-34	Sequence 34, App1
149	6	7.5	123	4	US-10-437-963-118361	Sequence 118361,	222	6	7.5	261	3	US-09-159-469-72	Sequence 72, App1
150	6	7.5	125	4	US-10-389-566-1697	Sequence 1697, App	223	6	7.5	261	3	US-09-798-042-72	Sequence 72, App1
151	6	7.5	125	4	US-10-389-566-2001	Sequence 2001, App	224	6	7.5	261	3	US-09-953-108-72	Sequence 72, App1
152	6	7.5	126	4	US-10-389-566-1742	Sequence 1742, App	225	6	7.5	265	4	US-10-270-845-1	Sequence 1, App1
153	6	7.5	132	4	US-10-425-115-313709	Sequence 313709,	226	6	7.5	265	4	US-10-224-356-16	Sequence 16, App1
154	6	7.5	133	4	US-10-424-599-248440	Sequence 248440,	227	6	7.5	265	4	US-10-440-366-16	Sequence 16, App1
155	6	7.5	135	4	US-10-767-701-34986	Sequence 34986, A	228	6	7.5	267	4	US-10-425-115-277798	Sequence 277798,
156	6	7.5	139	4	US-10-425-115-268856	Sequence 268856,	229	6	7.5	274	4	US-10-302-382-10	Sequence 10, App1
157	6	7.5	140	4	US-10-437-963-168880	Sequence 168880,	230	6	7.5	274	5	US-10-732-923-5847	Sequence 5847, Ap
158	6	7.5	144	4	US-10-082-828A-167	Sequence 167, App	231	6	7.5	275	4	US-10-369-493-19115	Sequence 19115, A
159	6	7.5	144	4	US-10-437-963-126470	Sequence 126470,	232	6	7.5	279	4	US-10-282-122A-72346	Sequence 72346, A
160	6	7.5	144	5	US-10-617-320-3320	Sequence 3320, App	233	6	7.5	280	4	US-10-282-122A-71523	Sequence 71523, A
161	6	7.5	146	4	US-11-057-807-167	Sequence 167, App	234	6	7.5	280	4	US-10-424-599-163943	Sequence 163943,
162	6	7.5	146	4	US-10-091-007-196	Sequence 196, App	235	6	7.5	281	4	US-10-767-701-32334	Sequence 32334, A
163	6	7.5	147	4	US-10-424-599-263420	Sequence 263420,	236	6	7.5	281	5	US-10-732-923-5848	Sequence 5848, Ap
164	6	7.5	148	4	US-10-424-599-147625	Sequence 147625,	237	6	7.5	282	3	US-09-815-242-5576	Sequence 5576, Ap
165	6	7.5	149	5	US-10-741-849-7294	Sequence 7294, App	238	6	7.5	285	4	US-10-156-761-7886	Sequence 7886, Ap
166	6	7.5	152	4	US-10-425-115-325011	Sequence 325011,	239	6	7.5	285	5	US-10-732-923-16991	Sequence 16991, A
167	6	7.5	153	4	US-10-425-115-243754	Sequence 243754,	240	6	7.5	287	4	US-10-424-599-265154	Sequence 265154,
168	6	7.5	156	5	US-10-732-923-4625	Sequence 4625, App	241	6	7.5	288	5	US-10-501-282-2	Sequence 2, App1
169	6	7.5	159	4	US-10-156-761-9215	Sequence 9215, App	242	6	7.5	289	4	US-10-282-122A-53218	Sequence 53218, A
170	6	7.5	161	3	US-09-798-042-106	Sequence 106, App	243	6	7.5	290	3	US-09-925-298-592	Sequence 592, App
171	6	7.5	161	3	US-09-953-108-106	Sequence 106, App	244	6	7.5	290	4	US-10-102-806-592	Sequence 592, App
172	6	7.5	166	3	US-09-864-408A-2368	Sequence 2368, App	245	6	7.5	292	3	US-09-815-242-12440	Sequence 12440, A
173	6	7.5	167	4	US-10-204-887-131	Sequence 131, App	246	6	7.5	292	4	US-10-282-122A-44114	Sequence 44114, A

247	6	7.5	292	4	US-10-425-115-309837	Sequence 309837,	320	6	7.5	387	4	US-10-290-386-140	Sequence 140, App
248	6	7.5	293	4	US-10-282-122A-60768	Sequence 60768, A	321	6	7.5	387	4	US-10-356-861-140	Sequence 140, App
249	6	7.5	295	5	US-10-721-922A-50	Sequence 50, Appl	322	6	7.5	387	4	US-10-309-584-140	Sequence 140, App
250	6	7.5	296	4	US-10-425-115-198890	Sequence 198890,	323	6	7.5	387	5	US-10-897-793-140	Sequence 140, App
251	6	7.5	297	4	US-10-264-213-233	Sequence 233, App	324	6	7.5	387	5	US-10-783-557-141	Sequence 141, App
252	6	7.5	299	4	US-10-424-598-182535	Sequence 182535,	325	6	7.5	389	4	US-10-243-552-341	Sequence 341, App
253	6	7.5	303	3	US-09-903-190-107	Sequence 107, App	326	6	7.5	390	4	US-10-112-944-331	Sequence 321, App
254	6	7.5	303	3	US-09-978-360A-763	Sequence 763, App	327	6	7.5	390	4	US-10-489-906-2	Sequence 2, Appl
255	6	7.5	303	4	US-10-424-599-229583	Sequence 229583,	328	6	7.5	391	4	US-10-437-963-155705	Sequence 155705,
256	6	7.5	303	4	US-10-408-765A-844	Sequence 844, App	329	6	7.5	391	4	US-10-437-963-193222	Sequence 193222,
257	6	7.5	303	4	US-10-408-765A-845	Sequence 845, App	330	6	7.5	394	4	US-10-156-761-10991	Sequence 10991, A
258	6	7.5	303	5	US-10-930-331-107	Sequence 107, App	331	6	7.5	397	4	US-10-369-493-261	Sequence 261, App
259	6	7.5	305	4	US-10-425-114-42718	Sequence 42718, A	332	6	7.5	398	4	US-10-282-122A-47016	Sequence 47016, A
260	6	7.5	306	4	US-10-264-213-139	Sequence 139, App	333	6	7.5	399	4	US-10-094-749-2219	Sequence 2219, Ap
261	6	7.5	306	4	US-10-282-122A-62082	Sequence 62082, A	334	6	7.5	399	4	US-10-369-493-671	Sequence 671, App
262	6	7.5	308	4	US-10-425-114-40549	Sequence 40549, A	335	6	7.5	400	4	US-10-437-963-156435	Sequence 156435,
263	6	7.5	308	4	US-10-282-122A-69373	Sequence 69373, A	336	6	7.5	403	4	US-10-369-493-194	Sequence 194, App
264	6	7.5	311	5	US-10-721-922A-52	Sequence 52, Appl	337	6	7.5	403	4	US-10-369-493-10827	Sequence 10827, A
265	6	7.5	314	4	US-10-425-114-63852	Sequence 63852, A	338	6	7.5	404	4	US-10-425-114-69708	Sequence 69708, A
266	6	7.5	314	5	US-10-639-194-6	Sequence 6, Appl	339	6	7.5	404	4	US-10-156-761-9220	Sequence 9220, Ap
267	6	7.5	316	5	US-10-639-194-2	Sequence 2, Appl	340	6	7.5	405	3	US-09-769-787-62	Sequence 62, Appl
268	6	7.5	318	5	US-10-639-194-10	Sequence 10, Appl	341	6	7.5	405	5	US-10-472-928-3640	Sequence 3640, Ap
269	6	7.5	319	4	US-10-174-693-323	Sequence 323, App	342	6	7.5	407	4	US-10-437-963-156447	Sequence 156447,
270	6	7.5	319	5	US-10-732-923-15987	Sequence 15987, A	343	6	7.5	407	4	US-10-425-115-212002	Sequence 212002,
271	6	7.5	320	4	US-10-437-963-135890	Sequence 135890,	344	6	7.5	409	4	US-10-781-142-1	Sequence 1, Appl
272	6	7.5	322	4	US-10-321-204-36	Sequence 36, Appl	345	6	7.5	410	4	US-10-369-493-366	Sequence 366, App
273	6	7.5	324	4	US-10-432-737-52	Sequence 52, Appl	346	6	7.5	410	4	US-10-437-963-184086	Sequence 184086,
274	6	7.5	325	5	US-10-732-923-19334	Sequence 19334, A	347	6	7.5	410	4	US-10-437-963-202231	Sequence 202231,
275	6	7.5	325	4	US-10-369-493-17720	Sequence 17720, A	348	6	7.5	411	4	US-10-389-566-1809	Sequence 1809, Ap
276	6	7.5	327	4	US-10-425-115-198882	Sequence 198882,	349	6	7.5	411	4	US-10-282-122A-59555	Sequence 59555, A
277	6	7.5	332	3	US-09-925-299-987	Sequence 987, App	350	6	7.5	411	4	US-10-282-122A-74947	Sequence 74947, A
278	6	7.5	332	5	US-09-925-299-987	Sequence 987, App	351	6	7.5	411	5	US-10-283-132A-75572	Sequence 75572, A
279	6	7.5	332	5	US-10-450-763-49200	Sequence 49200, A	352	6	7.5	411	5	US-10-732-923-5697	Sequence 5697, Ap
280	6	7.5	336	4	US-10-425-114-70192	Sequence 70192, A	353	6	7.5	411	5	US-10-732-923-5846	Sequence 5846, Ap
281	6	7.5	336	4	US-10-425-115-276729	Sequence 276729,	354	6	7.5	411	5	US-10-501-282-36	Sequence 36, Appl
282	6	7.5	337	4	US-10-437-963-112732	Sequence 112732,	355	6	7.5	413	3	US-09-821-803A-7	Sequence 7, Appl
283	6	7.5	339	4	US-10-781-014-380	Sequence 380, App	356	6	7.5	413	3	US-09-821-803A-8	Sequence 8, Appl
284	6	7.5	345	4	US-10-209-967-15	Sequence 15, Appl	357	6	7.5	413	4	US-10-270-845-13	Sequence 13, Appl
285	6	7.5	345	4	US-10-209-967-16	Sequence 16, Appl	358	6	7.5	413	4	US-10-270-845-14	Sequence 14, Appl
286	6	7.5	345	4	US-10-437-963-156412	Sequence 156412,	359	6	7.5	413	4	US-10-282-122A-77646	Sequence 77646, A
287	6	7.5	345	5	US-10-128-558-209	Sequence 209, App	360	6	7.5	413	5	US-10-498-698-1	Sequence 1, Appl
288	6	7.5	346	4	US-10-424-599-162560	Sequence 162560,	361	6	7.5	414	5	US-10-732-923-23190	Sequence 23190, A
289	6	7.5	348	4	US-10-437-963-136759	Sequence 136759,	362	6	7.5	416	4	US-10-210-281-14	Sequence 14, Appl
290	6	7.5	348	5	US-10-450-763-33541	Sequence 33541, A	363	6	7.5	417	6	US-11-097-143-21408	Sequence 21408, A
291	6	7.5	349	3	US-09-738-626-5897	Sequence 5897, Ap	364	6	7.5	418	4	US-10-282-122A-43285	Sequence 43285, A
292	6	7.5	350	4	US-10-437-963-184178	Sequence 184178,	365	6	7.5	419	4	US-10-425-114-70713	Sequence 70713, A
293	6	7.5	352	4	US-10-224-356-13	Sequence 13, Appl	366	6	7.5	420	4	US-10-282-122A-48931	Sequence 48931, A
294	6	7.5	353	5	US-10-501-282-1902	Sequence 1902, Ap	367	6	7.5	420	5	US-10-450-763-30672	Sequence 30672, A
295	6	7.5	356	4	US-10-408-765A-2059	Sequence 2059, Ap	368	6	7.5	422	4	US-10-437-963-104858	Sequence 104858,
296	6	7.5	360	6	US-11-097-143-10752	Sequence 10752, A	369	6	7.5	424	4	US-10-369-493-10059	Sequence 10059, A
297	6	7.5	360	6	US-10-437-963-155060	Sequence 155060,	370	6	7.5	429	4	US-10-369-493-2650	Sequence 2650, Ap
298	6	7.5	362	5	US-10-717-665-68	Sequence 68, Appl	371	6	7.5	430	4	US-10-437-963-155712	Sequence 155712,
299	6	7.5	369	4	US-10-424-599-171094	Sequence 171094,	372	6	7.5	433	3	US-09-946-290-14	Sequence 14, Appl
300	6	7.5	369	5	US-10-732-923-2849	Sequence 2849, Ap	373	6	7.5	433	4	US-10-369-493-22228	Sequence 22228, A
301	6	7.5	369	5	US-10-732-923-3249	Sequence 3249, Ap	374	6	7.5	433	4	US-10-437-963-113586	Sequence 113586,
302	6	7.5	371	4	US-10-424-599-193125	Sequence 193125,	375	6	7.5	433	5	US-10-324-035-14	Sequence 14, Appl
303	6	7.5	372	4	US-10-108-260A-4280	Sequence 4280, Ap	376	6	7.5	434	4	US-10-437-963-171802	Sequence 171802,
304	6	7.5	375	4	US-10-431-544-35	Sequence 35, Appl	377	6	7.5	435	4	US-10-437-963-155371	Sequence 155371,
305	6	7.5	375	4	US-10-437-963-115963	Sequence 115963,	378	6	7.5	436	5	US-10-732-923-8388	Sequence 8388, Ap
306	6	7.5	375	5	US-10-830-828-61	Sequence 61, Appl	379	6	7.5	439	4	US-10-382-248-30	Sequence 30, Appl
307	6	7.5	376	5	US-10-780-507-120	Sequence 120, App	380	6	7.5	439	4	US-10-425-115-338498	Sequence 338498,
308	6	7.5	378	5	US-10-501-282-1904	Sequence 1904, Ap	381	6	7.5	439	4	US-10-425-115-338501	Sequence 338501,
309	6	7.5	379	4	US-10-369-493-3015	Sequence 3015, Ap	382	6	7.5	440	4	US-10-437-963-149358	Sequence 149358,
310	6	7.5	381	3	US-09-764-903-42	Sequence 42, Appl	383	6	7.5	440	4	US-10-437-963-155659	Sequence 155659,
311	6	7.5	381	4	US-10-203-319A-26	Sequence 26, Appl	384	6	7.5	442	4	US-10-369-493-14197	Sequence 14197, A
312	6	7.5	382	4	US-10-282-122A-56872	Sequence 56872, A	385	6	7.5	449	4	US-10-369-493-2406	Sequence 2406, Ap
313	6	7.5	382	5	US-10-732-923-4753	Sequence 4753, Ap	386	6	7.5	449	4	US-10-323-281-102	Sequence 102, App
314	6	7.5	384	4	US-09-815-243-10742	Sequence 10742, A	387	6	7.5	451	4	US-10-607-631-18	Sequence 18, Appl
315	6	7.5	384	4	US-10-425-114-56302	Sequence 56302, A	388	6	7.5	452	4	US-10-425-114-66536	Sequence 66536, A
316	6	7.5	384	6	US-11-097-143-3378	Sequence 3378, Ap	389	6	7.5	453	4	US-10-369-493-11158	Sequence 11158, A
317	6	7.5	387	3	US-09-940-244-140	Sequence 140, App	390	6	7.5	453	4	US-10-471-115-12	Sequence 12, Appl
318	6	7.5	387	3	US-09-732-622A-140	Sequence 140, App	391	6	7.5	457	4	US-10-437-963-171647	Sequence 171647,
319	6	7.5	387	4	US-10-033-297-140	Sequence 140, App	392	6	7.5	459	4	US-10-369-493-11744	Sequence 11744, A

333	6	7.5	460	3	US-09-975-719-132	Sequence 132, App	466	6	7.5	538	4	US-10-245-033-50	Sequence 50, Appl
334	6	7.5	463	4	US-10-424-599-244931	Sequence 244931,	467	6	7.5	538	4	US-10-243-095-50	Sequence 50, Appl
335	6	7.5	467	4	US-10-437-963-156510	Sequence 156510,	468	6	7.5	538	4	US-10-243-185-50	Sequence 50, Appl
336	6	7.5	468	3	US-09-923-300-1661	Sequence 1661, Ap	469	6	7.5	538	4	US-10-245-427-50	Sequence 50, Appl
337	6	7.5	468	4	US-10-264-049-3018	Sequence 3018, Ap	470	6	7.5	538	4	US-10-245-473-50	Sequence 50, Appl
338	6	7.5	469	4	US-10-437-963-155757	Sequence 155757,	471	6	7.5	538	4	US-10-245-770-50	Sequence 50, Appl
339	6	7.5	470	4	US-10-437-963-139438	Sequence 139438,	472	6	7.5	538	4	US-10-245-877-50	Sequence 50, Appl
340	6	7.5	471	4	US-10-437-963-155372	Sequence 155372,	473	6	7.5	538	4	US-10-246-976-50	Sequence 50, Appl
341	6	7.5	474	4	US-10-282-122A-66211	Sequence 66211, A	474	6	7.5	538	4	US-10-243-320-50	Sequence 50, Appl
342	6	7.5	475	5	US-10-450-763-46256	Sequence 46256, A	475	6	7.5	538	4	US-10-242-743-50	Sequence 50, Appl
343	6	7.5	478	4	US-10-369-493-15107	Sequence 15107, A	476	6	7.5	538	4	US-10-242-845-50	Sequence 50, Appl
344	6	7.5	480	4	US-10-425-114-43517	Sequence 43517, A	477	6	7.5	538	4	US-10-237-636-50	Sequence 50, Appl
345	6	7.5	480	4	US-10-437-963-139538	Sequence 139538,	478	6	7.5	538	4	US-10-238-325-50	Sequence 50, Appl
346	6	7.5	480	4	US-10-437-963-155449	Sequence 155449,	479	6	7.5	538	4	US-10-238-346-50	Sequence 50, Appl
347	6	7.5	481	4	US-10-104-047-3799	Sequence 3799, Ap	480	6	7.5	538	4	US-10-238-411-50	Sequence 50, Appl
348	6	7.5	482	4	US-10-094-749-2966	Sequence 2966, Ap	481	6	7.5	538	4	US-10-243-124-50	Sequence 50, Appl
349	6	7.5	486	4	US-10-437-963-125679	Sequence 125679,	482	6	7.5	538	4	US-10-243-425-50	Sequence 50, Appl
350	6	7.5	487	4	US-10-369-493-14476	Sequence 14476, A	483	6	7.5	538	4	US-10-243-446-50	Sequence 50, Appl
351	6	7.5	487	6	US-11-097-143-6585	Sequence 6585, Ap	484	6	7.5	538	4	US-10-245-874-50	Sequence 50, Appl
352	6	7.5	489	4	US-10-437-963-155451	Sequence 155451,	485	6	7.5	538	4	US-10-242-653-50	Sequence 50, Appl
353	6	7.5	489	4	US-10-437-963-155665	Sequence 155665,	486	6	7.5	538	4	US-10-243-167-50	Sequence 50, Appl
354	6	7.5	494	4	US-10-425-114-64720	Sequence 64720, A	487	6	7.5	538	4	US-10-243-388-50	Sequence 50, Appl
355	6	7.5	495	4	US-10-369-493-23450	Sequence 23450, A	488	6	7.5	538	4	US-10-244-947-50	Sequence 50, Appl
356	6	7.5	495	4	US-10-282-122A-70223	Sequence 70223, A	489	6	7.5	538	4	US-10-244-968-50	Sequence 50, Appl
357	6	7.5	496	4	US-10-437-963-171669	Sequence 171669,	490	6	7.5	538	4	US-10-244-990-50	Sequence 50, Appl
358	6	7.5	496	5	US-10-739-930-10234	Sequence 10234, A	491	6	7.5	538	4	US-10-245-079-50	Sequence 50, Appl
359	6	7.5	497	4	US-10-282-122A-71807	Sequence 71807, A	492	6	7.5	538	4	US-10-245-127-50	Sequence 50, Appl
360	6	7.5	497	4	US-10-282-122A-74444	Sequence 74444, A	493	6	7.5	538	4	US-10-245-207-50	Sequence 50, Appl
361	6	7.5	498	4	US-10-437-963-150223	Sequence 150223,	494	6	7.5	538	4	US-10-245-646-50	Sequence 50, Appl
362	6	7.5	500	4	US-10-282-122A-57785	Sequence 57785, A	495	6	7.5	538	4	US-10-245-695-50	Sequence 50, Appl
363	6	7.5	501	4	US-10-369-493-10711	Sequence 10711, A	496	6	7.5	538	4	US-10-245-699-50	Sequence 50, Appl
364	6	7.5	502	4	US-10-437-963-152767	Sequence 152767,	497	6	7.5	538	4	US-10-245-737-50	Sequence 50, Appl
365	6	7.5	503	4	US-10-375-657-2	Sequence 2, Appli	498	6	7.5	538	4	US-10-245-878-50	Sequence 50, Appl
366	6	7.5	506	4	US-10-094-749-2229	Sequence 2229, Ap	499	6	7.5	538	4	US-10-245-890-50	Sequence 50, Appl
367	6	7.5	507	6	US-11-097-143-24531	Sequence 24531, A	500	6	7.5	538	4	US-10-245-899-50	Sequence 50, Appl
368	6	7.5	508	2	US-08-781-986A-5241	Sequence 5241, Ap	501	6	7.5	538	4	US-10-245-900-50	Sequence 50, Appl
369	6	7.5	508	4	US-10-329-624-5241	Sequence 5241, Ap	502	6	7.5	538	4	US-10-247-058-50	Sequence 50, Appl
370	6	7.5	508	4	US-10-437-963-141593	Sequence 141593,	503	6	7.5	538	4	US-10-245-454-50	Sequence 50, Appl
371	6	7.5	508	4	US-10-437-963-149381	Sequence 149381,	504	6	7.5	538	4	US-10-237-471-50	Sequence 50, Appl
372	6	7.5	514	4	US-10-425-115-221260	Sequence 221260,	505	6	7.5	538	4	US-10-238-261-50	Sequence 50, Appl
373	6	7.5	519	4	US-10-437-963-155750	Sequence 155750,	506	6	7.5	538	4	US-10-238-324-50	Sequence 50, Appl
374	6	7.5	520	4	US-10-437-963-112331	Sequence 112331,	507	6	7.5	538	4	US-10-241-860-50	Sequence 50, Appl
375	6	7.5	521	4	US-10-060-065-34	Sequence 34, Appl	508	6	7.5	538	4	US-10-242-172-50	Sequence 50, Appl
376	6	7.5	521	4	US-10-059-585-55	Sequence 55, Appl	509	6	7.5	538	4	US-10-242-652-50	Sequence 50, Appl
377	6	7.5	521	4	US-10-341-434-111	Sequence 11, App	510	6	7.5	538	4	US-10-242-990-50	Sequence 50, Appl
378	6	7.5	523	3	US-09-983-531A-24	Sequence 24, Appl	511	6	7.5	538	4	US-10-243-023-50	Sequence 50, Appl
379	6	7.5	528	4	US-10-781-142-6	Sequence 9, Appli	512	6	7.5	538	4	US-10-243-103-50	Sequence 50, Appl
380	6	7.5	529	4	US-10-781-142-13	Sequence 13, Appl	513	6	7.5	538	4	US-10-243-276-50	Sequence 50, Appl
381	6	7.5	529	4	US-10-781-142-9	Sequence 13, Appl	514	6	7.5	538	4	US-10-243-326-50	Sequence 50, Appl
382	6	7.5	533	4	US-10-369-493-17482	Sequence 17482, A	515	6	7.5	538	4	US-10-243-364-50	Sequence 50, Appl
383	6	7.5	536	4	US-10-104-047-2780	Sequence 2780, Ap	516	6	7.5	538	4	US-10-243-494-50	Sequence 50, Appl
384	6	7.5	538	4	US-10-245-752-50	Sequence 50, Appl	517	6	7.5	538	4	US-10-244-995-50	Sequence 50, Appl
385	6	7.5	538	4	US-10-245-859-50	Sequence 50, Appl	518	6	7.5	538	4	US-10-245-230-50	Sequence 50, Appl
386	6	7.5	538	4	US-10-245-103-50	Sequence 50, Appl	519	6	7.5	538	4	US-10-245-253-50	Sequence 50, Appl
387	6	7.5	538	4	US-10-245-107-50	Sequence 50, Appl	520	6	7.5	538	4	US-10-245-479-50	Sequence 50, Appl
388	6	7.5	538	4	US-10-245-143-50	Sequence 50, Appl	521	6	7.5	538	4	US-10-245-499-50	Sequence 50, Appl
389	6	7.5	538	4	US-10-245-771-50	Sequence 50, Appl	522	6	7.5	538	4	US-10-245-772-50	Sequence 50, Appl
390	6	7.5	538	4	US-10-245-851-50	Sequence 50, Appl	523	6	7.5	538	4	US-10-245-811-50	Sequence 50, Appl
391	6	7.5	538	4	US-10-245-883-50	Sequence 50, Appl	524	6	7.5	538	4	US-10-245-812-50	Sequence 50, Appl
392	6	7.5	538	4	US-10-237-535-50	Sequence 50, Appl	525	6	7.5	538	4	US-10-245-852-50	Sequence 50, Appl
393	6	7.5	538	4	US-10-238-183-50	Sequence 50, Appl	526	6	7.5	538	4	US-10-245-875-50	Sequence 50, Appl
394	6	7.5	538	4	US-10-238-283-50	Sequence 50, Appl	527	6	7.5	538	4	US-10-245-881-50	Sequence 50, Appl
395	6	7.5	538	4	US-10-238-370-50	Sequence 50, Appl	528	6	7.5	538	4	US-10-245-911-50	Sequence 50, Appl
396	6	7.5	538	4	US-10-245-055-50	Sequence 50, Appl	529	6	7.5	538	4	US-10-245-913-50	Sequence 50, Appl
397	6	7.5	538	4	US-10-245-147-50	Sequence 50, Appl	530	6	7.5	538	4	US-10-246-080-50	Sequence 50, Appl
398	6	7.5	538	4	US-10-245-730-50	Sequence 50, Appl	531	6	7.5	538	4	US-10-246-121-50	Sequence 50, Appl
399	6	7.5	538	4	US-10-245-739-50	Sequence 50, Appl	532	6	7.5	538	4	US-10-246-305-50	Sequence 50, Appl
400	6	7.5	538	4	US-10-246-210-50	Sequence 50, Appl	533	6	7.5	538	4	US-10-246-929-50	Sequence 50, Appl
401	6	7.5	538	4	US-10-233-136-50	Sequence 50, Appl	534	6	7.5	538	4	US-10-247-036-50	Sequence 50, Appl
402	6	7.5	538	4	US-10-243-049-50	Sequence 50, Appl	535	6	7.5	538	4	US-10-243-255-50	Sequence 50, Appl
403	6	7.5	538	4	US-10-243-409-50	Sequence 50, Appl	536	6	7.5	538	4	US-10-245-810-50	Sequence 50, Appl
404	6	7.5	538	4	US-10-245-621-50	Sequence 50, Appl	537	6	7.5	538	4	US-10-245-910-50	Sequence 50, Appl
405	6	7.5	538	4	US-10-245-880-50	Sequence 50, Appl	538	6	7.5	538	4	US-10-246-098-50	Sequence 50, Appl

539	6	7.5	538	4	US-10-237-496-50	Sequence 50, Appl	612	6	7.5	652	3	US-09-780-669-818	Sequence 818, App
540	6	7.5	538	4	US-10-242-074-50	Sequence 50, Appl	613	6	7.5	652	3	US-09-822-827-818	Sequence 818, App
541	6	7.5	538	4	US-10-242-505-50	Sequence 50, Appl	614	6	7.5	652	3	US-09-895-793-818	Sequence 818, App
542	6	7.5	538	4	US-10-242-574-50	Sequence 50, Appl	615	6	7.5	652	3	US-09-895-814-818	Sequence 818, App
543	6	7.5	538	4	US-10-243-261-50	Sequence 50, Appl	616	6	7.5	652	4	US-10-012-896-818	Sequence 818, App
544	6	7.5	538	4	US-10-243-282-50	Sequence 50, Appl	617	6	7.5	652	4	US-10-144-678A-818	Sequence 818, App
545	6	7.5	538	4	US-10-243-402-50	Sequence 50, Appl	618	6	7.5	652	4	US-10-294-025-818	Sequence 818, App
546	6	7.5	538	4	US-10-243-431-50	Sequence 50, Appl	619	6	7.5	652	5	US-10-511-556-17	Sequence 17, Appl
547	6	7.5	538	4	US-10-245-164-50	Sequence 50, Appl	620	6	7.5	652	5	US-10-511-556-19	Sequence 19, Appl
548	6	7.5	538	4	US-10-210-951-70	Sequence 70, Appl	621	6	7.5	675	5	US-10-732-923-23083	Sequence 23083, A
549	6	7.5	538	4	US-10-244-942-50	Sequence 50, Appl	622	6	7.5	675	5	US-10-739-930-10541	Sequence 10541, A
550	6	7.5	538	4	US-10-197-972-50	Sequence 50, Appl	623	6	7.5	686	3	US-09-983-531A-12	Sequence 12, Appl
551	6	7.5	538	4	US-10-211-884-70	Sequence 70, Appl	624	6	7.5	686	4	US-10-316-253-273	Sequence 273, App
552	6	7.5	538	4	US-10-238-196-50	Sequence 50, Appl	625	6	7.5	696	4	US-10-282-122A-70746	Sequence 70746, A
553	6	7.5	538	4	US-10-245-013-50	Sequence 50, Appl	626	6	7.5	696	4	US-10-437-963-142030	Sequence 142030, A
554	6	7.5	538	4	US-10-211-858-70	Sequence 70, Appl	627	6	7.5	697	5	US-10-450-763-41787	Sequence 41787, A
555	6	7.5	549	3	US-09-815-242-11206	Sequence 11206, A	628	6	7.5	704	4	US-10-418-819-2	Sequence 2, Appl
556	6	7.5	549	4	US-10-411-253-2	Sequence 2, Appl	629	6	7.5	704	4	US-10-418-819-8	Sequence 8, Appl
557	6	7.5	549	5	US-10-282-122A-58451	Sequence 58451, A	630	6	7.5	704	4	US-10-418-819-10	Sequence 10, Appl
558	6	7.5	549	5	US-10-741-600-1473	Sequence 1473, Ap	631	6	7.5	706	4	US-10-425-115-334013	Sequence 334013, A
559	6	7.5	549	5	US-10-714-470-1	Sequence 1, Appl	632	6	7.5	713	4	US-10-058-513-35	Sequence 35, Appl
560	6	7.5	549	5	US-10-714-470-3	Sequence 3, Appl	633	6	7.5	713	4	US-10-058-513-35	Sequence 35, Appl
561	6	7.5	549	5	US-10-732-923-18404	Sequence 18404, A	634	6	7.5	715	3	US-09-815-242-10450	Sequence 10450, A
562	6	7.5	550	4	US-10-411-253-4	Sequence 4, Appl	635	6	7.5	715	4	US-10-369-493-23660	Sequence 23660, A
563	6	7.5	555	2	US-08-808-031A-31	Sequence 31, Appl	636	6	7.5	715	4	US-10-282-122A-43223	Sequence 43223, A
564	6	7.5	557	4	US-10-282-122A-78003	Sequence 78003, A	637	6	7.5	715	4	US-10-282-122A-75843	Sequence 75843, A
565	6	7.5	557	5	US-10-732-923-18342	Sequence 18342, A	638	6	7.5	719	3	US-09-159-465-59	Sequence 59, Appl
566	6	7.5	558	4	US-10-053-248-10	Sequence 10, Appl	639	6	7.5	719	3	US-09-798-042-59	Sequence 59, Appl
567	6	7.5	558	4	US-10-364-748-2	Sequence 2, Appl	640	6	7.5	722	4	US-10-953-108-59	Sequence 120558, A
568	6	7.5	558	4	US-10-345-837-10	Sequence 10, Appl	641	6	7.5	722	4	US-10-437-963-120558	Sequence 120558, A
569	6	7.5	562	6	US-11-097-143-7800	Sequence 7800, Ap	642	6	7.5	723	6	US-11-097-143-4002	Sequence 4002, Ap
570	6	7.5	565	4	US-10-437-963-112333	Sequence 112333, A	643	6	7.5	723	6	US-10-437-963-120558	Sequence 120558, A
571	6	7.5	569	6	US-11-097-143-36531	Sequence 36531, A	644	6	7.5	727	4	US-10-437-963-194323	Sequence 194323, A
572	6	7.5	570	4	US-10-788-792-187	Sequence 187, App	645	6	7.5	729	6	US-10-369-493-23535	Sequence 23535, A
573	6	7.5	571	4	US-10-389-566-643	Sequence 643, App	646	6	7.5	735	3	US-09-978-295A-74	Sequence 74, Appl
574	6	7.5	574	4	US-10-389-566-654	Sequence 654, App	647	6	7.5	735	3	US-09-978-697-74	Sequence 74, Appl
575	6	7.5	574	4	US-10-389-566-654	Sequence 654, App	648	6	7.5	735	3	US-09-978-697-74	Sequence 74, Appl
576	6	7.5	577	4	US-10-425-115-198892	Sequence 198892, A	649	6	7.5	735	3	US-09-978-192A-74	Sequence 74, Appl
577	6	7.5	578	5	US-10-425-115-198880	Sequence 198880, A	650	6	7.5	735	3	US-09-978-192A-74	Sequence 74, Appl
578	6	7.5	581	3	US-09-949-029-38	Sequence 38, Appl	651	6	7.5	735	3	US-09-978-189-74	Sequence 74, Appl
579	6	7.5	581	6	US-11-097-143-2331	Sequence 2331, Ap	652	6	7.5	735	3	US-09-978-608A-74	Sequence 74, Appl
580	6	7.5	582	4	US-10-424-599-232754	Sequence 232754, A	653	6	7.5	735	3	US-09-978-608A-74	Sequence 74, Appl
581	6	7.5	586	2	US-08-808-031A-28	Sequence 28, Appl	654	6	7.5	735	3	US-09-978-608A-74	Sequence 74, Appl
582	6	7.5	588	4	US-10-369-493-21186	Sequence 21186, A	655	6	7.5	735	3	US-09-978-191A-74	Sequence 74, Appl
583	6	7.5	589	5	US-10-450-763-51530	Sequence 51530, A	656	6	7.5	735	3	US-09-978-403A-74	Sequence 74, Appl
584	6	7.5	593	4	US-10-437-963-189326	Sequence 189326, A	657	6	7.5	735	3	US-09-978-564A-74	Sequence 74, Appl
585	6	7.5	594	4	US-10-437-963-147363	Sequence 147363, A	658	6	7.5	735	3	US-09-978-833A-74	Sequence 74, Appl
586	6	7.5	594	5	US-10-450-763-49527	Sequence 49527, A	659	6	7.5	735	3	US-09-981-915A-74	Sequence 74, Appl
587	6	7.5	598	4	US-10-424-599-222753	Sequence 222753, A	660	6	7.5	735	3	US-09-978-824-74	Sequence 74, Appl
588	6	7.5	598	4	US-10-425-114-44126	Sequence 44126, A	661	6	7.5	735	3	US-09-918-585A-74	Sequence 74, Appl
589	6	7.5	599	4	US-10-389-647-688	Sequence 688, App	662	6	7.5	735	3	US-09-978-834A-74	Sequence 74, Appl
590	6	7.5	599	4	US-10-437-963-139771	Sequence 139771, A	663	6	7.5	735	3	US-09-978-423A-74	Sequence 74, Appl
591	6	7.5	599	4	US-10-425-115-219971	Sequence 219971, A	664	6	7.5	735	3	US-09-978-193A-74	Sequence 74, Appl
592	6	7.5	601	4	US-10-424-599-259258	Sequence 259258, A	665	6	7.5	735	3	US-09-999-830A-74	Sequence 74, Appl
593	6	7.5	605	4	US-10-425-115-360159	Sequence 360159, A	666	6	7.5	735	3	US-09-978-757A-74	Sequence 74, Appl
594	6	7.5	606	4	US-10-437-963-148183	Sequence 148183, A	667	6	7.5	735	3	US-09-978-187B-74	Sequence 74, Appl
595	6	7.5	607	5	US-10-732-923-23200	Sequence 23200, A	668	6	7.5	735	3	US-09-978-643A-74	Sequence 74, Appl
596	6	7.5	610	4	US-10-282-122A-53029	Sequence 53029, A	669	6	7.5	735	3	US-09-978-375A-74	Sequence 74, Appl
597	6	7.5	616	4	US-10-425-115-309918	Sequence 309918, A	670	6	7.5	735	3	US-09-978-298A-74	Sequence 74, Appl
598	6	7.5	617	5	US-10-732-923-3151	Sequence 3151, Ap	671	6	7.5	735	3	US-09-978-188A-74	Sequence 74, Appl
599	6	7.5	619	4	US-10-437-963-159314	Sequence 159314, A	672	6	7.5	735	3	US-09-978-681A-74	Sequence 74, Appl
600	6	7.5	623	4	US-10-437-963-201896	Sequence 201896, A	673	6	7.5	735	3	US-09-978-194A-74	Sequence 74, Appl
601	6	7.5	624	4	US-10-425-114-71490	Sequence 71490, A	674	6	7.5	735	3	US-09-999-829A-74	Sequence 74, Appl
602	6	7.5	624	4	US-10-437-963-138441	Sequence 138441, A	675	6	7.5	735	3	US-09-978-544A-74	Sequence 74, Appl
603	6	7.5	624	4	US-10-425-115-226416	Sequence 226416, A	676	6	7.5	735	3	US-09-978-665A-74	Sequence 74, Appl
604	6	7.5	633	4	US-10-425-114-43725	Sequence 43725, A	677	6	7.5	735	3	US-09-978-802A-74	Sequence 74, Appl
605	6	7.5	638	4	US-10-437-963-189105	Sequence 189105, A	678	6	7.5	735	3	US-09-978-665A-74	Sequence 74, Appl
606	6	7.5	639	4	US-10-437-963-189095	Sequence 189095, A	679	6	7.5	735	3	US-09-999-831A-74	Sequence 74, Appl
607	6	7.5	643	6	US-11-097-143-10962	Sequence 10962, A	680	6	7.5	735	4	US-09-978-824-74	Sequence 74, Appl
608	6	7.5	645	5	US-10-975-045-14	Sequence 14, Appl	681	6	7.5	735	4	US-10-052-586-88	Sequence 88, Appl
609	6	7.5	650	4	US-10-282-122A-48741	Sequence 48741, A	682	6	7.5	735	4	US-10-174-590-88	Sequence 88, Appl
610	6	7.5	651	4	US-10-058-513-3	Sequence 3, Appl	683	6	7.5	735	4	US-10-175-737-88	Sequence 88, Appl
611	6	7.5	652	3	US-09-759-143-818	Sequence 818, App	684	6	7.5	735	4	US-10-174-581-88	Sequence 88, Appl

831	6	7.5	735	4	US-10-196-745-88	Sequence 88, Appl	904	6	7.5	735	4	US-10-187-887-88	Sequence 88, Appl
832	6	7.5	735	4	US-10-196-762-88	Sequence 88, Appl	905	6	7.5	735	4	US-10-194-461-88	Sequence 88, Appl
833	6	7.5	735	4	US-10-197-695-88	Sequence 88, Appl	906	6	7.5	735	4	US-10-195-892-88	Sequence 88, Appl
834	6	7.5	735	4	US-10-195-894-88	Sequence 88, Appl	907	6	7.5	735	4	US-10-196-751-88	Sequence 88, Appl
835	6	7.5	735	4	US-10-176-484-88	Sequence 88, Appl	908	6	7.5	735	4	US-10-197-694-88	Sequence 88, Appl
836	6	7.5	735	4	US-10-176-753-88	Sequence 88, Appl	909	6	7.5	735	4	US-10-197-697-88	Sequence 88, Appl
837	6	7.5	735	4	US-10-176-917-88	Sequence 88, Appl	910	6	7.5	735	4	US-10-197-707-88	Sequence 88, Appl
838	6	7.5	735	4	US-10-176-982-88	Sequence 88, Appl	911	6	7.5	735	4	US-10-199-303-88	Sequence 88, Appl
839	6	7.5	735	4	US-10-179-506-88	Sequence 88, Appl	912	6	7.5	735	4	US-10-199-318-88	Sequence 88, Appl
840	6	7.5	735	4	US-10-179-513-88	Sequence 88, Appl	913	6	7.5	735	4	US-10-199-458-88	Sequence 88, Appl
841	6	7.5	735	4	US-10-179-514-88	Sequence 88, Appl	914	6	7.5	735	4	US-10-199-462-88	Sequence 88, Appl
842	6	7.5	735	4	US-10-179-522-88	Sequence 88, Appl	915	6	7.5	735	4	US-10-201-324-88	Sequence 88, Appl
843	6	7.5	735	4	US-10-180-556-88	Sequence 88, Appl	916	6	7.5	735	4	US-10-201-328-88	Sequence 88, Appl
844	6	7.5	735	4	US-10-180-560-88	Sequence 88, Appl	917	6	7.5	735	4	US-10-201-527-88	Sequence 88, Appl
845	6	7.5	735	4	US-10-183-015-88	Sequence 88, Appl	918	6	7.5	735	4	US-10-201-528-88	Sequence 88, Appl
846	6	7.5	735	4	US-10-184-615-88	Sequence 88, Appl	919	6	7.5	735	4	US-10-201-529-88	Sequence 88, Appl
847	6	7.5	735	4	US-10-184-620-88	Sequence 88, Appl	920	6	7.5	735	4	US-10-201-530-88	Sequence 88, Appl
848	6	7.5	735	4	US-10-184-643-88	Sequence 88, Appl	921	6	7.5	735	4	US-10-202-408-88	Sequence 88, Appl
849	6	7.5	735	4	US-10-184-656-88	Sequence 88, Appl	922	6	7.5	735	4	US-10-202-409-88	Sequence 88, Appl
850	6	7.5	735	4	US-10-192-010-88	Sequence 88, Appl	923	6	7.5	735	4	US-10-202-411-88	Sequence 88, Appl
851	6	7.5	735	4	US-10-205-908-88	Sequence 88, Appl	924	6	7.5	735	4	US-10-202-472-88	Sequence 88, Appl
852	6	7.5	735	4	US-10-017-081A-74	Sequence 74, Appl	925	6	7.5	735	4	US-10-205-502-88	Sequence 88, Appl
853	6	7.5	735	4	US-10-184-619-88	Sequence 88, Appl	926	6	7.5	735	4	US-10-205-507-88	Sequence 88, Appl
854	6	7.5	735	4	US-10-187-599-88	Sequence 88, Appl	927	6	7.5	735	4	US-10-205-511-88	Sequence 88, Appl
855	6	7.5	735	4	US-10-187-750-88	Sequence 88, Appl	928	6	7.5	735	4	US-10-205-902-88	Sequence 88, Appl
856	6	7.5	735	4	US-10-188-780-88	Sequence 88, Appl	929	6	7.5	735	4	US-10-205-907-88	Sequence 88, Appl
857	6	7.5	735	4	US-10-192-015-88	Sequence 88, Appl	930	6	7.5	735	4	US-10-167-749-74	Sequence 74, Appl
858	6	7.5	735	4	US-10-194-394-88	Sequence 88, Appl	931	6	7.5	735	4	US-10-176-484-88	Sequence 88, Appl
859	6	7.5	735	4	US-10-194-425-88	Sequence 88, Appl	932	6	7.5	735	4	US-10-194-456-88	Sequence 88, Appl
860	6	7.5	735	4	US-10-194-485-88	Sequence 88, Appl	933	6	7.5	735	4	US-10-196-758-88	Sequence 88, Appl
861	6	7.5	735	4	US-10-195-885-88	Sequence 88, Appl	934	6	7.5	735	4	US-10-198-770-88	Sequence 88, Appl
862	6	7.5	735	4	US-10-195-899-88	Sequence 88, Appl	935	6	7.5	735	4	US-10-199-308-88	Sequence 88, Appl
863	6	7.5	735	4	US-10-196-748-88	Sequence 88, Appl	936	6	7.5	735	4	US-10-200-617-88	Sequence 88, Appl
864	6	7.5	735	4	US-10-196-750-88	Sequence 88, Appl	937	6	7.5	735	4	US-10-205-893-88	Sequence 88, Appl
865	6	7.5	735	4	US-10-197-699-88	Sequence 88, Appl	938	6	7.5	735	4	US-10-205-897-88	Sequence 88, Appl
866	6	7.5	735	4	US-10-197-700-88	Sequence 88, Appl	939	6	7.5	735	4	US-10-195-896-88	Sequence 88, Appl
867	6	7.5	735	4	US-10-197-705-88	Sequence 88, Appl	940	6	7.5	735	4	US-10-180-550-88	Sequence 88, Appl
868	6	7.5	735	4	US-10-197-708-88	Sequence 88, Appl	941	6	7.5	735	4	US-10-183-014-88	Sequence 88, Appl
869	6	7.5	735	4	US-10-198-764-88	Sequence 88, Appl	942	6	7.5	735	4	US-10-187-738-88	Sequence 88, Appl
870	6	7.5	735	4	US-10-198-765-88	Sequence 88, Appl	943	6	7.5	735	4	US-10-187-740-88	Sequence 88, Appl
871	6	7.5	735	4	US-10-198-768-88	Sequence 88, Appl	944	6	7.5	735	4	US-10-187-883-88	Sequence 88, Appl
872	6	7.5	735	4	US-10-198-769-88	Sequence 88, Appl	945	6	7.5	735	4	US-10-194-363-88	Sequence 88, Appl
873	6	7.5	735	4	US-10-199-305-88	Sequence 88, Appl	946	6	7.5	735	4	US-10-194-460-88	Sequence 88, Appl
874	6	7.5	735	4	US-10-199-306-88	Sequence 88, Appl	947	6	7.5	735	4	US-10-194-463-88	Sequence 88, Appl
875	6	7.5	735	4	US-10-199-310-88	Sequence 88, Appl	948	6	7.5	735	4	US-10-194-484-88	Sequence 88, Appl
876	6	7.5	735	4	US-10-199-311-88	Sequence 88, Appl	949	6	7.5	735	4	US-10-195-884-88	Sequence 88, Appl
877	6	7.5	735	4	US-10-199-314-88	Sequence 88, Appl	950	6	7.5	735	4	US-10-196-744-88	Sequence 88, Appl
878	6	7.5	735	4	US-10-199-317-88	Sequence 88, Appl	951	6	7.5	735	4	US-10-196-755-88	Sequence 88, Appl
879	6	7.5	735	4	US-10-199-665-88	Sequence 88, Appl	952	6	7.5	735	4	US-10-197-704-88	Sequence 88, Appl
880	6	7.5	735	4	US-10-199-666-88	Sequence 88, Appl	953	6	7.5	735	4	US-10-197-710-88	Sequence 88, Appl
881	6	7.5	735	4	US-10-199-669-88	Sequence 88, Appl	954	6	7.5	735	4	US-10-198-758-88	Sequence 88, Appl
882	6	7.5	735	4	US-10-201-534-88	Sequence 88, Appl	955	6	7.5	735	4	US-10-198-766-88	Sequence 88, Appl
883	6	7.5	735	4	US-10-201-770-88	Sequence 88, Appl	956	6	7.5	735	4	US-10-199-304-88	Sequence 88, Appl
884	6	7.5	735	4	US-10-201-855-88	Sequence 88, Appl	957	6	7.5	735	4	US-10-199-309-88	Sequence 88, Appl
885	6	7.5	735	4	US-10-201-856-88	Sequence 88, Appl	958	6	7.5	735	4	US-10-199-313-88	Sequence 88, Appl
886	6	7.5	735	4	US-10-202-469-88	Sequence 88, Appl	959	6	7.5	735	4	US-10-199-456-88	Sequence 88, Appl
887	6	7.5	735	4	US-10-202-470-88	Sequence 88, Appl	960	6	7.5	735	4	US-10-201-323-88	Sequence 88, Appl
888	6	7.5	735	4	US-10-202-476-88	Sequence 88, Appl	961	6	7.5	735	4	US-10-202-412-88	Sequence 88, Appl
889	6	7.5	735	4	US-10-202-934-88	Sequence 88, Appl	962	6	7.5	735	4	US-10-206-919-88	Sequence 88, Appl
890	6	7.5	735	4	US-10-202-935-88	Sequence 88, Appl	963	6	7.5	735	4	US-10-206-922-88	Sequence 88, Appl
891	6	7.5	735	4	US-10-202-936-88	Sequence 88, Appl	964	6	7.5	735	4	US-10-206-924-88	Sequence 88, Appl
892	6	7.5	735	4	US-10-202-939-88	Sequence 88, Appl	965	6	7.5	735	4	US-10-206-928-88	Sequence 88, Appl
893	6	7.5	735	4	US-10-205-504-88	Sequence 88, Appl	966	6	7.5	735	4	US-10-207-914-88	Sequence 88, Appl
894	6	7.5	735	4	US-10-205-509-88	Sequence 88, Appl	967	6	7.5	735	4	US-10-207-921-88	Sequence 88, Appl
895	6	7.5	735	4	US-10-205-895-88	Sequence 88, Appl	968	6	7.5	735	4	US-10-207-922-88	Sequence 88, Appl
896	6	7.5	735	4	US-10-205-899-88	Sequence 88, Appl	969	6	7.5	735	4	US-10-208-027-88	Sequence 88, Appl
897	6	7.5	735	4	US-10-205-900-88	Sequence 88, Appl	970	6	7.5	735	4	US-10-196-757-88	Sequence 88, Appl
898	6	7.5	735	4	US-10-205-908-88	Sequence 88, Appl	971	6	7.5	735	4	US-10-196-754-88	Sequence 88, Appl
899	6	7.5	735	4	US-10-195-890-88	Sequence 88, Appl	972	6	7.5	735	4	US-10-013-921A-74	Sequence 74, Appl
900	6	7.5	735	4	US-10-183-002-88	Sequence 88, Appl	973	6	7.5	735	4	US-10-174-571-88	Sequence 88, Appl
901	6	7.5	735	4	US-10-184-621-88	Sequence 88, Appl	974	6	7.5	735	4	US-10-176-746-88	Sequence 88, Appl
902	6	7.5	735	4	US-10-184-638-88	Sequence 88, Appl	975	6	7.5	735	4	US-10-176-923-88	Sequence 88, Appl
903	6	7.5	735	4	US-10-187-752-88	Sequence 88, Appl	976	6	7.5	735	4	US-10-183-011-88	Sequence 88, Appl

977 6 7.5 735 4 US-10-184-633-88 Sequence 88, Appl
978 6 7.5 735 4 US-10-184-633-88 Sequence 88, Appl
979 6 7.5 735 4 US-10-187-742-88 Sequence 88, Appl
980 6 7.5 735 4 US-10-187-748-88 Sequence 88, Appl
981 6 7.5 735 4 US-10-188-765-88 Sequence 88, Appl
982 6 7.5 735 4 US-10-188-771-88 Sequence 88, Appl
983 6 7.5 735 4 US-10-192-006-88 Sequence 88, Appl
984 6 7.5 735 4 US-10-192-008-88 Sequence 88, Appl
985 6 7.5 735 4 US-10-192-009-88 Sequence 88, Appl
986 6 7.5 735 4 US-10-192-012-88 Sequence 88, Appl
987 6 7.5 735 4 US-10-192-014-88 Sequence 88, Appl
988 6 7.5 735 4 US-10-192-016-88 Sequence 88, Appl
989 6 7.5 735 4 US-10-194-362-88 Sequence 88, Appl
990 6 7.5 735 4 US-10-194-364-88 Sequence 88, Appl
991 6 7.5 735 4 US-10-194-395-88 Sequence 88, Appl
992 6 7.5 735 4 US-10-194-424-88 Sequence 88, Appl
993 6 7.5 735 4 US-10-194-458-88 Sequence 88, Appl
994 6 7.5 735 4 US-10-194-459-88 Sequence 88, Appl
995 6 7.5 735 4 US-10-194-488-88 Sequence 88, Appl
996 6 7.5 735 4 US-10-195-886-88 Sequence 88, Appl
997 6 7.5 735 4 US-10-195-891-88 Sequence 88, Appl
998 6 7.5 735 4 US-10-196-746-88 Sequence 88, Appl
999 6 7.5 735 4 US-10-196-752-88 Sequence 88, Appl
1000 6 7.5 735 4 US-10-196-753-88 Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-08-592-711-6
; Sequence 6, Application US/08592711
; Publication No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992

; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-592-711-6
Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQBPQRETLKAIHYALNCCGLAGGVQFISDICKPKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTQBPQRETLKAIHYALNCCGLAGGVQFISDICKPKDV 171
QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191
RESULT 2
US-09-183-055-6
; Sequence 6, Application US/09183055
; Publication No. US20020076407A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,055
; FILING DATE: 30-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992

```

; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 36119-125US8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6564
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-183-055-6

; Query Match 100.0%; Score 80; DB 3; Length 227;
; Best Local Similarity 100.0%; Pred. No. 6.5e-75;
; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 3
US-09-350-202-6
; Sequence 6, Application US/09350202
; Publication No. US20030099643A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993

```

```

; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy B.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-350-202-6

; Query Match 100.0%; Score 80; DB 3; Length 227;
; Best Local Similarity 100.0%; Pred. No. 6.5e-75;
; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGVQFISDIPKKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 4
US-10-390-330-6
; Sequence 5, Application US/10390330
; Publication No. US20040001829A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation
; TITLE OF INVENTION: Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/390,330
; FILING DATE: March 17, 2003
; CLASSIFICATION:

```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,816A
; FILING DATE: May 4, 1995
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-390-330-6

Query Match          100.0%; Score 80; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 5
US-10-473-127-1723
; Sequence 1723, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match          100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 6
US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match          100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 7
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
```

```
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1723

Query Match          100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 6
US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match          100.0%; Score 80; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNNKLTKDPEQRETLKAHYALNCCGLAGGVQEFISDIPCKDV 171

QY 61 LETFTVKSCPDAlKEVFDNK 80
Db 172 LETFTVKSCPDAlKEVFDNK 191

RESULT 7
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
```

TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS: ADDRESSER: Human Genome Sciences, Inc.

STREET: 9410 Key West Ave

CITY: Rockville

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/156,136

FILING DATE: 29-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA: APPLICATION NUMBER: US/09/010,146

FILING DATE: <Unknown>

APPLICATION NUMBER: WO US98/00959

FILING DATE: 21-JAN-1998

ATTORNEY/AGENT INFORMATION: NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF354PCT

TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 228 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-10-156-136-39

Query Match 100.0%; Score 80; DB 4; Length 228;

Best Local Similarity 100.0%; Pred. No. 6.5e-75;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60

Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 172

QY 61 LETFTVKSCPDAIKEVFNK 80

Db 173 LETFTVKSCPDAIKEVFNK 192

RESULT 8

US-10-331-496A-41

Sequence 41, Application US/10331496A

Publication No. US2003028305A1

GENERAL INFORMATION: APPLICANT: FRANTZ, GRETCHEN

PRIOR APPLICATION NUMBER: US 60/345,444

PRIOR FILING DATE: 2002-01-02

PRIOR APPLICATION NUMBER: US 60/351,885

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 60/360,066

PRIOR FILING DATE: 2002-02-25

PRIOR APPLICATION NUMBER: US 60/362,004

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/366,869

PRIOR FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: US 60/366,284

PRIOR FILING DATE: 2002-03-21

PRIOR APPLICATION NUMBER: US 60/368,679

PRIOR FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: US 60/404,809

PRIOR FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: US 60/405,645

PRIOR FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 95

SEQ ID NO 41

LENGTH: 228

TYPE: PRT

ORGANISM: Homo sapien

US-10-331-496A-41

Query Match 100.0%; Score 80; DB 4; Length 228;

Best Local Similarity 100.0%; Pred. No. 6.5e-75;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60

Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 172

QY 61 LETFTVKSCPDAIKEVFNK 80

Db 173 LETFTVKSCPDAIKEVFNK 192

RESULT 9

US-10-619-323-1

Sequence 1, Application US/10619323

Publication No. US20040136985A1

GENERAL INFORMATION: APPLICANT: Jennings, Lisa K.

APPLICANT: Longhurst, Celia M.

APPLICANT: Cook, George A.

APPLICANT: Bao, Jianxiong

APPLICANT: Zhang, Chunxiang

APPLICANT: White, Melanie M.

APPLICANT: Crossno, Jr., Joseph T.

APPLICANT: Lu, Yi

TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS

FILE REFERENCE: 20609/241

CURRENT APPLICATION NUMBER: US/10/619,323

CURRENT FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: 60/395,864

PRIOR FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 228

TYPE: PRT

ORGANISM: Homosapien

US-10-619-323-1

Query Match 100.0%; Score 80; DB 4; Length 228;

Best Local Similarity 100.0%; Pred. No. 6.5e-75;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60

Db 113 HKDEVIKEVQEFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 172

QY 61 LETFTVKSCPDAIKEVFNK 80

Db 173 LETFTVKSCPDAIKEVFNK 192

RESULT 9

US-10-619-323-1

Sequence 1, Application US/10619323

Publication No. US20040136985A1

GENERAL INFORMATION: APPLICANT: Jennings, Lisa K.

APPLICANT: Longhurst, Celia M.

APPLICANT: Cook, George A.

APPLICANT: Bao, Jianxiong

APPLICANT: Zhang, Chunxiang

APPLICANT: White, Melanie M.

APPLICANT: Crossno, Jr., Joseph T.

APPLICANT: Lu, Yi

TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS

FILE REFERENCE: 20609/241

CURRENT APPLICATION NUMBER: US/10/619,323

CURRENT FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: 60/395,864

PRIOR FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 228

TYPE: PRT

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FILE REFERENCE: P5014R1-PCT

CURRENT APPLICATION NUMBER: US/10/331,496A

CURRENT FILING DATE: 2002-12-30

US-10-331-496A-41

Sequence 41, Application US/10331496A

Publication No. US2003028305A1

GENERAL INFORMATION: APPLICANT: FRANTZ, GRETCHEN

APPLICANT: HILLAN, KENNETH J.

APPLICANT: PHILLIPS, HEIDI S.

APPLICANT: POLAKIS, PAUL

APPLICANT: SMITH, VICTORIA

APPLICANT: SPENCER, SUSAN D.

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WU, THOMAS D.

APPLICANT: ZHANG, ZEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FILE REFERENCE: P5014R1-PCT

CURRENT APPLICATION NUMBER: US/10/331,496A

CURRENT FILING DATE: 2002-12-30

US-10-331-496A-41

Sequence 41, Application US/10331496A

Publication No. US2003028305A1

GENERAL INFORMATION: APPLICANT: FRANTZ, GRETCHEN

APPLICANT: HILLAN, KENNETH J.

APPLICANT: PHILLIPS, HEIDI S.

APPLICANT: POLAKIS, PAUL

APPLICANT: SMITH, VICTORIA

APPLICANT: SPENCER, SUSAN D.

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WU, THOMAS D.

APPLICANT: ZHANG, ZEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FILE REFERENCE: P5014R1-PCT

CURRENT APPLICATION NUMBER: US/10/331,496A

CURRENT FILING DATE: 2002-12-30

US-10-331-496A-41

Sequence 41, Application US/10331496A

Publication No. US2003028305A1

GENERAL INFORMATION: APPLICANT: FRANTZ, GRETCHEN

APPLICANT: HILLAN, KENNETH J.

APPLICANT: PHILLIPS, HEIDI S.

APPLICANT: POLAKIS, PAUL

```
Qy 61 LETFTVKSCPDAlKEVFDNK 80
    |||||
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 10
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97

Query Match 100.0%; Score 80; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 60
    |||||
Db 113 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80
    |||||
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 11
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match 100.0%; Score 80; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 60
    |||||
Db 113 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80
    |||||
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 12
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715

Query Match 100.0%; Score 80; DB 5; Length 238;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 60
    |||||
Db 113 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80
    |||||
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 13
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
Qy 61 LETFTVKSCPDAlKEVFDNK 80
    |||||
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 12
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715

Query Match 100.0%; Score 80; DB 5; Length 238;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 60
    |||||
Db 113 HKDEVKEVQFYKDTYNNKLTQDEPQRETLLKAIHYALNCCGLAGGVQFISDlCPKKDV 172

Qy 61 LETFTVKSCPDAlKEVFDNK 80
    |||||
Db 173 LETFTVKSCPDAlKEVFDNK 192

RESULT 13
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 1716
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1716

Query Match      100.0%; Score 80; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 60
Db 113 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 172

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192
```

```
RESULT 14
US-10-473-127-1718
; Sequence 1718, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1718
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1718
```

```
Query Match      100.0%; Score 80; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 60
Db 113 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 172

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192
```

```
RESULT 15
US-10-473-127-1719
; Sequence 1719, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
```

```
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1719
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1719

Query Match      100.0%; Score 80; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 60
Db 113 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGGVEQFISDIPKDV 172

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 173 LETFTVKSCPDAIKEVFDNK 192

Search completed: January 20, 2006, 17:47:42
Job time : 99.3846 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:42:32 ; Search time 8.46154 Seconds
(without alignments)
95.811 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192

Perfect score: 80

Sequence: 1 HXDEVIKEVQEPYKDTYNKL.....LEFTTVKSCPDIAKEVFNK 80

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 10133881 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA_New.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	228	6	US-10-821-234-1266
2	6	7.5	20	7	US-11-022-562-157
3	6	7.5	20	7	US-11-022-562-158
4	6	7.5	31	7	US-11-145-035-45
5	6	7.5	122	6	US-10-467-657-606
6	6	7.5	259	6	US-10-467-657-2734
7	6	7.5	274	6	US-10-883-512-108
8	6	7.5	303	5	US-09-978-360A-763
9	6	7.5	316	6	US-10-510-386-244
10	6	7.5	405	6	US-10-873-528-62
11	6	7.5	408	6	US-10-467-657-8004
12	6	7.5	409	6	US-10-978-927-1
13	6	7.5	521	7	US-11-109-156-34
14	6	7.5	528	6	US-10-978-927-6
15	6	7.5	529	6	US-10-821-234-1520
16	6	7.5	529	6	US-10-978-927-9
17	6	7.5	529	6	US-10-978-927-13
18	6	7.5	549	6	US-10-995-561-909
19	6	7.5	549	7	US-11-194-246-431
20	6	7.5	572	7	US-11-052-554A-129
21	6	7.5	645	6	US-10-821-234-1409
22	6	7.5	745	6	US-10-995-561-659
23	6	7.5	745	7	US-11-109-156-14
24	6	7.5	879	7	US-11-022-562-340
25	6	7.5	909	7	US-11-186-284-2
					Sequence 1266, Ap
					Sequence 157, App
					Sequence 158, App
					Sequence 45, Appl
					Sequence 606, App
					Sequence 2734, Ap
					Sequence 108, App
					Sequence 763, App
					Sequence 244, App
					Sequence 62, Appl
					Sequence 8004, Ap
					Sequence 1, Appli
					Sequence 34, Appl
					Sequence 6, Appli
					Sequence 1520, Ap
					Sequence 9, Appli
					Sequence 13, Appl
					Sequence 909, App
					Sequence 431, App
					Sequence 129, App
					Sequence 1409, Ap
					Sequence 659, App
					Sequence 14, Appl
					Sequence 340, App
					Sequence 2, Appli

6	7.5	913	6	US-10-821-234-1040	Sequence 1040, Ap
6	7.5	1012	6	US-10-995-561-908	Sequence 908, App
6	7.5	1213	7	US-11-074-176-256	Sequence 256, App
6	7.5	1244	7	US-11-052-554A-130	Sequence 130, App
6	7.5	1381	7	US-11-052-554A-138	Sequence 138, App
6	7.5	4384	6	US-10-821-234-1120	Sequence 1120, Ap
5	6.2	10	6	US-10-859-643-185	Sequence 185, App
5	6.2	10	7	US-11-097-864-185	Sequence 185, App
5	6.2	10	7	US-11-097-912-185	Sequence 185, App
5	6.2	19	6	US-10-880-238-119	Sequence 119, App
5	6.2	20	6	US-10-485-788A-630	Sequence 630, App
5	6.2	20	7	US-11-133-465A-6	Sequence 6, Appli
5	6.2	36	5	US-09-978-360A-549	Sequence 549, App
5	6.2	37	6	US-10-957-351-6	Sequence 6, Appli
5	6.2	65	5	US-09-978-360A-764	Sequence 764, App
5	6.2	66	6	US-10-467-657-3594	Sequence 3594, Ap
5	6.2	66	6	US-10-467-657-6436	Sequence 6436, Ap
5	6.2	66	6	US-10-467-657-8428	Sequence 8428, Ap
5	6.2	91	7	US-11-046-786-1	Sequence 1, Appli
5	6.2	95	6	US-10-485-788A-788	Sequence 788, App
5	6.2	95	7	US-11-053-076-170	Sequence 170, App
5	6.2	96	6	US-10-467-657-4198	Sequence 4198, Ap
5	6.2	106	7	US-11-074-176-288	Sequence 288, App
5	6.2	107	6	US-10-793-626-1586	Sequence 1586, Ap
5	6.2	111	5	US-09-978-360A-799	Sequence 799, App
5	6.2	112	5	US-09-978-360A-507	Sequence 507, App
5	6.2	121	7	US-11-074-176-86	Sequence 86, Appl
5	6.2	129	6	US-10-485-517-304	Sequence 304, App
5	6.2	129	6	US-10-485-517-365	Sequence 365, App
5	6.2	134	6	US-10-793-626-1382	Sequence 1382, Ap
5	6.2	141	6	US-10-467-657-7286	Sequence 7286, Ap
5	6.2	143	7	US-11-120-308-56	Sequence 56, Appl
5	6.2	144	6	US-11-194-246-420	Sequence 420, App
5	6.2	155	6	US-10-793-626-3088	Sequence 3088, Ap
5	6.2	156	6	US-10-793-626-1222	Sequence 1222, Ap
5	6.2	165	7	US-11-052-554A-191	Sequence 191, App
5	6.2	170	7	US-11-069-642-12	Sequence 12, Appl
5	6.2	174	6	US-10-485-517-225	Sequence 225, App
5	6.2	175	6	US-10-873-528-97	Sequence 97, Appl
5	6.2	175	7	US-11-133-465A-1	Sequence 1, Appli
5	6.2	182	6	US-10-821-234-1114	Sequence 1114, Ap
5	6.2	185	6	US-10-967-527A-10	Sequence 10, Appl
5	6.2	190	7	US-11-069-601-13	Sequence 13, Appl
5	6.2	193	7	US-11-052-554A-76	Sequence 76, Appl
5	6.2	193	7	US-11-052-554A-196	Sequence 196, App
5	6.2	196	7	US-11-065-943-51	Sequence 51, Appl
5	6.2	201	6	US-10-793-626-312	Sequence 312, App
5	6.2	201	6	US-10-467-657-3482	Sequence 3482, Ap
5	6.2	203	6	US-11-080-991-8	Sequence 8, Appli
5	6.2	204	7	US-11-022-562-222	Sequence 222, App
5	6.2	207	6	US-10-454-437-302	Sequence 302, App
5	6.2	210	6	US-09-978-360A-534	Sequence 534, App
5	6.2	211	5	US-10-965-972-1	Sequence 1, Appli
5	6.2	211	7	US-11-186-284-22	Sequence 22, Appl
5	6.2	214	7	US-11-096-051-16	Sequence 16, Appl
5	6.2	215	6	US-10-873-528-13	Sequence 13, Appl
5	6.2	226	6	US-10-878-556A-106	Sequence 106, App
5	6.2	226	7	US-11-052-554A-11	Sequence 11, Appl
5	6.2	230	6	US-10-884-730-372	Sequence 372, App
5	6.2	230	6	US-10-884-730-375	Sequence 375, App
5	6.2	233	6	US-10-884-730-377	Sequence 377, App
5	6.2	233	6	US-10-793-626-416	Sequence 416, App
5	6.2	236	7	US-11-100-183-15	Sequence 15, Appl
5	6.2	238	7	US-11-052-554A-38	Sequence 38, Appl
5	6.2	238	7	US-11-052-554A-51	Sequence 51, Appl
5	6.2	238	7	US-11-052-554A-52	Sequence 52, Appl
5	6.2	240	7	US-11-100-183-17	Sequence 17, Appl
5	6.2	241	7	US-11-100-183-19	Sequence 19, Appl
5	6.2	244	7	US-11-055-822-1148	Sequence 1148, Ap
5	6.2	247	6	US-10-453-372-1200	Sequence 1200, Ap
5	6.2	249	6	US-10-485-517-157	Sequence 157, App
5	6.2	256	6	US-10-510-386-112	Sequence 112, App

99	5	6.2	257	7	US-11-135-855-42	Sequence 42, Appl	172	5	6.2	397	6	US-10-878-556A-189	Sequence 189, App
100	5	6.2	259	6	US-10-793-626-2958	Sequence 2958, Ap	173	5	6.2	397	6	US-10-995-561-928	Sequence 928, App
101	5	6.2	259	7	US-11-118-855-1	Sequence 1, Appl1	174	5	6.2	397	6	US-10-995-561-929	Sequence 53, Appl
102	5	6.2	260	7	US-11-055-822-436	Sequence 436, App	175	5	6.2	399	7	US-11-065-943-53	Sequence 53, Appl1
103	5	6.2	261	6	US-10-467-657-5896	Sequence 5896, Ap	176	5	6.2	400	6	US-10-453-372-140	Sequence 140, App
104	5	6.2	262	6	US-10-453-372-1192	Sequence 1192, Ap	177	5	6.2	400	6	US-10-453-372-152	Sequence 152, App
105	5	6.2	262	6	US-10-453-372-1196	Sequence 1196, Ap	178	5	6.2	401	6	US-10-821-234-881	Sequence 881, App
106	5	6.2	263	6	US-10-467-657-6188	Sequence 6188, Ap	179	5	6.2	401	6	US-10-517-939-246	Sequence 246, App
107	5	6.2	266	6	US-10-467-657-5258	Sequence 5258, Ap	180	5	6.2	405	6	US-10-821-234-1357	Sequence 1357, Ap
108	5	6.2	266	6	US-11-055-822-1138	Sequence 1138, Ap	181	5	6.2	410	6	US-10-793-626-3258	Sequence 3258, Ap
109	5	6.2	268	6	US-10-821-234-866	Sequence 866, App	182	5	6.2	410	7	US-11-159-428-10	Sequence 10, Appl
110	5	6.2	269	6	US-10-453-372-1194	Sequence 1194, Ap	183	5	6.2	415	7	US-11-055-822-816	Sequence 816, App
111	5	6.2	271	7	US-11-052-554A-225	Sequence 225, App	184	5	6.2	416	6	US-10-641-678-73	Sequence 73, Appl
112	5	6.2	272	6	US-10-485-517-279	Sequence 279, App	185	5	6.2	420	6	US-10-131-826A-260	Sequence 260, App
113	5	6.2	273	6	US-10-793-626-84	Sequence 84, Appl	186	5	6.2	426	6	US-10-467-962B-85	Sequence 85, Appl
114	5	6.2	276	6	US-10-821-234-1501	Sequence 1501, Ap	187	5	6.2	426	6	US-10-525-710-28	Sequence 28, Appl
115	5	6.2	279	6	US-10-793-626-2998	Sequence 2998, Ap	188	5	6.2	430	7	US-11-055-822-814	Sequence 814, App
116	5	6.2	280	6	US-10-873-528-49	Sequence 49, Appl	189	5	6.2	430	6	US-10-949-720-410	Sequence 410, App
117	5	6.2	287	6	US-10-467-657-5866	Sequence 5866, Ap	190	5	6.2	433	7	US-11-070-080-12	Sequence 12, Appl
118	5	6.2	288	6	US-10-508-263-72	Sequence 72, Appl	191	5	6.2	437	7	US-11-194-246-124	Sequence 324, App
119	5	6.2	294	6	US-10-467-657-4688	Sequence 4688, Ap	192	5	6.2	441	7	US-11-196-475-120	Sequence 120, App
120	5	6.2	295	6	US-10-793-626-2998	Sequence 2998, Ap	193	5	6.2	442	7	US-11-055-822-814	Sequence 814, App
121	5	6.2	296	7	US-11-196-475-22	Sequence 22, Appl	194	5	6.2	444	6	US-10-467-657-2414	Sequence 2414, Ap
122	5	6.2	296	7	US-11-037-243-85	Sequence 85, Appl	195	5	6.2	445	6	US-10-454-437-312	Sequence 312, App
123	5	6.2	296	7	US-11-156-084-285	Sequence 285, App	196	5	6.2	445	7	US-11-082-389-376	Sequence 376, App
124	5	6.2	297	6	US-10-878-556A-119	Sequence 119, App	197	5	6.2	447	6	US-10-467-657-4034	Sequence 4034, Ap
125	5	6.2	301	6	US-10-793-626-3176	Sequence 3176, Ap	198	5	6.2	447	6	US-10-467-657-7050	Sequence 7050, Ap
126	5	6.2	301	6	US-10-979-871-2	Sequence 2, Appl1	199	5	6.2	450	7	US-11-087-100-20	Sequence 20, Appl
127	5	6.2	302	7	US-11-024-959-262	Sequence 262, App	200	5	6.2	450	7	US-11-087-100-28	Sequence 28, Appl
128	5	6.2	305	7	US-11-137-465-56	Sequence 56, Appl	201	5	6.2	450	7	US-11-087-084-20	Sequence 20, Appl
129	5	6.2	309	7	US-11-156-084-200	Sequence 200, App	202	5	6.2	450	7	US-11-087-084-28	Sequence 28, Appl
130	5	6.2	311	6	US-10-055-877-181	Sequence 181, App	203	5	6.2	450	7	US-11-087-085-20	Sequence 20, Appl
131	5	6.2	311	6	US-10-055-877-182	Sequence 182, App	204	5	6.2	450	7	US-11-087-085-28	Sequence 28, Appl
132	5	6.2	312	6	US-10-467-657-5318	Sequence 5318, Ap	205	5	6.2	454	7	US-11-196-475-116	Sequence 116, App
133	5	6.2	313	6	US-10-467-657-3982	Sequence 3982, Ap	206	5	6.2	458	7	US-11-124-368A-316	Sequence 316, App
134	5	6.2	313	6	US-10-467-657-8140	Sequence 8140, Ap	207	5	6.2	461	6	US-10-878-556A-162	Sequence 162, App
135	5	6.2	313	7	US-11-052-554A-247	Sequence 247, App	208	5	6.2	468	7	US-11-122-144-8	Sequence 8, Appl1
136	5	6.2	320	6	US-10-467-657-424	Sequence 424, App	209	5	6.2	469	6	US-10-793-626-276	Sequence 276, App
137	5	6.2	320	6	US-11-052-554A-239	Sequence 239, App	210	5	6.2	469	6	US-10-821-234-1151	Sequence 1151, Ap
138	5	6.2	321	6	US-11-052-554A-239	Sequence 133, App	211	5	6.2	474	6	US-10-467-657-5978	Sequence 5978, Ap
139	5	6.2	323	6	US-10-508-263-52	Sequence 52, Appl	212	5	6.2	474	6	US-10-467-657-7518	Sequence 7518, Ap
140	5	6.2	323	7	US-11-156-084-294	Sequence 294, App	213	5	6.2	474	7	US-11-076-733-11	Sequence 11, Appl
141	5	6.2	323	6	US-11-156-084-336	Sequence 336, App	214	5	6.2	476	7	US-11-074-176-122	Sequence 122, App
142	5	6.2	331	6	US-10-821-234-1650	Sequence 1650, Ap	215	5	6.2	476	7	US-11-055-822-942	Sequence 942, App
143	5	6.2	331	6	US-10-949-720-405	Sequence 405, App	216	5	6.2	476	7	US-11-055-822-962	Sequence 962, App
144	5	6.2	338	6	US-10-793-626-2868	Sequence 2868, Ap	217	5	6.2	477	6	US-10-793-626-3250	Sequence 3250, Ap
145	5	6.2	338	6	US-10-821-234-1418	Sequence 1418, Ap	218	5	6.2	480	6	US-10-878-556A-198	Sequence 198, App
146	5	6.2	338	7	US-11-186-284-109	Sequence 109, App	219	5	6.2	484	7	US-11-024-959-351	Sequence 351, App
147	5	6.2	341	6	US-10-454-437-176	Sequence 176, App	220	5	6.2	486	6	US-10-467-657-950	Sequence 950, App
148	5	6.2	341	6	US-10-454-437-244	Sequence 244, App	221	5	6.2	490	7	US-11-063-343-31	Sequence 31, Appl
149	5	6.2	348	6	US-10-793-626-2866	Sequence 2866, Ap	222	5	6.2	490	7	US-11-124-368A-223	Sequence 223, App
150	5	6.2	354	6	US-10-878-556A-164	Sequence 164, App	223	5	6.2	497	6	US-10-763-712A-24	Sequence 24, Appl
151	5	6.2	356	6	US-10-055-877-184	Sequence 184, App	224	5	6.2	497	6	US-10-763-712A-91	Sequence 91, Appl
152	5	6.2	356	6	US-10-055-877-185	Sequence 185, App	225	5	6.2	502	6	US-10-131-826A-548	Sequence 548, App
153	5	6.2	357	6	US-10-517-939-100	Sequence 100, App	226	5	6.2	502	6	US-10-689-742-148	Sequence 148, App
154	5	6.2	358	6	US-10-485-517-227	Sequence 227, App	227	5	6.2	507	6	US-10-878-556A-23	Sequence 23, Appl
155	5	6.2	360	7	US-11-052-554A-376	Sequence 376, App	228	5	6.2	519	7	US-11-093-631-10	Sequence 10, Appl
156	5	6.2	360	7	US-11-019-711-67	Sequence 67, Appl	229	5	6.2	521	6	US-10-821-234-1546	Sequence 1546, Ap
157	5	6.2	374	6	US-10-467-657-3420	Sequence 3420, Ap	230	5	6.2	522	6	US-10-949-720-425	Sequence 425, App
158	5	6.2	377	7	US-11-152-892-8	Sequence 8, Appl1	231	5	6.2	523	6	US-10-641-678-45	Sequence 45, Appl
159	5	6.2	378	7	US-11-152-892-7	Sequence 7, Appl1	232	5	6.2	525	7	US-11-082-389-36	Sequence 36, Appl
160	5	6.2	380	7	US-11-196-475-118	Sequence 118, App	233	5	6.2	526	6	US-10-467-657-2186	Sequence 2186, Ap
161	5	6.2	382	5	US-09-978-360A-425	Sequence 425, App	234	5	6.2	526	6	US-10-641-678-46	Sequence 46, Appl
162	5	6.2	382	6	US-10-467-657-7540	Sequence 7540, Ap	235	5	6.2	531	6	US-10-878-556A-90	Sequence 90, Appl
163	5	6.2	383	7	US-11-147-360-2	Sequence 2, Appl1	236	5	6.2	531	7	US-10-453-372-132	Sequence 132, App
164	5	6.2	388	6	US-10-467-657-8788	Sequence 8788, Ap	237	5	6.2	531	7	US-11-124-368A-314	Sequence 314, App
165	5	6.2	390	6	US-10-453-372-130	Sequence 130, App	238	5	6.2	532	6	US-10-821-234-1071	Sequence 1071, Ap
166	5	6.2	393	6	US-10-453-372-134	Sequence 134, App	239	5	6.2	533	7	US-11-230-995-3	Sequence 3, Appl1
167	5	6.2	393	7	US-11-196-475-114	Sequence 114, App	240	5	6.2	536	6	US-10-821-231C-1	Sequence 1, Appl1
168	5	6.2	395	6	US-10-454-437-208	Sequence 208, App	241	5	6.2	536	7	US-11-124-368A-315	Sequence 315, App
169	5	6.2	395	6	US-10-454-437-210	Sequence 210, App	242	5	6.2	537	6	US-10-949-720-424	Sequence 424, App
170	5	6.2	397	6	US-10-485-517-172	Sequence 172, App	243	5	6.2	538	7	US-11-167-856-20	Sequence 20, Appl
171	5	6.2	397	6	US-10-467-657-4202	Sequence 4202, Ap	244	5	6.2	539	6	US-10-793-626-790	Sequence 790, App

245	5	6.2	541	7	US-11-118-855-26	Sequence 26, Appl	318	5	6.2	724	7	US-11-053-100-41	Sequence 41, Appl
246	5	6.2	542	7	US-11-074-176-30	Sequence 30, Appl	319	5	6.2	726	7	US-11-052-554A-127	Sequence 127, Appl
247	5	6.2	543	6	US-10-467-657-1020	Sequence 1020, Ap	320	5	6.2	746	7	US-11-052-554A-57	Sequence 57, Appl
248	5	6.2	544	7	US-11-082-389-34	Sequence 34, Appl	321	5	6.2	747	7	US-11-052-554A-148	Sequence 148, Appl
249	5	6.2	545	7	US-11-082-389-86	Sequence 86, Appl	322	5	6.2	749	7	US-11-052-554A-148	Sequence 148, Appl
250	5	6.2	547	7	US-11-082-389-86	Sequence 86, Appl	323	5	6.2	758	7	US-11-024-959-347	Sequence 347, Appl
251	5	6.2	548	6	US-10-949-720-387	Sequence 387, Appl	324	5	6.2	767	7	US-11-052-554A-154	Sequence 154, Appl
252	5	6.2	555	6	US-10-763-712A-30	Sequence 30, Appl	325	5	6.2	771	6	US-10-949-720-389	Sequence 389, Appl
253	5	6.2	556	6	US-10-995-561-766	Sequence 766, Appl	326	5	6.2	777	6	US-10-467-657-2474	Sequence 2474, Ap
254	5	6.2	556	6	US-10-995-561-767	Sequence 767, Appl	327	5	6.2	798	7	US-11-107-028-2	Sequence 2, Appl
255	5	6.2	563	7	US-11-113-224-18	Sequence 18, Appl	328	5	6.2	812	7	US-11-107-028-2	Sequence 1, Appl
256	5	6.2	564	7	US-11-133-360-11	Sequence 11, Appl	329	5	6.2	856	6	US-10-467-657-8334	Sequence 8334, Ap
257	5	6.2	564	7	US-11-133-360-11	Sequence 11, Appl	330	5	6.2	868	6	US-10-995-561-792	Sequence 792, Appl
258	5	6.2	564	7	US-11-133-360-15	Sequence 15, Appl	331	5	6.2	871	6	US-10-859-643-765	Sequence 765, Appl
259	5	6.2	564	7	US-11-133-360-17	Sequence 17, Appl	332	5	6.2	871	7	US-11-097-864-765	Sequence 765, Appl
260	5	6.2	564	7	US-11-133-346-11	Sequence 11, Appl	333	5	6.2	871	7	US-11-097-912-765	Sequence 765, Appl
261	5	6.2	564	7	US-11-133-346-13	Sequence 13, Appl	334	5	6.2	874	7	US-11-053-100-42	Sequence 42, Appl
262	5	6.2	564	7	US-11-133-346-15	Sequence 15, Appl	335	5	6.2	875	6	US-10-859-643-743	Sequence 743, Appl
263	5	6.2	564	7	US-11-133-346-17	Sequence 17, Appl	336	5	6.2	875	6	US-10-859-643-745	Sequence 745, Appl
264	5	6.2	568	6	US-10-793-626-2482	Sequence 2482, Ap	337	5	6.2	875	6	US-10-859-643-747	Sequence 747, Appl
265	5	6.2	570	6	US-10-949-720-386	Sequence 386, Ap	338	5	6.2	875	6	US-10-859-643-747	Sequence 747, Appl
266	5	6.2	570	6	US-10-949-720-412	Sequence 412, Ap	339	5	6.2	875	6	US-10-859-643-748	Sequence 748, Appl
267	5	6.2	572	6	US-10-454-437-68	Sequence 68, Appl	340	5	6.2	875	6	US-11-097-864-743	Sequence 743, Appl
268	5	6.2	574	7	US-11-053-100-40	Sequence 40, Appl	341	5	6.2	875	7	US-11-097-864-745	Sequence 745, Appl
269	5	6.2	577	7	US-11-074-176-184	Sequence 184, Appl	342	5	6.2	875	7	US-11-097-864-747	Sequence 747, Appl
270	5	6.2	578	7	US-11-037-243-100	Sequence 100, Appl	343	5	6.2	875	7	US-11-097-864-748	Sequence 748, Appl
271	5	6.2	579	6	US-10-821-234-1352	Sequence 1352, Ap	344	5	6.2	875	7	US-11-097-864-751	Sequence 751, Appl
272	5	6.2	580	6	US-10-453-372-138	Sequence 138, Ap	345	5	6.2	875	7	US-11-097-912-743	Sequence 743, Appl
273	5	6.2	580	6	US-10-453-372-144	Sequence 144, Appl	346	5	6.2	875	7	US-11-097-912-745	Sequence 745, Appl
274	5	6.2	584	6	US-10-454-437-66	Sequence 66, Appl	347	5	6.2	875	7	US-11-097-912-747	Sequence 747, Appl
275	5	6.2	585	6	US-10-821-234-875	Sequence 875, Appl	348	5	6.2	875	7	US-11-097-912-748	Sequence 748, Appl
276	5	6.2	587	6	US-10-453-372-964	Sequence 964, Appl	349	5	6.2	885	6	US-10-793-626-1660	Sequence 1660, Ap
277	5	6.2	588	7	US-11-196-475-122	Sequence 122, Appl	350	5	6.2	906	7	US-11-124-635-4	Sequence 4, Appl
278	5	6.2	591	6	US-10-453-372-952	Sequence 952, Appl	351	5	6.2	907	7	US-11-103-957-82	Sequence 82, Appl
279	5	6.2	594	6	US-10-453-372-956	Sequence 956, Appl	352	5	6.2	932	7	US-11-017-550-65	Sequence 65, Appl
280	5	6.2	596	6	US-10-467-657-3952	Sequence 3952, Ap	353	5	6.2	934	7	US-11-077-386-17	Sequence 17, Appl
281	5	6.2	596	6	US-10-453-372-964	Sequence 964, Ap	354	5	6.2	959	6	US-10-453-372-1074	Sequence 1074, Ap
282	5	6.2	604	6	US-10-467-657-2280	Sequence 2280, Ap	355	5	6.2	964	7	US-11-137-465-58	Sequence 58, Appl
283	5	6.2	612	7	US-11-186-284-136	Sequence 136, Appl	356	5	6.2	965	7	US-11-113-424-2	Sequence 2, Appl
284	5	6.2	614	7	US-11-165-576-2	Sequence 2, Appl	357	5	6.2	965	7	US-11-147-047-51	Sequence 51, Appl
285	5	6.2	618	6	US-10-821-234-1481	Sequence 1481, Ap	358	5	6.2	980	7	US-11-064-246-10	Sequence 10, Appl
286	5	6.2	620	6	US-10-131-826A-324	Sequence 324, Appl	359	5	6.2	980	6	US-10-949-720-395	Sequence 395, Appl
287	5	6.2	620	7	US-11-186-284-134	Sequence 134, Appl	360	5	6.2	990	6	US-10-821-234-1201	Sequence 1201, Ap
288	5	6.2	621	6	US-10-821-234-1376	Sequence 1376, Ap	361	5	6.2	1015	6	US-10-467-657-180	Sequence 180, Appl
289	5	6.2	622	7	US-11-021-441-35	Sequence 35, Appl	362	5	6.2	1015	6	US-10-467-657-3764	Sequence 3764, Ap
290	5	6.2	622	7	US-11-147-360-4	Sequence 4, Appl	363	5	6.2	1021	6	US-10-453-372-1076	Sequence 1076, Ap
291	5	6.2	622	7	US-11-155-288-17	Sequence 17, Appl	364	5	6.2	1025	6	US-10-453-372-1068	Sequence 1068, Ap
292	5	6.2	630	7	US-11-155-288-18	Sequence 18, Appl	365	5	6.2	1025	6	US-10-453-372-1070	Sequence 1070, Ap
293	5	6.2	633	6	US-10-453-372-1072	Sequence 1072, Ap	366	5	6.2	1063	6	US-11-120-308-186	Sequence 186, Appl
294	5	6.2	633	6	US-10-453-372-1078	Sequence 1078, Ap	367	5	6.2	1063	6	US-10-453-372-1066	Sequence 1066, Ap
295	5	6.2	636	6	US-10-763-712A-29	Sequence 29, Appl	368	5	6.2	1068	7	US-11-191-374-45	Sequence 45, Appl
296	5	6.2	636	6	US-10-763-712A-93	Sequence 93, Appl	369	5	6.2	1068	7	US-11-191-375-45	Sequence 45, Appl
297	5	6.2	642	6	US-10-453-372-962	Sequence 962, Appl	370	5	6.2	1068	7	US-11-191-375-45	Sequence 45, Appl
298	5	6.2	646	6	US-10-453-372-958	Sequence 958, Appl	371	5	6.2	1068	6	US-10-964-313-2	Sequence 2, Appl
299	5	6.2	646	6	US-10-453-372-960	Sequence 960, Appl	372	5	6.2	1124	7	US-11-195-197-9	Sequence 9, Appl
300	5	6.2	648	6	US-10-501-039-6	Sequence 6, Appl	373	5	6.2	1126	7	US-11-075-185-3	Sequence 3, Appl
301	5	6.2	648	6	US-10-793-626-568	Sequence 568, Appl	374	5	6.2	1145	6	US-10-793-626-1432	Sequence 1432, Ap
302	5	6.2	650	6	US-10-453-372-966	Sequence 966, Appl	375	5	6.2	1147	6	US-10-615-668-5	Sequence 5, Appl
303	5	6.2	664	7	US-11-080-991-40	Sequence 40, Appl	376	5	6.2	1167	7	US-11-052-554A-121	Sequence 121, Appl
304	5	6.2	667	7	US-11-156-163-4	Sequence 4, Appl	377	5	6.2	1174	7	US-11-053-100-43	Sequence 43, Appl
305	5	6.2	668	6	US-10-453-372-950	Sequence 950, Appl	378	5	6.2	1192	6	US-10-858-730-72	Sequence 72, Appl
306	5	6.2	668	6	US-10-453-372-968	Sequence 968, Appl	379	5	6.2	1206	6	US-10-858-730-73	Sequence 73, Appl
307	5	6.2	668	6	US-10-453-372-970	Sequence 970, Appl	380	5	6.2	1206	6	US-10-467-657-72	Sequence 72, Appl
308	5	6.2	675	6	US-10-467-657-4004	Sequence 4004, Ap	381	5	6.2	1206	6	US-10-467-657-3892	Sequence 3892, Ap
309	5	6.2	677	6	US-10-131-826A-230	Sequence 230, Appl	382	5	6.2	1215	6	US-10-964-313-6	Sequence 6, Appl
310	5	6.2	683	7	US-11-103-957-84	Sequence 84, Appl	383	5	6.2	1216	6	US-10-873-528-12	Sequence 12, Appl
311	5	6.2	684	6	US-10-793-626-2098	Sequence 2098, Ap	384	5	6.2	1259	6	US-10-467-657-5510	Sequence 5510, Ap
312	5	6.2	690	7	US-11-052-554A-232	Sequence 232, Appl	385	5	6.2	1308	7	US-11-113-202-16	Sequence 16, Appl
313	5	6.2	697	7	US-11-082-389-362	Sequence 362, Appl	386	5	6.2	1313	7	US-11-091-668-4	Sequence 4, Appl
314	5	6.2	703	6	US-10-467-657-7158	Sequence 7158, Ap	387	5	6.2	1323	6	US-11-019-939-312	Sequence 312, Appl
315	5	6.2	710	7	US-11-151-601-23	Sequence 23, Appl	388	5	6.2	1327	7	US-11-019-711-70	Sequence 70, Appl
316	5	6.2	712	7	US-11-037-243-69	Sequence 69, Appl	389	5	6.2	1342	7	US-11-115-639-2	Sequence 2, Appl
317	5	6.2	716	7	US-11-150-845-16	Sequence 16, Appl	390	5	6.2	1342	7	US-11-115-639-3	Sequence 3, Appl

391	5	6.2	1342	7	US-11-115-639-4	Sequence 4, Appli	464	4	5.0	8	7	US-11-045-024-3091	Sequence 3091, Ap
392	5	6.2	1342	7	US-11-115-639-5	Sequence 5, Appli	465	4	5.0	8	7	US-11-045-024-9415	Sequence 9415, Ap
393	5	6.2	1342	7	US-11-115-639-6	Sequence 6, Appli	466	4	5.0	8	7	US-11-045-024-10717	Sequence 10717, A
394	5	6.2	1390	6	US-10-951-351-1	Sequence 1, Appli	467	4	5.0	8	7	US-11-045-024-11485	Sequence 11485, A
395	5	6.2	1417	7	US-11-052-554A-8	Sequence 8, Appli	468	4	5.0	8	7	US-11-045-024-12493	Sequence 12493, A
396	5	6.2	1538	7	US-11-052-554A-146	Sequence 146, App	469	4	5.0	9	6	US-10-491-096-29	Sequence 29, Appl
397	5	6.2	1562	7	US-11-052-554A-211	Sequence 211, App	470	4	5.0	9	6	US-10-859-643-284	Sequence 284, App
398	5	6.2	1590	6	US-10-055-877-1146	Sequence 146, App	471	4	5.0	9	6	US-10-859-643-662	Sequence 662, App
399	5	6.2	1681	7	US-11-019-711-20	Sequence 20, Appl	472	4	5.0	9	7	US-11-044-051-111	Sequence 111, App
400	5	6.2	1697	7	US-11-019-711-68	Sequence 68, Appl	473	4	5.0	9	7	US-11-073-112-14	Sequence 14, Appl
401	5	6.2	1723	7	US-11-019-711-18	Sequence 18, Appl	474	4	5.0	9	7	US-11-097-864-284	Sequence 284, App
402	5	6.2	1730	7	US-11-192-967-4	Sequence 4, Appli	475	4	5.0	9	7	US-11-097-864-662	Sequence 662, App
403	5	6.2	1730	7	US-11-193-715-4	Sequence 4, Appli	476	4	5.0	9	7	US-11-097-912-284	Sequence 284, App
404	5	6.2	1766	7	US-11-075-185-10	Sequence 10, Appl	477	4	5.0	9	7	US-11-097-912-662	Sequence 662, App
405	5	6.2	1786	7	US-11-196-400-3	Sequence 3, Appli	478	4	5.0	9	7	US-11-045-024-8133	Sequence 8133, Ap
406	5	6.2	1966	7	US-11-126-313-32	Sequence 32, Appl	479	4	5.0	9	7	US-11-045-024-8136	Sequence 8136, Ap
407	5	6.2	1976	7	US-11-069-834-52	Sequence 52, Appl	480	4	5.0	9	7	US-11-033-039-785	Sequence 785, App
408	5	6.2	1976	7	US-11-069-834-54	Sequence 54, Appl	481	4	5.0	9	7	US-11-033-039-809	Sequence 809, App
409	5	6.2	1992	7	US-11-013-759-3	Sequence 3, Appli	482	4	5.0	9	7	US-11-033-039-810	Sequence 810, App
410	5	6.2	1992	7	US-11-013-759-13	Sequence 13, Appl	483	4	5.0	10	6	US-10-431-096-28	Sequence 28, Appl
411	5	6.2	2047	7	US-11-013-759-4	Sequence 4, Appli	484	4	5.0	10	6	US-10-491-096-138	Sequence 138, App
412	5	6.2	2047	7	US-11-013-759-7	Sequence 7, Appli	485	4	5.0	10	6	US-10-929-988-17	Sequence 17, Appl
413	5	6.2	2048	7	US-11-116-939-6	Sequence 6, Appli	486	4	5.0	10	6	US-10-880-238-30	Sequence 30, Appl
414	5	6.2	2053	7	US-11-013-759-9	Sequence 9, Appli	487	4	5.0	10	6	US-10-880-238-33	Sequence 33, Appl
415	5	6.2	2059	7	US-11-087-100-4	Sequence 4, Appli	488	4	5.0	10	6	US-10-859-643-76	Sequence 76, Appl
416	5	6.2	2059	7	US-11-087-084-4	Sequence 4, Appli	489	4	5.0	10	6	US-10-859-643-202	Sequence 202, App
417	5	6.2	2059	7	US-11-087-085-4	Sequence 4, Appli	490	4	5.0	10	6	US-10-859-643-205	Sequence 205, App
418	5	6.2	2097	7	US-11-075-185-8	Sequence 8, Appli	491	4	5.0	10	6	US-10-859-643-309	Sequence 309, App
419	5	6.2	2204	7	US-11-052-554A-174	Sequence 174, App	492	4	5.0	10	6	US-10-859-643-322	Sequence 322, App
420	5	6.2	2312	7	US-11-126-313-34	Sequence 34, Appl	493	4	5.0	10	7	US-11-097-864-76	Sequence 76, Appl
421	5	6.2	2333	6	US-10-453-372-170	Sequence 170, App	494	4	5.0	10	7	US-11-097-864-205	Sequence 202, App
422	5	6.2	2551	7	US-11-052-554A-368	Sequence 368, App	495	4	5.0	10	7	US-11-097-864-205	Sequence 205, App
423	5	6.2	2630	7	US-11-186-731-2	Sequence 2, Appli	496	4	5.0	10	7	US-11-097-864-309	Sequence 309, App
424	5	6.2	2647	6	US-10-821-234-1303	Sequence 1303, Ap	497	4	5.0	10	7	US-11-097-864-322	Sequence 322, App
425	5	6.2	2657	6	US-10-821-234-1262	Sequence 1262, Ap	498	4	5.0	10	7	US-11-097-912-76	Sequence 76, Appl
426	5	6.2	2662	6	US-10-453-372-114	Sequence 114, App	499	4	5.0	10	7	US-11-097-912-202	Sequence 202, App
427	5	6.2	2715	7	US-11-096-051-2	Sequence 2, Appli	500	4	5.0	10	7	US-11-097-912-305	Sequence 305, App
428	5	6.2	2715	7	US-11-113-424-51	Sequence 51, Appl	501	4	5.0	10	7	US-11-097-912-309	Sequence 309, App
429	5	6.2	2721	7	US-11-096-051-10	Sequence 10, Appl	502	4	5.0	10	7	US-11-097-912-322	Sequence 322, App
430	5	6.2	2724	6	US-10-453-372-148	Sequence 148, App	503	4	5.0	10	7	US-11-045-024-2670	Sequence 2670, Ap
431	5	6.2	2725	7	US-11-096-051-8	Sequence 8, Appli	504	4	5.0	10	7	US-11-045-024-5455	Sequence 5455, Ap
432	5	6.2	2733	6	US-10-453-372-136	Sequence 136, App	505	4	5.0	10	7	US-11-045-024-8134	Sequence 8134, Ap
433	5	6.2	2733	6	US-10-453-372-142	Sequence 142, App	506	4	5.0	10	7	US-11-045-024-10712	Sequence 10712, A
434	5	6.2	2733	6	US-10-453-372-146	Sequence 146, App	507	4	5.0	10	7	US-11-045-024-12490	Sequence 12490, A
435	5	6.2	2733	6	US-10-453-372-150	Sequence 150, App	508	4	5.0	11	6	US-10-982-891-25	Sequence 25, Appl
436	5	6.2	2733	6	US-10-453-372-154	Sequence 154, App	509	4	5.0	11	6	US-10-859-643-763	Sequence 763, App
437	5	6.2	2759	6	US-10-453-372-168	Sequence 168, App	510	4	5.0	11	7	US-11-097-864-763	Sequence 763, App
438	5	6.2	2759	6	US-10-453-372-116	Sequence 116, App	511	4	5.0	11	7	US-11-097-912-763	Sequence 763, App
439	5	6.2	2769	7	US-11-113-424-14	Sequence 14, Appl	512	4	5.0	11	7	US-11-045-024-2687	Sequence 2687, Ap
440	5	6.2	2828	7	US-11-080-991-54	Sequence 54, Appl	513	4	5.0	11	7	US-11-045-024-8280	Sequence 8280, Ap
441	5	6.2	2828	7	US-11-186-284-49	Sequence 49, Appl	514	4	5.0	11	7	US-11-045-024-14491	Sequence 14491, A
442	5	6.2	3003	6	US-10-453-372-1080	Sequence 1080, Ap	515	4	5.0	11	7	US-11-189-321-9	Sequence 9, Appli
443	5	6.2	3056	7	US-11-109-156-20	Sequence 20, Appl	516	4	5.0	11	7	US-11-116-144-226	Sequence 226, App
444	5	6.2	3073	7	US-11-143-980-50	Sequence 50, Appl	517	4	5.0	11	7	US-11-116-144-227	Sequence 227, App
445	5	6.2	3353	7	US-11-037-243-64	Sequence 64, Appl	518	4	5.0	12	6	US-10-982-891-30	Sequence 30, Appl
446	5	6.2	3361	6	US-10-453-372-1082	Sequence 1082, Ap	519	4	5.0	12	6	US-10-632-350-82	Sequence 82, Appl
447	5	6.2	3507	7	US-11-075-185-7	Sequence 7, Appli	520	4	5.0	12	6	US-10-893-584-111	Sequence 111, App
448	5	6.2	3623	6	US-10-995-561-593	Sequence 593, App	521	4	5.0	12	6	US-11-073-457-82	Sequence 82, Appl
449	5	6.2	3674	7	US-11-000-463-454	Sequence 454, App	522	4	5.0	12	7	US-11-073-460-82	Sequence 82, Appl
450	5	6.2	3689	7	US-11-075-185-4	Sequence 4, Appli	523	4	5.0	12	7	US-11-098-763-31	Sequence 31, Appl
451	5	6.2	3803	6	US-10-995-561-773	Sequence 773, App	524	4	5.0	12	7	US-11-043-693-7	Sequence 7, Appli
452	5	6.2	3960	6	US-10-995-561-771	Sequence 771, App	525	4	5.0	12	7	US-11-127-877-540	Sequence 540, App
453	5	6.2	4374	7	US-11-128-572-2	Sequence 2, Appli	526	4	5.0	12	7	US-11-033-039-483	Sequence 483, App
454	5	6.2	5335	6	US-10-995-561-777	Sequence 777, App	527	4	5.0	12	7	US-11-033-039-522	Sequence 522, App
455	5	6.2	5406	6	US-10-995-561-774	Sequence 774, App	528	4	5.0	13	6	US-10-503-575-80	Sequence 80, Appl
456	5	6.2	5415	6	US-10-995-561-779	Sequence 779, App	529	4	5.0	13	6	US-10-716-189-8	Sequence 8, Appli
457	5	6.2	5464	6	US-10-995-561-775	Sequence 775, App	530	4	5.0	13	6	US-10-511-559-882	Sequence 882, App
458	5	6.2	5712	7	US-11-143-980-47	Sequence 47, Appl	531	4	5.0	13	6	US-10-511-559-883	Sequence 883, App
459	5	6.2	7102	7	US-11-143-980-48	Sequence 48, Appl	532	4	5.0	13	6	US-10-511-559-884	Sequence 884, App
460	5	6.2	7968	7	US-11-186-731-5	Sequence 5, Appli	533	4	5.0	13	6	US-10-511-559-903	Sequence 903, App
461	5	6.2	7968	7	US-11-143-980-49	Sequence 49, Appl	534	4	5.0	13	6	US-10-511-559-904	Sequence 904, App
462	4	5.0	7	6	US-10-753-537-7	Sequence 7, Appli	535	4	5.0	13	6	US-10-511-559-905	Sequence 905, App
463	4	5.0	7	7	US-11-039-268-7	Sequence 7, Appli	536	4	5.0	13	6	US-10-511-559-906	Sequence 906, App

537	4	5.0	13	6	US-10-467-657-9104	Sequence 9104, Ap	610	4	5.0	22	7	US-11-107-029-23	Sequence 23, Appl
538	4	5.0	13	6	US-10-889-197-3	Sequence 3, Appli	611	4	5.0	22	7	US-11-107-029-27	Sequence 27, Appl
539	4	5.0	13	7	US-11-064-774A-136	Sequence 136, App	612	4	5.0	23	7	US-11-107-029-25	Sequence 25, Appl
540	4	5.0	13	7	US-11-033-039-800	Sequence 800, App	613	4	5.0	24	5	US-09-978-360A-474	Sequence 474, App
541	4	5.0	13	7	US-11-033-039-821	Sequence 821, App	614	4	5.0	24	6	US-10-957-887B-122	Sequence 122, App
542	4	5.0	13	7	US-11-041-893-77	Sequence 77, Appl	615	4	5.0	29	7	US-11-089-601-10	Sequence 10, Appl
543	4	5.0	14	7	US-11-045-024-14251	Sequence 14251, A	616	4	5.0	29	7	US-11-188-281-10	Sequence 10, Appl
544	4	5.0	14	7	US-11-033-039-1444	Sequence 1444, Ap	617	4	5.0	30	7	US-11-033-039-679	Sequence 679, App
545	4	5.0	14	7	US-11-033-039-1450	Sequence 1450, Ap	618	4	5.0	31	7	US-11-106-932-12	Sequence 12, Appl
546	4	5.0	15	7	US-11-106-932-72	Sequence 72, Appl	619	4	5.0	32	6	US-10-467-657-1306	Sequence 1306, Ap
547	4	5.0	15	7	US-11-107-029-28	Sequence 28, Appl	620	4	5.0	32	6	US-10-746-959C-7	Sequence 7, Appli
548	4	5.0	15	7	US-11-107-029-29	Sequence 29, Appl	621	4	5.0	32	7	US-11-033-039-525	Sequence 525, App
549	4	5.0	15	7	US-11-107-029-32	Sequence 32, Appl	622	4	5.0	33	7	US-11-121-301-49	Sequence 49, Appl
550	4	5.0	15	7	US-11-033-039-1443	Sequence 1443, Ap	623	4	5.0	33	7	US-11-121-301-50	Sequence 50, Appl
551	4	5.0	15	7	US-11-041-893-5	Sequence 5, Appli	624	4	5.0	33	7	US-11-121-301-74	Sequence 74, Appl
552	4	5.0	15	7	US-11-041-893-16	Sequence 16, Appl	625	4	5.0	34	6	US-10-816-768-30	Sequence 30, Appl
553	4	5.0	15	7	US-11-041-893-210	Sequence 210, App	626	4	5.0	34	6	US-10-816-768-31	Sequence 31, Appl
554	4	5.0	15	7	US-11-051-481-52	Sequence 52, Appl	627	4	5.0	34	6	US-10-816-768-33	Sequence 33, Appl
555	4	5.0	16	6	US-10-631-558-8	Sequence 8, Appli	628	4	5.0	34	7	US-11-068-783-88	Sequence 88, Appl
556	4	5.0	16	7	US-11-017-550-78	Sequence 78, Appl	629	4	5.0	34	7	US-11-121-301-14	Sequence 14, Appl
557	4	5.0	16	7	US-11-089-764-34	Sequence 34, Appl	630	4	5.0	34	7	US-11-122-795-15	Sequence 15, Appl
558	4	5.0	16	7	US-11-089-764-35	Sequence 35, Appl	631	4	5.0	35	6	US-10-816-768-1	Sequence 1, Appli
559	4	5.0	16	7	US-11-107-029-22	Sequence 22, Appl	632	4	5.0	35	6	US-10-467-657-1036	Sequence 1036, Ap
560	4	5.0	16	7	US-11-107-029-26	Sequence 26, Appl	633	4	5.0	35	6	US-10-431-638-25	Sequence 25, Appl
561	4	5.0	16	7	US-11-033-039-1442	Sequence 1442, Ap	634	4	5.0	35	6	US-10-957-351-34	Sequence 34, Appl
562	4	5.0	17	7	US-11-033-039-1448	Sequence 1448, Ap	635	4	5.0	36	6	US-10-467-657-3056	Sequence 3056, Ap
563	4	5.0	17	7	US-11-062-186-54	Sequence 54, Appl	636	4	5.0	37	6	US-10-467-657-8849	Sequence 8849, App
564	4	5.0	17	7	US-11-033-039-1441	Sequence 1441, Ap	637	4	5.0	38	6	US-10-467-657-2998	Sequence 2998, App
565	4	5.0	17	7	US-11-033-039-1447	Sequence 1447, Ap	638	4	5.0	38	7	US-11-212-443-144	Sequence 144, App
566	4	5.0	18	7	US-11-092-496-21	Sequence 21, Appl	639	4	5.0	38	7	US-11-212-443-145	Sequence 145, App
567	4	5.0	18	7	US-11-076-164-24	Sequence 24, Appl	640	4	5.0	38	7	US-11-212-443-146	Sequence 146, App
568	4	5.0	18	7	US-11-106-415-216	Sequence 216, App	641	4	5.0	39	7	US-11-196-400-23	Sequence 23, Appl
569	4	5.0	18	7	US-11-106-415-230	Sequence 230, App	642	4	5.0	41	6	US-10-467-657-6206	Sequence 6206, Ap
570	4	5.0	18	7	US-11-106-415-254	Sequence 254, App	643	4	5.0	41	6	US-10-467-657-8759	Sequence 8759, App
571	4	5.0	18	7	US-11-106-415-270	Sequence 270, App	644	4	5.0	41	6	US-10-916-827-38	Sequence 38, Appl
572	4	5.0	18	7	US-11-106-415-339	Sequence 339, App	645	4	5.0	42	6	US-10-518-159-2	Sequence 2, Appli
573	4	5.0	18	7	US-11-106-415-340	Sequence 340, App	646	4	5.0	42	6	US-10-518-159-4	Sequence 4, Appli
574	4	5.0	18	7	US-11-106-415-343	Sequence 343, App	647	4	5.0	42	6	US-10-986-501-166	Sequence 166, App
575	4	5.0	18	7	US-11-106-415-344	Sequence 344, App	648	4	5.0	42	6	US-10-467-657-1478	Sequence 1478, App
576	4	5.0	18	7	US-11-106-415-348	Sequence 348, App	649	4	5.0	42	6	US-10-957-887B-119	Sequence 119, App
577	4	5.0	18	7	US-11-106-415-354	Sequence 354, App	650	4	5.0	42	7	US-11-090-787-1	Sequence 1, Appli
578	4	5.0	18	7	US-11-106-415-357	Sequence 357, App	651	4	5.0	42	7	US-11-090-787-2	Sequence 2, Appli
579	4	5.0	18	7	US-11-106-415-360	Sequence 360, App	652	4	5.0	42	7	US-11-090-825-1	Sequence 1, Appli
580	4	5.0	18	7	US-11-106-415-388	Sequence 388, App	653	4	5.0	42	7	US-11-090-825-2	Sequence 2, Appli
581	4	5.0	18	7	US-11-033-039-1440	Sequence 1440, Ap	654	4	5.0	43	6	US-10-952-535A-40	Sequence 40, Appl
582	4	5.0	18	7	US-11-033-039-1446	Sequence 1446, Ap	655	4	5.0	43	6	US-10-623-155-482	Sequence 482, App
583	4	5.0	19	6	US-10-503-575-125	Sequence 125, App	656	4	5.0	43	6	US-10-957-887B-28	Sequence 28, Appl
584	4	5.0	19	6	US-10-503-575-131	Sequence 131, App	657	4	5.0	43	6	US-10-957-887B-64	Sequence 64, Appl
585	4	5.0	19	6	US-10-503-575-314	Sequence 314, App	658	4	5.0	43	6	US-10-957-887B-77	Sequence 77, Appl
586	4	5.0	19	6	US-10-503-575-315	Sequence 315, App	659	4	5.0	43	6	US-10-957-887B-78	Sequence 78, Appl
587	4	5.0	19	6	US-10-503-575-317	Sequence 317, App	660	4	5.0	43	6	US-10-957-887B-79	Sequence 79, Appl
588	4	5.0	19	6	US-10-503-575-319	Sequence 319, App	661	4	5.0	43	6	US-10-957-887B-80	Sequence 80, Appl
589	4	5.0	19	6	US-10-503-575-321	Sequence 321, App	662	4	5.0	43	6	US-10-957-887B-159	Sequence 159, App
590	4	5.0	19	7	US-11-145-566-9	Sequence 9, Appli	663	4	5.0	43	6	US-10-957-887B-160	Sequence 160, App
591	4	5.0	19	7	US-11-212-443-153	Sequence 153, App	664	4	5.0	43	6	US-10-957-887B-163	Sequence 163, App
592	4	5.0	19	7	US-11-212-443-154	Sequence 154, App	665	4	5.0	43	6	US-10-957-887B-164	Sequence 164, App
593	4	5.0	19	7	US-11-212-443-155	Sequence 155, App	666	4	5.0	43	6	US-10-957-887B-165	Sequence 165, App
594	4	5.0	19	7	US-11-033-039-1439	Sequence 1439, Ap	667	4	5.0	43	6	US-10-957-887B-222	Sequence 222, App
595	4	5.0	19	7	US-11-033-039-1439	Sequence 1445, Ap	668	4	5.0	43	6	US-10-957-887B-224	Sequence 224, App
596	4	5.0	20	6	US-10-623-155-400	Sequence 400, App	669	4	5.0	43	6	US-10-957-887B-223	Sequence 223, App
597	4	5.0	20	6	US-10-623-155-401	Sequence 401, App	670	4	5.0	43	6	US-10-957-887B-224	Sequence 224, App
598	4	5.0	20	6	US-10-623-155-457	Sequence 457, App	671	4	5.0	43	6	US-10-957-887B-233	Sequence 233, App
599	4	5.0	20	6	US-10-623-155-508	Sequence 508, App	672	4	5.0	43	6	US-10-957-887B-234	Sequence 234, App
600	4	5.0	20	6	US-10-623-155-509	Sequence 509, App	673	4	5.0	43	6	US-10-957-887B-236	Sequence 236, App
601	4	5.0	20	7	US-11-106-415-290	Sequence 290, App	674	4	5.0	43	6	US-10-957-887B-237	Sequence 237, App
602	4	5.0	20	7	US-11-106-415-307	Sequence 307, App	675	4	5.0	43	6	US-10-957-887B-262	Sequence 262, App
603	4	5.0	20	7	US-11-106-415-311	Sequence 311, App	676	4	5.0	43	6	US-10-957-887B-303	Sequence 303, App
604	4	5.0	20	7	US-11-106-415-324	Sequence 324, App	677	4	5.0	43	7	US-11-108-001-4	Sequence 4, Appli
605	4	5.0	20	7	US-11-106-415-324	Sequence 328, App	678	4	5.0	44	6	US-10-957-887B-1	Sequence 1, Appli
606	4	5.0	21	6	US-10-986-501-358	Sequence 358, App	679	4	5.0	44	6	US-10-957-887B-4	Sequence 4, Appli
607	4	5.0	21	6	US-10-939-890-472	Sequence 472, App	680	4	5.0	44	6	US-10-957-887B-116	Sequence 116, App
608	4	5.0	21	6	US-10-939-890-504	Sequence 504, App	681	4	5.0	44	6	US-10-957-887B-173	Sequence 173, App
609	4	5.0	21	6	US-10-939-890-511	Sequence 511, App	682	4	5.0	44	6	US-10-957-887B-294	Sequence 294, App

683	4	5.0	45	6	US-10-986-501-170	Sequence 170, App	756	4	5.0	78	6	US-10-467-657-1764	Sequence 1764, Ap
684	4	5.0	45	6	US-10-957-887B-185	Sequence 185, App	757	4	5.0	78	6	US-10-467-657-3038	Sequence 3038, Ap
685	4	5.0	46	6	US-11-000-463-742	Sequence 742, App	758	4	5.0	78	6	US-11-082-389-170	Sequence 170, App
686	4	5.0	46	6	US-10-828-033-32	Sequence 32, Appl	759	4	5.0	80	6	US-10-986-501-200	Sequence 200, App
687	4	5.0	46	6	US-10-828-033-34	Sequence 34, Appl	760	4	5.0	80	6	US-10-467-657-5282	Sequence 5282, Ap
688	4	5.0	46	6	US-10-957-887B-33	Sequence 33, Appl	761	4	5.0	81	6	US-10-467-657-2490	Sequence 2490, Ap
689	4	5.0	46	6	US-10-957-887B-198	Sequence 198, App	762	4	5.0	81	6	US-10-467-657-5668	Sequence 5668, Ap
690	4	5.0	46	6	US-10-957-887B-275	Sequence 275, App	763	4	5.0	81	6	US-10-467-657-8338	Sequence 8338, Ap
691	4	5.0	46	6	US-10-957-887B-276	Sequence 276, App	764	4	5.0	81	6	US-10-467-657-8352	Sequence 8352, Ap
692	4	5.0	46	6	US-10-957-351-5	Sequence 5, Appl	765	4	5.0	82	6	US-11-053-076-287	Sequence 287, App
693	4	5.0	46	6	US-11-000-463-306	Sequence 306, App	766	4	5.0	83	6	US-10-467-657-7970	Sequence 7970, Ap
694	4	5.0	46	7	US-11-000-463-778	Sequence 778, App	767	4	5.0	83	7	US-11-089-426-21	Sequence 21, Appl
695	4	5.0	47	6	US-10-467-657-2348	Sequence 2348, Ap	768	4	5.0	83	7	US-11-000-463-246	Sequence 246, App
696	4	5.0	47	6	US-10-467-657-2350	Sequence 2350, Ap	769	4	5.0	85	6	US-10-986-501-129	Sequence 129, App
697	4	5.0	47	6	US-10-467-657-5500	Sequence 5500, Ap	770	4	5.0	85	6	US-10-467-657-3090	Sequence 3090, Ap
698	4	5.0	47	6	US-11-068-783-108	Sequence 108, App	771	4	5.0	85	6	US-10-485-788A-660	Sequence 660, App
699	4	5.0	47	7	US-11-000-463-414	Sequence 414, App	772	4	5.0	85	7	US-11-053-076-23	Sequence 23, Appl
700	4	5.0	47	7	US-11-000-463-886	Sequence 886, App	773	4	5.0	85	7	US-11-076-164-43	Sequence 43, Appl
701	4	5.0	48	6	US-10-467-657-6820	Sequence 6820, Ap	774	4	5.0	87	6	US-10-467-657-7678	Sequence 7678, Ap
702	4	5.0	48	6	US-10-467-657-7896	Sequence 7896, Ap	775	4	5.0	87	6	US-10-485-788A-729	Sequence 729, App
703	4	5.0	48	7	US-11-123-896-282	Sequence 282, App	776	4	5.0	87	7	US-11-053-076-99	Sequence 99, Appl
704	4	5.0	49	6	US-10-485-517-334	Sequence 334, App	777	4	5.0	88	6	US-10-467-657-5480	Sequence 5480, Ap
705	4	5.0	49	6	US-10-967-527A-15	Sequence 15, Appl	778	4	5.0	88	7	US-11-135-855-32	Sequence 32, Appl
706	4	5.0	49	6	US-10-467-657-8236	Sequence 8236, Ap	779	4	5.0	89	6	US-10-485-788A-754	Sequence 754, App
707	4	5.0	49	6	US-10-431-638-35	Sequence 35, Appl	780	4	5.0	89	6	US-10-485-788A-789	Sequence 789, App
708	4	5.0	50	6	US-10-986-501-216	Sequence 216, App	781	4	5.0	89	7	US-11-053-076-131	Sequence 131, App
709	4	5.0	50	6	US-10-982-727-63	Sequence 63, Appl	782	4	5.0	89	7	US-11-053-076-171	Sequence 171, App
710	4	5.0	50	6	US-10-982-727-64	Sequence 64, Appl	783	4	5.0	89	7	US-10-485-788A-829	Sequence 829, App
711	4	5.0	50	6	US-10-729-121-32	Sequence 32, Appl	784	4	5.0	90	6	US-10-485-788A-832	Sequence 832, App
712	4	5.0	51	6	US-10-467-657-816	Sequence 816, App	785	4	5.0	90	7	US-11-053-076-214	Sequence 214, App
713	4	5.0	51	7	US-11-000-463-256	Sequence 256, App	786	4	5.0	90	7	US-11-053-076-217	Sequence 217, App
714	4	5.0	51	7	US-11-000-463-443	Sequence 443, App	787	4	5.0	91	6	US-10-954-468-48	Sequence 48, Appl
715	4	5.0	51	7	US-11-000-463-728	Sequence 728, App	788	4	5.0	91	7	US-11-051-481-49	Sequence 49, Appl
716	4	5.0	52	6	US-10-914-165-6	Sequence 6, Appl	789	4	5.0	92	6	US-10-821-234-1505	Sequence 1505, Ap
717	4	5.0	52	7	US-11-000-463-266	Sequence 266, App	790	4	5.0	92	6	US-10-467-657-2068	Sequence 2068, Ap
718	4	5.0	52	7	US-11-000-463-738	Sequence 738, App	791	4	5.0	92	6	US-10-467-657-3456	Sequence 3456, Ap
719	4	5.0	54	6	US-10-467-657-3784	Sequence 784, Ap	792	4	5.0	92	6	US-10-467-657-7806	Sequence 7806, Ap
720	4	5.0	54	7	US-11-000-463-712	Sequence 712, App	793	4	5.0	94	6	US-10-467-657-2090	Sequence 2090, Ap
721	4	5.0	55	5	US-09-978-360A-457	Sequence 457, App	794	4	5.0	94	6	US-10-485-788A-662	Sequence 662, App
722	4	5.0	55	6	US-10-467-657-4466	Sequence 4466, App	795	4	5.0	94	6	US-10-485-788A-776	Sequence 776, App
723	4	5.0	59	5	US-09-978-360A-730	Sequence 730, App	796	4	5.0	94	6	US-10-485-788A-802	Sequence 802, App
724	4	5.0	59	6	US-10-467-657-4896	Sequence 4896, Ap	797	4	5.0	94	7	US-11-053-076-25	Sequence 25, Appl
725	4	5.0	60	6	US-10-467-657-4114	Sequence 4114, Ap	798	4	5.0	94	7	US-11-053-076-158	Sequence 158, App
726	4	5.0	60	6	US-10-467-657-4940	Sequence 4940, Ap	799	4	5.0	94	7	US-11-053-076-184	Sequence 184, App
727	4	5.0	60	6	US-10-467-657-8454	Sequence 8454, Ap	800	4	5.0	94	7	US-11-055-822-828	Sequence 828, App
728	4	5.0	61	6	US-10-467-657-1506	Sequence 1506, Ap	801	4	5.0	95	6	US-10-467-657-2136	Sequence 2136, Ap
729	4	5.0	61	6	US-10-467-657-5574	Sequence 5674, Ap	802	4	5.0	95	6	US-10-467-657-2922	Sequence 2922, Ap
730	4	5.0	62	6	US-10-888-613B-86	Sequence 86, Appl	803	4	5.0	95	6	US-10-485-788A-659	Sequence 659, App
731	4	5.0	64	7	US-11-102-978-5	Sequence 5, Appl	804	4	5.0	95	6	US-10-485-788A-663	Sequence 663, App
732	4	5.0	65	6	US-10-467-657-7770	Sequence 7770, Ap	805	4	5.0	95	7	US-11-053-076-22	Sequence 22, Appl
733	4	5.0	66	6	US-10-986-501-160	Sequence 160, App	806	4	5.0	95	7	US-11-053-076-26	Sequence 26, Appl
734	4	5.0	66	6	US-10-467-657-2890	Sequence 2890, Ap	807	4	5.0	96	6	US-10-821-234-1351	Sequence 1351, Ap
735	4	5.0	67	7	US-11-068-717-13	Sequence 13, Appl	808	4	5.0	96	6	US-10-467-657-5492	Sequence 5492, Ap
736	4	5.0	67	7	US-11-074-176-302	Sequence 302, App	809	4	5.0	96	6	US-10-925-366A-222	Sequence 222, App
737	4	5.0	68	6	US-10-467-657-1436	Sequence 1436, Ap	810	4	5.0	96	6	US-10-485-788A-766	Sequence 766, App
738	4	5.0	68	6	US-10-467-657-3384	Sequence 3384, Ap	811	4	5.0	96	7	US-11-053-076-143	Sequence 143, App
739	4	5.0	68	6	US-10-467-657-7534	Sequence 7534, Ap	812	4	5.0	96	7	US-11-019-711-92	Sequence 92, Appl
740	4	5.0	69	7	US-10-467-657-5932	Sequence 5932, Ap	813	4	5.0	96	7	US-11-019-711-93	Sequence 93, Appl
741	4	5.0	69	7	US-11-051-481-50	Sequence 50, Appl	814	4	5.0	97	6	US-10-467-657-2016	Sequence 2016, Ap
742	4	5.0	70	6	US-10-467-657-4972	Sequence 4972, Ap	815	4	5.0	97	6	US-10-995-561-900	Sequence 900, App
743	4	5.0	70	7	US-11-021-441-116	Sequence 116, App	816	4	5.0	97	6	US-10-485-788A-676	Sequence 676, App
744	4	5.0	71	6	US-10-467-657-4162	Sequence 4162, Ap	817	4	5.0	97	6	US-10-485-788A-791	Sequence 791, App
745	4	5.0	71	7	US-11-000-463-369	Sequence 369, App	818	4	5.0	97	6	US-10-485-788A-795	Sequence 795, App
746	4	5.0	71	7	US-11-000-463-841	Sequence 841, App	819	4	5.0	97	6	US-10-485-788A-820	Sequence 820, App
747	4	5.0	72	6	US-10-467-657-2816	Sequence 2816, Ap	820	4	5.0	97	7	US-11-053-076-42	Sequence 42, Appl
748	4	5.0	72	6	US-10-528-031-2	Sequence 2, Appl	821	4	5.0	97	7	US-11-053-076-173	Sequence 173, App
749	4	5.0	73	6	US-10-467-657-8832	Sequence 8832, Ap	822	4	5.0	97	7	US-11-053-076-177	Sequence 177, App
750	4	5.0	74	6	US-10-467-657-1976	Sequence 1976, Ap	823	4	5.0	97	7	US-11-053-076-205	Sequence 205, App
751	4	5.0	75	6	US-10-986-501-139	Sequence 139, App	824	4	5.0	97	7	US-11-000-463-870	Sequence 870, App
752	4	5.0	75	6	US-10-986-501-143	Sequence 143, App	825	4	5.0	98	6	US-10-816-768-41	Sequence 41, Appl
753	4	5.0	76	7	US-11-123-896-281	Sequence 281, App	826	4	5.0	98	6	US-10-816-768-42	Sequence 42, Appl
754	4	5.0	77	7	US-11-132-142-19	Sequence 19, Appl	827	4	5.0	98	6	US-10-816-768-44	Sequence 44, Appl
755	4	5.0	78	6	US-10-986-501-357	Sequence 357, App	828	4	5.0	98	6	US-10-467-657-3490	Sequence 3490, Ap

829	4	5.0	98	6	US-10-467-657-4746	Sequence 4746, Ap	902	4	5.0	102	7	US-11-064-774A-347	Sequence 347, App
830	4	5.0	98	6	US-10-467-657-6904	Sequence 6904, Ap	903	4	5.0	102	7	US-11-064-774A-353	Sequence 353, App
831	4	5.0	98	6	US-10-467-657-7082	Sequence 7082, Ap	904	4	5.0	102	7	US-11-064-774A-355	Sequence 355, App
832	4	5.0	98	6	US-10-467-657-8586	Sequence 8586, Ap	905	4	5.0	102	7	US-11-064-774A-361	Sequence 361, App
833	4	5.0	98	6	US-10-485-788A-717	Sequence 717, App	906	4	5.0	102	7	US-11-064-774A-363	Sequence 363, App
834	4	5.0	98	7	US-11-053-076-87	Sequence 87, Appl	907	4	5.0	102	7	US-11-064-774A-369	Sequence 369, App
835	4	5.0	98	7	US-11-000-463-944	Sequence 944, App	908	4	5.0	102	7	US-11-064-774A-371	Sequence 371, App
836	4	5.0	99	6	US-10-467-657-5934	Sequence 5934, Ap	909	4	5.0	102	7	US-11-064-774A-377	Sequence 377, App
837	4	5.0	100	6	US-10-467-657-9162	Sequence 9162, Ap	910	4	5.0	102	7	US-11-064-774A-379	Sequence 379, App
838	4	5.0	100	6	US-10-454-437-18	Sequence 18, Appl	911	4	5.0	102	7	US-11-064-774A-385	Sequence 385, App
839	4	5.0	100	7	US-11-107-096-1	Sequence 1, Appl1	912	4	5.0	102	7	US-11-064-774A-387	Sequence 387, App
840	4	5.0	101	6	US-10-793-626-446	Sequence 446, App	913	4	5.0	102	7	US-11-064-774A-393	Sequence 393, App
841	4	5.0	101	6	US-10-467-657-120	Sequence 120, App	914	4	5.0	102	7	US-11-064-774A-395	Sequence 395, App
842	4	5.0	101	6	US-10-467-657-2338	Sequence 2338, Ap	915	4	5.0	102	7	US-11-064-774A-401	Sequence 401, App
843	4	5.0	101	6	US-10-467-657-5360	Sequence 5360, Ap	916	4	5.0	102	7	US-11-064-774A-403	Sequence 403, App
844	4	5.0	101	6	US-10-928-446A-141	Sequence 141, App	917	4	5.0	102	7	US-11-064-774A-409	Sequence 409, App
845	4	5.0	101	6	US-10-928-446A-142	Sequence 142, App	918	4	5.0	102	7	US-11-064-774A-411	Sequence 411, App
846	4	5.0	101	6	US-10-485-788A-683	Sequence 683, App	919	4	5.0	102	7	US-11-064-774A-417	Sequence 417, App
847	4	5.0	101	7	US-11-082-544-28	Sequence 28, Appl	920	4	5.0	102	7	US-11-064-774A-419	Sequence 419, App
848	4	5.0	101	7	US-11-053-076-51	Sequence 51, Appl	921	4	5.0	102	7	US-11-064-774A-425	Sequence 425, App
849	4	5.0	101	7	US-10-689-742-21	Sequence 297, App	922	4	5.0	102	7	US-11-064-774A-427	Sequence 427, App
850	4	5.0	102	6	US-10-689-742-21	Sequence 297, App	923	4	5.0	102	7	US-11-064-774A-429	Sequence 429, App
851	4	5.0	102	6	US-10-689-742-44	Sequence 44, Appl	924	4	5.0	102	7	US-11-064-774A-1209	Sequence 1209, Ap
852	4	5.0	102	6	US-10-793-626-122	Sequence 122, App	925	4	5.0	103	6	US-10-986-501-169	Sequence 15, Appl
853	4	5.0	102	6	US-10-821-234-1245	Sequence 1245, Ap	926	4	5.0	103	6	US-10-793-626-556	Sequence 169, App
854	4	5.0	102	6	US-10-928-446A-143	Sequence 143, App	927	4	5.0	103	6	US-10-793-626-1762	Sequence 556, App
855	4	5.0	102	6	US-10-928-446A-144	Sequence 144, App	928	4	5.0	103	6	US-10-467-657-3940	Sequence 1762, Ap
856	4	5.0	102	6	US-10-928-446A-145	Sequence 145, App	929	4	5.0	103	6	US-10-485-788A-740	Sequence 3040, Ap
857	4	5.0	102	6	US-10-928-446A-146	Sequence 146, App	930	4	5.0	103	6	US-11-053-076-110	Sequence 740, App
858	4	5.0	102	6	US-10-928-446A-147	Sequence 147, App	931	4	5.0	103	7	US-11-090-916-6	Sequence 6, Appli
859	4	5.0	102	7	US-11-064-774A-177	Sequence 177, App	932	4	5.0	103	7	US-11-064-774A-181	Sequence 181, App
860	4	5.0	102	7	US-11-064-774A-179	Sequence 179, App	933	4	5.0	103	7	US-11-064-774A-183	Sequence 183, App
861	4	5.0	102	7	US-11-064-774A-185	Sequence 185, App	934	4	5.0	103	7	US-11-064-774A-189	Sequence 189, App
862	4	5.0	102	7	US-11-064-774A-187	Sequence 187, App	935	4	5.0	103	7	US-11-064-774A-191	Sequence 191, App
863	4	5.0	102	7	US-11-064-774A-193	Sequence 193, App	936	4	5.0	103	7	US-11-064-774A-197	Sequence 197, App
864	4	5.0	102	7	US-11-064-774A-195	Sequence 195, App	937	4	5.0	103	7	US-11-064-774A-199	Sequence 199, App
865	4	5.0	102	7	US-11-064-774A-201	Sequence 201, App	938	4	5.0	103	7	US-11-064-774A-205	Sequence 205, App
866	4	5.0	102	7	US-11-064-774A-203	Sequence 203, App	939	4	5.0	103	7	US-11-064-774A-207	Sequence 207, App
867	4	5.0	102	7	US-11-064-774A-209	Sequence 209, App	940	4	5.0	103	7	US-11-064-774A-213	Sequence 213, App
868	4	5.0	102	7	US-11-064-774A-211	Sequence 211, App	941	4	5.0	103	7	US-11-064-774A-215	Sequence 215, App
869	4	5.0	102	7	US-11-064-774A-217	Sequence 217, App	942	4	5.0	103	7	US-11-064-774A-221	Sequence 221, App
870	4	5.0	102	7	US-11-064-774A-219	Sequence 219, App	943	4	5.0	103	7	US-11-064-774A-223	Sequence 223, App
871	4	5.0	102	7	US-11-064-774A-225	Sequence 225, App	944	4	5.0	103	7	US-11-064-774A-229	Sequence 229, App
872	4	5.0	102	7	US-11-064-774A-227	Sequence 227, App	945	4	5.0	103	7	US-11-064-774A-231	Sequence 231, App
873	4	5.0	102	7	US-11-064-774A-233	Sequence 233, App	946	4	5.0	103	7	US-11-064-774A-237	Sequence 237, App
874	4	5.0	102	7	US-11-064-774A-235	Sequence 235, App	947	4	5.0	103	7	US-11-064-774A-239	Sequence 239, App
875	4	5.0	102	7	US-11-064-774A-241	Sequence 241, App	948	4	5.0	103	7	US-11-064-774A-245	Sequence 245, App
876	4	5.0	102	7	US-11-064-774A-243	Sequence 243, App	949	4	5.0	103	7	US-11-064-774A-247	Sequence 247, App
877	4	5.0	102	7	US-11-064-774A-249	Sequence 249, App	950	4	5.0	103	7	US-11-064-774A-253	Sequence 253, App
878	4	5.0	102	7	US-11-064-774A-251	Sequence 251, App	951	4	5.0	103	7	US-11-064-774A-255	Sequence 255, App
879	4	5.0	102	7	US-11-064-774A-257	Sequence 257, App	952	4	5.0	103	7	US-11-064-774A-261	Sequence 261, App
880	4	5.0	102	7	US-11-064-774A-259	Sequence 259, App	953	4	5.0	103	7	US-11-064-774A-263	Sequence 263, App
881	4	5.0	102	7	US-11-064-774A-265	Sequence 265, App	954	4	5.0	103	7	US-11-064-774A-269	Sequence 269, App
882	4	5.0	102	7	US-11-064-774A-267	Sequence 267, App	955	4	5.0	103	7	US-11-064-774A-271	Sequence 271, App
883	4	5.0	102	7	US-11-064-774A-273	Sequence 273, App	956	4	5.0	103	7	US-11-064-774A-277	Sequence 277, App
884	4	5.0	102	7	US-11-064-774A-275	Sequence 275, App	957	4	5.0	103	7	US-11-064-774A-279	Sequence 279, App
885	4	5.0	102	7	US-11-064-774A-281	Sequence 281, App	958	4	5.0	103	7	US-11-064-774A-285	Sequence 285, App
886	4	5.0	102	7	US-11-064-774A-283	Sequence 283, App	959	4	5.0	103	7	US-11-064-774A-287	Sequence 287, App
887	4	5.0	102	7	US-11-064-774A-289	Sequence 289, App	960	4	5.0	103	7	US-11-064-774A-293	Sequence 293, App
888	4	5.0	102	7	US-11-064-774A-291	Sequence 291, App	961	4	5.0	103	7	US-11-064-774A-295	Sequence 295, App
889	4	5.0	102	7	US-11-064-774A-297	Sequence 297, App	962	4	5.0	103	7	US-11-064-774A-301	Sequence 301, App
890	4	5.0	102	7	US-11-064-774A-299	Sequence 299, App	963	4	5.0	103	7	US-11-064-774A-303	Sequence 303, App
891	4	5.0	102	7	US-11-064-774A-305	Sequence 305, App	964	4	5.0	103	7	US-11-064-774A-309	Sequence 309, App
892	4	5.0	102	7	US-11-064-774A-307	Sequence 307, App	965	4	5.0	103	7	US-11-064-774A-311	Sequence 311, App
893	4	5.0	102	7	US-11-064-774A-313	Sequence 313, App	966	4	5.0	103	7	US-11-064-774A-317	Sequence 317, App
894	4	5.0	102	7	US-11-064-774A-315	Sequence 315, App	967	4	5.0	103	7	US-11-064-774A-319	Sequence 319, App
895	4	5.0	102	7	US-11-064-774A-321	Sequence 321, App	968	4	5.0	103	7	US-11-064-774A-325	Sequence 325, App
896	4	5.0	102	7	US-11-064-774A-323	Sequence 323, App	969	4	5.0	103	7	US-11-064-774A-327	Sequence 327, App
897	4	5.0	102	7	US-11-064-774A-329	Sequence 329, App	970	4	5.0	103	7	US-11-064-774A-333	Sequence 333, App
898	4	5.0	102	7	US-11-064-774A-331	Sequence 331, App	971	4	5.0	103	7	US-11-064-774A-335	Sequence 335, App
899	4	5.0	102	7	US-11-064-774A-337	Sequence 337, App	972	4	5.0	103	7	US-11-064-774A-341	Sequence 341, App
900	4	5.0	102	7	US-11-064-774A-339	Sequence 339, App	973	4	5.0	103	7	US-11-064-774A-343	Sequence 343, App
901	4	5.0	102	7	US-11-064-774A-345	Sequence 345, App	974	4	5.0	103	7	US-11-064-774A-349	Sequence 349, App

975 4 5.0 103 7 US-11-064-774A-351 Sequence 351, App
976 4 5.0 103 7 US-11-064-774A-357 Sequence 357, App
977 4 5.0 103 7 US-11-064-774A-359 Sequence 359, App
978 4 5.0 103 7 US-11-064-774A-365 Sequence 365, App
979 4 5.0 103 7 US-11-064-774A-367 Sequence 367, App
980 4 5.0 103 7 US-11-064-774A-373 Sequence 373, App
981 4 5.0 103 7 US-11-064-774A-375 Sequence 375, App
982 4 5.0 103 7 US-11-064-774A-381 Sequence 381, App
983 4 5.0 103 7 US-11-064-774A-383 Sequence 383, App
984 4 5.0 103 7 US-11-064-774A-389 Sequence 389, App
985 4 5.0 103 7 US-11-064-774A-391 Sequence 391, App
986 4 5.0 103 7 US-11-064-774A-397 Sequence 397, App
987 4 5.0 103 7 US-11-064-774A-399 Sequence 399, App
988 4 5.0 103 7 US-11-064-774A-405 Sequence 405, App
989 4 5.0 103 7 US-11-064-774A-407 Sequence 407, App
990 4 5.0 103 7 US-11-064-774A-413 Sequence 413, App
991 4 5.0 103 7 US-11-064-774A-415 Sequence 415, App
992 4 5.0 103 7 US-11-064-774A-421 Sequence 421, App
993 4 5.0 103 7 US-11-064-774A-423 Sequence 423, App
994 4 5.0 103 7 US-11-064-774A-429 Sequence 429, App
995 4 5.0 103 7 US-11-064-774A-431 Sequence 431, App
996 4 5.0 103 7 US-11-194-246-412 Sequence 412, App
997 4 5.0 103 7 US-11-064-174-42 Sequence 42, Appl
998 4 5.0 104 6 US-10-467-657-6588 Sequence 6588, Ap
999 4 5.0 104 6 US-10-485-788A-835 Sequence 835, App
1000 4 5.0 104 7 US-11-053-076-220 Sequence 220, App

ALIGNMENTS

RESULT 1
US-10-821-234-1266
; Sequence 1266, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1266
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1266
Query Match 100.0%; Score 80; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.6e-78;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEPYKDTYKLTQRETKLAIHYALNCCGLAGVQFTSDICPKKDV 60
DB 113 HKDEVIKEVQEPYKDTYKLTQRETKLAIHYALNCCGLAGVQFTSDICPKKDV 172
QY 61 LETFTVKSCPDAIKEVFDNK 80
DB 173 LETFTVKSCPDAIKEVFDNK 192
RESULT 2
US-11-022-562-157
; Sequence 157, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.

; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-157
Query Match 7.5%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 DAIKEV 76
DB 12 DAIKEV 17
RESULT 3
US-11-022-562-158
; Sequence 158, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-158
Query Match 7.5%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 DAIKEV 76
DB 2 DAIKEV 7
RESULT 4
US-11-145-035-45
; Sequence 45, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: RAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124

; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-145-035-45

Query Match 7.5%; Score 6; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQR 28
|||
Db 1 KDEPQR 6

RESULT 5
US-10-467-657-606
; Sequence 606, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 606
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-606

Query Match 7.5%; Score 6; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GGVEQF 50
|||
Db 28 GGVEQF 33

RESULT 6
US-10-467-657-2734
; Sequence 2734, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2734
; LENGTH: 259

; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2734

Query Match 7.5%; Score 6; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GLAGGV 47
|||
Db 140 GLAGGV 145

RESULT 7
US-10-883-512-108
; Sequence 108, Application US/10883512
; Publication No. US20060005265A1
; GENERAL INFORMATION:
; APPLICANT: Bughrara, Suleiman
; APPLICANT: Han, Zhao
; APPLICANT: Wang, Yuxia
; TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation
; FILE REFERENCE: MSU-08807
; CURRENT APPLICATION NUMBER: US/10/883,512
; CURRENT FILING DATE: 2004-07-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 108
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-883-512-108

Query Match 7.5%; Score 6; DB 6; Length 274;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 KKDVL 62
|||
Db 184 KKDVL 189

RESULT 8
US-09-978-360A-763
; Sequence 763, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122

; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 763
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-978-360A-763

Query Match 7.5%; Score 6; DB 5; Length 303;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CGLAGG 46
Db 249 CGLAGG 254

RESULT 9
US-10-510-386-244
; Sequence 244, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 244
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-244

Query Match 7.5%; Score 6; DB 6; Length 316;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 KEVFDN 79
Db 302 KEVFDN 307

RESULT 10
US-10-873-528-62
; Sequence 62, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip W
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19

; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 62
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-62

Query Match 7.5%; Score 6; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 DVLETF 64
Db 178 DVLETF 183

RESULT 11
US-10-467-657-8004
; Sequence 8004, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8004
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8004

Query Match 7.5%; Score 6; DB 6; Length 408;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 GVEQFI 51
Db 228 GVEQFI 233

RESULT 12
US-10-978-927-1
; Sequence 1, Application US/10978927
; Publication No. US20060009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE REFERENCE: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =

; OTHER INFORMATION: Synthetic Construct
US-10-978-927-1

Query Match 7.5%; Score 6; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EVFDNK 80
|||||
Db 255 EVFDNK 260

RESULT 13

US-11-109-156-34
; Sequence 34, Application US/11109156
; Publication No. US20050250144A1

; GENERAL INFORMATION:

; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo

; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; FILE REFERENCE: 06501-099002

; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 521

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-34

Query Match 7.5%; Score 6; DB 7; Length 521;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 KEVFON 79
|||||
Db 32 KEVFON 37

RESULT 14

US-10-978-927-6
; Sequence 6, Application US/10978927
; Publication No. US20060009406A1

; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-6

Query Match 7.5%; Score 6; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EVFDNK 80
|||||
Db 374 EVFDNK 379

RESULT 15

US-10-821-234-1520
; Sequence 1520, Application US/10821234
; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1520
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1520

Query Match 7.5%; Score 6; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 EVFDNK 80
|||||
Db 375 EVFDNK 380

Search completed: January 20, 2006, 17:47:41
Job time : 10.4615 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:35:41 ; Search time 18.4615 Seconds
(without alignments)
416.939 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192

Perfect score: 80

Sequence: 1 HKDEVIKEVQEFYKDYTNKL.....LEFTVKSCPDAIKVFDNK 80

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	228	1 A40402	CD9 antigen [valid
2	38	47.5	228	1 A42929	CD9 antigen - gree
3	15	18.8	226	1 S3262	CD9 antigen - rat
4	13	16.2	226	1 JX0221	CD9 antigen - bovi
5	13	16.2	226	2 I49589	antigen - mouse
6	7	8.8	100	2 T07054	cysteine proteinas
7	7	8.8	276	2 A72276	phosphate ABC tran
8	7	8.8	516	2 B64551	oligopeptide ABC t
9	7	8.8	980	2 T00045	cellohextrin phosph
10	7	8.8	1302	2 T23236	hypothetical prote
11	6	7.5	15	2 S03353	plastocyanin - Mic
12	6	7.5	57	2 H35057	MHC class II histo
13	6	7.5	60	2 H82927	hypothetical prote
14	6	7.5	66	2 PQ0469	cysteine proteinas
15	6	7.5	68	2 D64538	hypothetical prote
16	6	7.5	83	2 D56604	M protein precuro
17	6	7.5	84	2 S61082	cytochrome c6 - re
18	6	7.5	85	1 JCS849	cytochrome c6 - re
19	6	7.5	85	2 JCS849	nonhistone chromos
20	6	7.5	89	1 NSBQH7	nonhistone chromos
21	6	7.5	89	2 S11349	nonhistone chromos
22	6	7.5	89	2 S38666	nonhistone chromos
23	6	7.5	90	1 NSCHH7	nonhistone chromos
24	6	7.5	90	2 S03700	nonhistone chromos
25	6	7.5	90	2 S01946	nonhistone chromos
26	6	7.5	92	2 T07051	cysteine proteinas
27	6	7.5	92	2 S78005	cuticle structural
28	6	7.5	93	2 A95121	hypothetical prote
29	6	7.5	93	2 F97990	hypothetical prote

hypothetical prote
probable minor tai
probable minor tai
probable minor tai
hypothetical prote
hypothetical prote
cytochrome c553 -
hypothetical prote
hypothetical prote
protein Tf685.6 [i
hypothetical prote
NADP-reducing hydr
probable minor tai
probable tail comp
plastocyanin precu
probable minor tai
hypothetical prote
minor tail protein
probable tail comp
nitric-oxide reduc
hypothetical prote
hypothetical prote
conserved hypothet
flagellar protein
hypothetical prote
hypothetical prote
sensor protein chv
hypothetical prote
pilus assembly pro
hypothetical prote
ribosomal protein
acetyltransferase,
TATA-binding trans
probable membrane
hypothetical cytos
conserved hypothet
transcription regu
transcription regu
ORF13 - Agrobacter
chemotaxis protein
Spi20 env protein
hypothetical prote
oncofetal protein
hypothetical prote
probable phosphos
probable transcrip
acetoacetate decar
hypothetical prote
capsular polysacch
purine nucleotide
phosphoprotein pho
conserved hypothet
hypothetical prote
probable integral
ABC transporter (A
minor tail protein
coproporphyrinogen
phosphodiesterase
conserved hypothet
conserved hypothet
hypothetical prote
conserved hypothet
hypothetical prote
unknown protein li
hypothetical prote
endopeptidase (EC
3alpha-hydroxyster
probable transcrip
hypothetical prote
probable oxidoredu
probable dehydroge

103	6	7.5	324	2	E91144	probable dehydroge	176	6	7.5	453	2	AG1267	ribonuclease G hom
104	6	7.5	324	2	JS0688	hypothetical 35k p	177	6	7.5	454	2	G72452	probable glucamate
105	6	7.5	325	2	A10445	probable zinc-bind	178	6	7.5	461	2	AB1649	conserved hypot het
106	6	7.5	325	2	C36718	pyruvate dehydroge	179	6	7.5	462	2	S52528	UAI1 protein - yea
107	6	7.5	326	2	T19451	hypothetical prote	180	6	7.5	473	2	T29622	hypothetical prote
108	6	7.5	326	2	D82374	zinc-binding alcoh	181	6	7.5	474	2	F83550	serine proteinase
109	6	7.5	327	2	G83921	hypothetical prote	182	6	7.5	481	2	T01850	UTP-glucose glucos
110	6	7.5	338	2	B69439	signal-transducin	183	6	7.5	482	2	T49079	serine-type carbox
111	6	7.5	344	2	S76268	probable UDP-3-O- [184	6	7.5	483	2	H90210	hypothetical prote
112	6	7.5	345	1	B46113	protein kinase (EC	185	6	7.5	487	2	T33192	hypothetical prote
113	6	7.5	348	2	B69790	hypothetical prote	186	6	7.5	488	2	T27532	hypothetical prote
114	6	7.5	348	2	S44628	f22b7.1 protein -	187	6	7.5	493	2	B97460	betaine aldehyde d
115	6	7.5	348	2	E69162	sulfate transport	188	6	7.5	493	2	A26278	betaine aldehyde d
116	6	7.5	355	2	T49753	related to feebly	189	6	7.5	494	2	B86671	lysine-tRNA ligase
117	6	7.5	357	2	T12464	hypothetical prote	190	6	7.5	495	2	C89778	hypothetical prote
118	6	7.5	365	2	PQ0839	envelope protein -	191	6	7.5	495	2	A75608	aldehyde dehydroge
119	6	7.5	365	2	PQ0840	envelope protein -	192	6	7.5	495	2	S55273	amine oxidase (fla
120	6	7.5	365	2	S43780	peridinin-chloroph	193	6	7.5	501	2	T31265	aldehyde dehydroge
121	6	7.5	365	2	PQ0838	envelope protein -	194	6	7.5	501	2	S66763	hypothetical prote
122	6	7.5	369	2	A96513	probable cyclin, 2	195	6	7.5	505	1	S71413	betaine-aldehyde d
123	6	7.5	371	2	T31874	hypothetical prote	196	6	7.5	521	1	A56968	phosphoprotein pho
124	6	7.5	372	2	H97277	glycosyltransferas	197	6	7.5	521	1	S35067	phosphoprotein pho
125	6	7.5	375	2	S64621	biotin synthase (E	198	6	7.5	521	2	A33257	phosphoprotein pho
126	6	7.5	375	2	T19038	hypothetical prote	199	6	7.5	521	2	A33264	phosphoprotein pho
127	6	7.5	375	2	T32251	hypothetical prote	200	6	7.5	522	1	TSBVSS	protein disulfide-
128	6	7.5	377	2	E83220	hypothetical prote	201	6	7.5	528	2	I48253	beta-N-acetylhexos
129	6	7.5	379	2	E72274	cystathionine gamm	202	6	7.5	529	1	AOHUBA	beta-N-acetylhexos
130	6	7.5	379	2	B69344	hypothetical prote	203	6	7.5	531	2	T49058	hypothetical prote
131	6	7.5	380	2	G64309	hypothetical prote	204	6	7.5	533	2	B84148	hypothetical prote
132	6	7.5	380	2	H75009	hypothetical prote	205	6	7.5	535	2	D84340	hypothetical prote
133	6	7.5	387	2	E83679	multidrug-efflux t	206	6	7.5	549	2	JC5926	secreted klocho pr
134	6	7.5	388	1	VCVGTB	coat protein - tom	207	6	7.5	549	2	S04845	ig heavy chain pre
135	6	7.5	389	2	T33340	hypothetical prote	208	6	7.5	553	2	H82189	iron-sulfur cluate
136	6	7.5	389	2	T27574	hypothetical prote	209	6	7.5	554	2	B72362	hydroxy-acid deh
137	6	7.5	392	1	H65004	hypothetical prote	210	6	7.5	557	2	AB0170	30S ribosomal prot
138	6	7.5	392	2	AG2377	phosphate-binding	211	6	7.5	561	2	T51417	protein kinase-lik
139	6	7.5	392	2	G85873	probable transport	212	6	7.5	570	2	JC5722	vacuolar protein s
140	6	7.5	392	2	F91029	probable transport	213	6	7.5	572	2	S73730	MG307 homolog H08
141	6	7.5	394	2	B84016	aryldialkylphospha	214	6	7.5	579	2	S51528	D-lactate dehydrog
142	6	7.5	395	2	H90421	hypothetical prote	215	6	7.5	584	2	S06318	endoplasmic reticu
143	6	7.5	397	2	G71031	probable DNA-direc	216	6	7.5	585	2	E97232	probable signal tr
144	6	7.5	398	2	E70113	acetyl-CoA C-acety	217	6	7.5	592	2	G35115	hypothetical prote
145	6	7.5	399	2	A75269	acetyl-CoA acetyl t	218	6	7.5	592	2	D75421	conserved hypot het
146	6	7.5	399	2	H84108	ABC transporter BH	219	6	7.5	599	2	E83241	hypothetical prote
147	6	7.5	400	2	T35019	beta-ketoadipyl-Co	220	6	7.5	607	2	F90413	AAA family ATPase
148	6	7.5	400	2	JC2473	doc2 protein - hum	221	6	7.5	612	2	E81287	probable sugar tra
149	6	7.5	403	2	C70815	probable beta-keto	222	6	7.5	625	2	F81287	probable sugar tra
150	6	7.5	403	2	E87179	probable beta-keto	223	6	7.5	629	2	E72297	methionine-tRNA li
151	6	7.5	403	2	T16242	hypothetical prote	224	6	7.5	631	2	JC5803	ring finger protei
152	6	7.5	404	2	T35428	probable acetyl co	225	6	7.5	632	2	UC7155	brain finger prote
153	6	7.5	404	2	T35256	probable thiolase	226	6	7.5	632	2	T48316	hypothetical prote
154	6	7.5	405	2	E95205	preproteins translo	227	6	7.5	638	1	ISMSER	protein disulfide-
155	6	7.5	409	2	C41872	groEL 3'-region hy	228	6	7.5	640	2	T45924	protein kinase-lik
156	6	7.5	411	2	AH0807	probable membrane	229	6	7.5	643	1	S32476	protein disulfide-
157	6	7.5	412	2	E88736	protein f33D4.6a [230	6	7.5	645	1	A23723	protein disulfide-
158	6	7.5	413	2	G82422	anaerobic glycerol	231	6	7.5	646	1	S16654	RNA-directed DNA p
159	6	7.5	414	1	D42594	N-carbamyl-L-amino	232	6	7.5	660	2	T28111	hypothetical prote
160	6	7.5	417	2	I84434	Rhesus-like protei	233	6	7.5	672	2	T32557	hypothetical prote
161	6	7.5	418	2	E91037	hypothetical prote	234	6	7.5	676	2	T40772	hypothetical prote
162	6	7.5	418	2	G85881	hypothetical prote	235	6	7.5	695	2	S49163	transferrin precu
163	6	7.5	418	2	B65013	hypothetical prote	236	6	7.5	696	2	A90959	probable tail prot
164	6	7.5	420	2	T08005	flavonol 3-O-gluc	237	6	7.5	696	2	C85807	hypothetical prote
165	6	7.5	422	2	AB1154	D-tagatose-bisphos	238	6	7.5	708	2	JC4384	gelatinase B (EC 3
166	6	7.5	422	2	C82666	conserved hypot het	239	6	7.5	708	2	S62907	gelatinase B (EC 3
167	6	7.5	428	2	D81255	histidinol dehydro	240	6	7.5	713	2	JC2522	nuclear autoantige
168	6	7.5	429	2	S75245	N-acetylmornithine	241	6	7.5	715	1	DEECFS	formate dehydrogen
169	6	7.5	429	2	G37114	hypothetical prote	242	6	7.5	715	2	JC4560	methyilmalonyl-CoA
170	6	7.5	433	2	S73790	probable serine/th	243	6	7.5	715	2	E91261	formate dehydrogen
171	6	7.5	435	2	F96939	TPR repeats contai	244	6	7.5	715	2	A86102	formate dehydrogen
172	6	7.5	438	2	G87290	major facilitator	245	6	7.5	715	2	AB1021	formate dehydrogen
173	6	7.5	439	2	C64401	hypothetical prote	246	6	7.5	720	2	T47221	replication licens
174	6	7.5	448	2	B71319	probable acetate k	247	6	7.5	724	1	QOBBE15	U189 protein - hum
175	6	7.5	448	2	S39348	26S ATP/ubiquitin-	248	6	7.5	728	2	T26607	hypothetical prote

249	6	7.5	729	1	A34796	kinesin-related pr	322	6	7.5	1774	2	S13178	6-methylsalicylic
250	6	7.5	729	2	B70333	hypothetical prote	323	6	7.5	1802	2	S52611	TyB protein - Yeas
251	6	7.5	729	3	F97321	membrane export pr	324	6	7.5	1803	2	S56894	TyB protein - Yeas
252	6	7.5	734	2	AF2001	hypothetical prote	325	6	7.5	1820	2	T19430	hypothetical prote
253	6	7.5	736	2	H75460	conserved hypotet	326	6	7.5	1944	2	T40065	tRNA-splicing endo
254	6	7.5	752	2	F81203	maltose phosphoryl	327	6	7.5	2238	1	RRVUBY	genome polyprotein
255	6	7.5	752	2	C81781	probable maltose p	328	6	7.5	2326	2	T29140	hypothetical prote
256	6	7.5	756	2	S40305	multicystatin - po	329	6	7.5	2802	2	F97686	cyclic beta-(1-2)
257	6	7.5	758	2	E83884	hypothetical prote	330	6	7.5	2831	2	AI2911	beta (1->2) glucan
258	6	7.5	774	1	P31V50	RNA-directed RNA p	331	6	7.5	3110	2	AC0116	probable virulence
259	6	7.5	774	2	S13670	basic polymerase 2	332	6	7.5	3394	2	T18501	hypothetical prote
260	6	7.5	778	2	E70320	polyribonucleotide	333	6	7.5	4377	2	A55575	ankyrin 3, long ep
261	6	7.5	778	2	D85055	probable polyprote	334	6	7.5	4558	2	C82199	RTX toxin RtxA VCI
262	6	7.5	790	2	T49414	related to ahmp1 p	335	5	6.2	33	2	A61232	relaxin - oranguta
263	6	7.5	796	2	T19683	hypothetical prote	336	5	6.2	39	2	S42781	pregnancy-associat
264	6	7.5	821	1	S73253	endopeptidase Clp	337	5	6.2	39	2	S23804	homeotic protein 1
265	6	7.5	832	2	B96702	hypothetical prote	338	5	6.2	39	2	S23803	homeotic protein 1
266	6	7.5	853	2	A28668	DNA mismatch repai	339	5	6.2	40	2	H81591	E2 glycoprotein -
267	6	7.5	855	2	AH0853	probable permease,	340	5	6.2	40	2	PQ0560	hypothetical prote
268	6	7.5	863	2	G96964	env protein gp120(341	5	6.2	41	2	PQ0561	nonstructural prot
269	6	7.5	869	2	A47665	S-layer protein pr	342	5	6.2	41	2	PQ0562	nonstructural prot
270	6	7.5	874	2	JC4930	env polyprotein pr	343	5	6.2	41	2	PQ0563	nonstructural prot
271	6	7.5	880	1	VCLJ52	env polyprotein pr	344	5	6.2	41	2	PQ0564	nonstructural prot
272	6	7.5	881	2	S03068	26S proteasome reg	345	5	6.2	41	2	PQ0565	nonstructural prot
273	6	7.5	887	2	TS2488	env polyprotein -	346	5	6.2	46	2	C83437	hypothetical prote
274	6	7.5	889	1	VCLJG5	hypothetical prote	347	5	6.2	49	2	T37008	hypothetical prote
275	6	7.5	899	2	T42976	hypothetical prote	348	5	6.2	55	2	B46485	Ig epsilon chain C
276	6	7.5	904	2	T03806	hypothetical prote	349	5	6.2	56	2	B89903	hypothetical prote
277	6	7.5	920	2	S53961	hypothetical prote	350	5	6.2	57	2	G35057	MHC class II histo
278	6	7.5	932	2	S65214	probable alpha/gam	351	5	6.2	57	2	C35058	probable collagen
279	6	7.5	940	2	H86420	probable receptor-	352	5	6.2	58	2	B43928	integrase - Staphy
280	6	7.5	945	2	F83925	oxoglutarate dehyd	353	5	6.2	59	1	R8BPL5	probable gas vesic
281	6	7.5	947	2	T20156	hypothetical prote	354	5	6.2	60	2	T34737	hypothetical prote
282	6	7.5	954	2	S57108	hypothetical prote	355	5	6.2	61	2	D97920	hypothetical prote
283	6	7.5	967	2	S28428	phosphoenolpyruvat	356	5	6.2	63	1	H64095	carbon storage reg
284	6	7.5	1003	1	PRVZAM	spheroidin precurs	357	5	6.2	63	1	FECLC	ferredoxin [4Fe-4S
285	6	7.5	1005	2	F90099	hypothetical prote	358	5	6.2	63	2	C59147	conotoxin Gm5.1 pr
286	6	7.5	1012	2	JC5925	membrane klotho pr	359	5	6.2	64	2	H91000	hypothetical prote
287	6	7.5	1031	2	A29839	RAD2 protein - yea	360	5	6.2	64	2	B90779	hypothetical prote
288	6	7.5	1091	2	F83928	hypothetical prote	361	5	6.2	65	1	A22810	small acid-soluble
289	6	7.5	1104	1	A36866	microbial collagen	362	5	6.2	66	2	B87379	ribosomal protein H
290	6	7.5	1108	2	T31335	hgIC protein - Ana	363	5	6.2	66	2	S14932	ribosomal protein
291	6	7.5	1109	2	AC2475	heterocyst glycoli	364	5	6.2	67	2	B71666	proteinase A inhib
292	6	7.5	1137	2	G84581	copia-like retroel	365	5	6.2	68	1	IABY3	hypothetical prote
293	6	7.5	1146	2	B70376	reverse gyrase - A	366	5	6.2	68	1	QOHSNB	hypothetical prote
294	6	7.5	1166	2	C84532	copia-like retroel	367	5	6.2	68	2	B84267	hypothetical prote
295	6	7.5	1175	2	S51005	protein-tyrosine-p	368	5	6.2	68	2	C71970	hypothetical prote
296	6	7.5	1181	2	T19736	hypothetical prote	369	5	6.2	69	2	S14074	hypothetical prote
297	6	7.5	1187	1	JC4155	probable helicase	371	5	6.2	70	2	S34217	acclimation protei
298	6	7.5	1189	1	JC2366	probable membrane	372	5	6.2	71	2	T03353	gene e14 protein -
299	6	7.5	1218	2	T30447	hypothetical prote	373	5	6.2	71	2	D82686	hypothetical prote
300	6	7.5	1228	2	S59681	probable lipoprote	374	5	6.2	73	2	G89307	protein TolC3.2 [i
301	6	7.5	1235	2	C69165	transferrin-like p	375	5	6.2	75	1	BVECRY	tray protein - Bac
302	6	7.5	1244	2	S73731	hypothetical prote	376	5	6.2	75	2	A13305	hypothetical prote
303	6	7.5	1274	2	T10729	hypothetical prote	377	5	6.2	76	2	S55527	H+-exporting ATPas
304	6	7.5	1308	2	T05178	hypothetical prote	378	5	6.2	76	2	E59472	conserved hypotet
305	6	7.5	1322	2	B71440	probable retroelem	379	5	6.2	76	2	S69162	serine proteinase
306	6	7.5	1333	2	E84601	copia-like polypro	380	5	6.2	76	2	S69163	hypothetical prote
307	6	7.5	1363	2	T47492	hypothetical glyci	381	5	6.2	77	2	H96955	CT659 hypotetical
308	6	7.5	1381	2	E70806	natural killer cel	382	5	6.2	78	2	B86580	conserved hypotet
309	6	7.5	1402	1	A47328	TyB protein - yeas	383	5	6.2	78	2	H72043	hypothetical prote
310	6	7.5	1465	2	S31262	DNA-directed DNA p	384	5	6.2	78	2	B75193	proteinase A inhib
311	6	7.5	1467	2	PC1253	synaptonemal compl	385	5	6.2	79	2	AB1238	B. subtilis ynfef p
312	6	7.5	1468	2	S58250	natural killer cel	386	5	6.2	79	2	AG1600	B. subtilis ynfef p
313	6	7.5	1505	2	T31418	mitotic spindle pr	387	5	6.2	79	2	F72354	hypothetical prote
314	6	7.5	1507	2	B47328	peroxisome prolif	388	5	6.2	79	2	B69874	hypothetical prote
315	6	7.5	1513	2	T02885	hypothetical prote	389	5	6.2	79	2	T02461	hypothetical prote
316	6	7.5	1560	2	T25421	hypothetical prote	390	5	6.2	79	2	T04983	hypothetical prote
317	6	7.5	1653	2	T14758	protein kinase GCN	391	5	6.2	80	2	F75598	hypothetical prote
318	6	7.5	1657	2	T25421	hypothetical prote	392	5	6.2	81	2	S38696	class II histocomp
319	6	7.5	1659	1	OKBYN2	zinc finger protei	393	5	6.2	81	2	T30937	reverse transcript
320	6	7.5	1663	2	T28923		394	5	6.2	81	2	T30937	
321	6	7.5	1706	2	I84499								

395	5	6.2	81	2	F75409	hypothetical prote	468	5	6.2	100	2	AD0434	probable anti-sigm
396	5	6.2	81	2	T31199	hypothetical prote	469	5	6.2	101	2	A82058	ribosomal protein
397	5	6.2	82	2	S06772	ribulose-bisphosph	470	5	6.2	101	2	A27819	anti-lipopolysacch
398	5	6.2	82	2	I61834	gene MHC DQ-beta 1	471	5	6.2	101	2	AB0506	probable transcrip
399	5	6.2	82	2	I61811	gene MHC DQ-beta 1	472	5	6.2	101	2	B91275	hypothetical prote
400	5	6.2	82	2	I61810	gene MHC DQ-beta 1	473	5	6.2	101	2	B86116	hypothetical prote
401	5	6.2	82	2	I61815	gene MHC DQ-beta 1	474	5	6.2	101	2	S56419	hypothetical 10.9K
402	5	6.2	82	2	I36924	gene MHC DQ-beta 1	475	5	6.2	102	2	H71221	hypothetical prote
403	5	6.2	83	2	S38693	class II histocomp	476	5	6.2	102	2	S69741	hypothetical prote
404	5	6.2	83	2	S38690	class II histocomp	477	5	6.2	102	2	B75020	hypothetical prote
405	5	6.2	83	2	S38698	class II histocomp	478	5	6.2	102	2	C86654	hypothetical prote
406	5	6.2	83	2	S38699	class II histocomp	479	5	6.2	102	2	F71206	hypothetical prote
407	5	6.2	83	2	S38694	class II histocomp	480	5	6.2	103	2	B25913	Ig heavy chain pre
408	5	6.2	83	2	G88921	ribosomal protein	481	5	6.2	103	2	B87522	conserved hypotet
409	5	6.2	84	2	B98922	hypothetical prote	482	5	6.2	104	1	H64327	conserved hypotet
410	5	6.2	85	2	AC1066	hypothetical prote	483	5	6.2	104	2	H75140	hypothetical prote
411	5	6.2	85	2	AH1010	conserved hypotet	484	5	6.2	104	2	H82793	transposase Orfa X
412	5	6.2	85	2	S31018	gene 73 protein -	485	5	6.2	104	2	A90174	hypothetical prote
413	5	6.2	86	1	Q1BP67	gene 1.6 protein -	486	5	6.2	105	2	A97683	hypothetical prote
414	5	6.2	86	2	C83838	hypothetical prote	487	5	6.2	105	2	A12907	hypothetical prote
415	5	6.2	87	2	B32360	shiga-like toxin I	488	5	6.2	105	2	G71102	hypothetical prote
416	5	6.2	87	2	B45823	shiga-like toxin I	489	5	6.2	105	2	S76770	hypothetical prote
417	5	6.2	87	2	I83832	shiga-like toxin I	490	5	6.2	105	2	T32799	hypothetical prote
418	5	6.2	87	2	B53890	verocytotoxin B ch	491	5	6.2	106	2	S22067	hypothetical prote
419	5	6.2	87	2	I76712	variant shiga-like	492	5	6.2	106	2	F69184	hypothetical prote
420	5	6.2	87	2	B84034	PTS system, histid	493	5	6.2	106	2	S46028	hypothetical prote
421	5	6.2	88	2	A69341	cobalt transport p	494	5	6.2	106	2	AD2795	conserved hypotet
422	5	6.2	88	2	A57711	diazepam-binding i	495	5	6.2	106	2	D97574	hypothetical prote
423	5	6.2	88	2	A47760	retrovirus-related	496	5	6.2	107	2	T02814	thioredoxin TRXRp1
424	5	6.2	88	2	D64562	hypothetical prote	497	5	6.2	107	2	A27646	Ig heavy chain V r
425	5	6.2	88	2	F97888	degenerative trans	498	5	6.2	107	2	D71678	hypothetical prote
426	5	6.2	89	1	S42609	shiga-like toxin -	499	5	6.2	107	2	H86788	hypothetical prote
427	5	6.2	89	1	JN0726	Shiga-like toxin I	500	5	6.2	107	2	T51193	small zinc finger-
428	5	6.2	89	1	XVBEP9	Shiga-like toxin c	501	5	6.2	107	2	S07818	homeotic protein H
429	5	6.2	89	1	XVEBBD	Shigella toxin cha	502	5	6.2	108	1	PVNESB	parvalbumin beta -
430	5	6.2	89	2	S58344	Shiga-like toxin I	503	5	6.2	109	1	W7WL39	E7 protein - human
431	5	6.2	89	2	F90779	Shiga toxin 2 subu	504	5	6.2	109	2	D47056	cur regulatory pro
432	5	6.2	89	2	H85640	Shiga toxin 2 subu	505	5	6.2	109	2	AF0940	conserved hypotet
433	5	6.2	89	2	E91000	Shiga toxin 1 subu	506	5	6.2	109	2	C97849	hypothetical prote
434	5	6.2	89	2	G85845	Shiga toxin i subu	507	5	6.2	110	2	B72496	hypothetical prote
435	5	6.2	89	2	A60279	shiga-like toxin I	508	5	6.2	110	2	A96907	hypothetical prote
436	5	6.2	89	2	I69156	shiga-like toxin I	509	5	6.2	110	2	S72390	hypothetical prote
437	5	6.2	89	2	S01033	shiga-like toxin I	510	5	6.2	112	2	E97732	ferredoxin (import
438	5	6.2	89	2	B53887	Shiga-like toxin I	511	5	6.2	112	2	A71731	ferredoxin [2Fe-2S
439	5	6.2	89	2	F97816	SOS ribosomal prot	512	5	6.2	112	2	B47033	AadA2 - Pseudomona
440	5	6.2	89	2	A69513	hypothetical prote	513	5	6.2	112	2	G83169	conserved hypotet
441	5	6.2	89	2	B49754	hypothetical prote	514	5	6.2	113	1	HVMSAM	Ig heavy chain V r
442	5	6.2	89	2	T51191	small zinc finger-	515	5	6.2	113	2	G87110	SOS ribosomal prot
443	5	6.2	89	2	T51192	small zinc finger-	516	5	6.2	113	2	C70927	probable ribosomal
444	5	6.2	90	2	A13583	hypothetical prote	517	5	6.2	113	2	JC2026	cell specific 10K
445	5	6.2	91	2	B82893	hypothetical prote	518	5	6.2	114	2	B97117	ribosomal protein
446	5	6.2	91	2	T42310	hypothetical prote	519	5	6.2	114	2	AC1298	ribosomal protein
447	5	6.2	92	2	G82236	glutaredoxin [simi	520	5	6.2	114	2	F83959	ribosomal protein
448	5	6.2	92	2	F69522	conserved hypotet	521	5	6.2	114	2	AC1670	ribosomal protein
449	5	6.2	92	2	B71637	hypothetical prote	522	5	6.2	114	2	A13284	hypothetical prote
450	5	6.2	93	2	A97190	hypothetical prote	523	5	6.2	115	1	A46279	guanylin precursor
451	5	6.2	93	2	A95377	hypothetical prote	524	5	6.2	115	2	S53841	hypothetical prote
452	5	6.2	94	2	I48172	glial fibrillary a	525	5	6.2	115	2	T34723	hypothetical prote
453	5	6.2	94	2	D64679	hypothetical prote	526	5	6.2	115	2	D95035	hypothetical prote
454	5	6.2	95	2	AC1040	hypothetical prote	527	5	6.2	115	2	A97911	transposase (impor
455	5	6.2	96	1	UGMS	uterooglobin precu	528	5	6.2	115	2	B97962	transposase (impor
456	5	6.2	96	2	A52274	phosphodiesterase	529	5	6.2	115	2	F97873	transposase (impor
457	5	6.2	96	2	A36581	polychlorinated bi	530	5	6.2	115	2	B98100	transposase (impor
458	5	6.2	97	2	T44733	hypothetical prote	531	5	6.2	115	2	T36886	hypothetical prote
459	5	6.2	97	2	T45416	hypothetical prote	532	5	6.2	116	1	A45434	ribosomal protein
460	5	6.2	98	1	B64377	conserved hypotet	533	5	6.2	116	2	S26328	Ig heavy chain V r
461	5	6.2	98	2	C86517	hypothetical prote	534	5	6.2	116	2	S78140	ribosomal protein
462	5	6.2	98	2	T22503	hypothetical prote	535	5	6.2	116	2	D89857	SOS ribosomal prot
463	5	6.2	98	2	T24286	hypothetical prote	536	5	6.2	116	2	T34780	ribosomal protein
464	5	6.2	98	2	D72106	hypothetical prote	537	5	6.2	116	2	JC5188	sporulation-specif
465	5	6.2	99	1	Q8BPB7	host specificity p	538	5	6.2	116	2	G64433	hypothetical prote
466	5	6.2	99	2	B37775	phoR protein - Pse	539	5	6.2	116	2	A72272	conserved hypotet
467	5	6.2	99	2	C70941	hypothetical prote	540	5	6.2	116	2	T03489	conserved hypotet

541	5	6.2	116	2	AH1174	B. subtilis YqkP	614	5	6.2	133	2	T36401	hypothetical prote
542	5	6.2	117	2	AC2149	hypothetical prote	615	5	6.2	133	2	E82390	hypothetical prote
543	5	6.2	117	2	A72286	hypothetical prote	616	5	6.2	133	2	T49231	hypothetical prote
544	5	6.2	117	2	C90437	conserved hypotet	617	5	6.2	133	2	AE1435	PTS system, fructo
545	5	6.2	118	2	E69696	ribosomal protein	618	5	6.2	134	2	G89937	cytidine deaminase
546	5	6.2	118	2	E97289	uncharacterized co	619	5	6.2	134	2	D64381	conserved hypotet
547	5	6.2	118	2	D64347	hypothetical prote	620	5	6.2	134	2	G72465	hypothetical prote
548	5	6.2	118	2	C84181	hypothetical prote	621	5	6.2	134	2	AB2765	conserved hypotet
549	5	6.2	118	2	AH0986	phage-like lysozym	622	5	6.2	134	2	AB0784	conserved hypotet
550	5	6.2	119	2	S47942	ribosomal protein	623	5	6.2	134	2	T25527	hypothetical prote
551	5	6.2	119	2	S50634	ribosomal protein	624	5	6.2	135	2	PN0494	NAD ADP-ribosyltra
552	5	6.2	120	2	B72346	chemotaxis respons	625	5	6.2	135	2	S60977	probable membrane
553	5	6.2	120	2	F86871	hypothetical prote	626	5	6.2	135	2	S55647	hypothetical prote
554	5	6.2	120	2	JC4754	hypothetical 13.6k	627	5	6.2	135	2	D89805	hypothetical prote
555	5	6.2	120	2	G86654	transcription regu	628	5	6.2	135	2	A13164	hypothetical prote
556	5	6.2	121	1	PSGNAM	phospholipase A2 h	629	5	6.2	135	2	G96691	hypothetical prote
557	5	6.2	121	2	D86783	50S ribosomal prot	630	5	6.2	136	2	PN0529	G protein-coupled
558	5	6.2	121	2	G81121	hypothetical prote	631	5	6.2	136	2	F84234	hypothetical prote
559	5	6.2	121	2	G64315	hypothetical prote	632	5	6.2	137	2	S68429	myotoxin precursor
560	5	6.2	122	2	G69532	conserved hypotet	633	5	6.2	137	2	C70461	hypothetical prote
561	5	6.2	122	2	A41810	transcription fact	634	5	6.2	137	2	A69127	hypothetical prote
562	5	6.2	122	2	F98001	transposase [impor	635	5	6.2	137	2	F69507	c-myc binding prot
563	5	6.2	122	2	AG0221	conserved hypotet	636	5	6.2	137	2	B72720	hypothetical prote
564	5	6.2	123	1	RSRT35	ribosomal protein	637	5	6.2	138	2	D83824	transcription regu
565	5	6.2	123	2	E97918	conserved hypotet	638	5	6.2	138	2	A95133	IS630-Spn1, transp
566	5	6.2	123	2	F95047	conserved hypotet	639	5	6.2	138	2	A97032	transcription regu
567	5	6.2	123	2	H72698	hypothetical prote	640	5	6.2	139	1	MN21C	nonstructural prot
568	5	6.2	123	2	A69884	cell wall protein	641	5	6.2	139	2	T36603	hypothetical prote
569	5	6.2	123	2	T00711	hypothetical prote	642	5	6.2	139	2	C83597	hypothetical prote
570	5	6.2	124	1	RSRRA	ribosomal protein	643	5	6.2	139	2	AH0372	probable exported
571	5	6.2	124	2	E70148	ribosomal protein	644	5	6.2	140	2	C97710	nucleoside-diphosp
572	5	6.2	124	2	I40348	ribosomal protein	645	5	6.2	140	2	T15738	hypothetical prote
573	5	6.2	124	2	I40350	ribosomal protein	646	5	6.2	141	2	A11105	ribosomal protein
574	5	6.2	124	2	AF3345	LSU ribosomal prot	647	5	6.2	141	2	A11467	ribosomal protein
575	5	6.2	125	2	D97595	ribosomal protein	648	5	6.2	141	2	AE1255	transcription regu
576	5	6.2	125	2	AC2817	50S ribosomal prote	649	5	6.2	141	2	T46654	transcription regu
577	5	6.2	125	2	S35629	hypothetical prote	650	5	6.2	141	2	AB1618	transcription regu
578	5	6.2	125	2	D34829	sigma lbnS protein	651	5	6.2	141	2	B82779	hypothetical prote
579	5	6.2	126	2	S42643	ubiquitin / riboso	652	5	6.2	141	2	F71176	hypothetical prote
580	5	6.2	126	2	S52355	copper resistance	653	5	6.2	143	1	FQBOGM	granulocyte-macrop
581	5	6.2	126	2	A84567	hypothetical prote	654	5	6.2	143	2	AC2693	transcription regu
582	5	6.2	127	1	I53651	hydrophilic protei	655	5	6.2	143	2	E69065	molybdopterin bios
583	5	6.2	127	2	I46269	granulocyte-macrop	656	5	6.2	143	2	S43071	hypothetical prote
584	5	6.2	127	2	H87310	ribosomal protein	657	5	6.2	143	2	T45444	hypothetical prote
585	5	6.2	127	2	A58933	ribosomal protein	658	5	6.2	143	2	D82797	phage-related repr
586	5	6.2	127	2	H90460	conserved hypotet	659	5	6.2	144	1	A61632	granulocyte-macrop
587	5	6.2	127	2	T07301	cell division topo	660	5	6.2	144	2	JH0469	granulocyte-macrop
588	5	6.2	127	2	E83500	hypothetical prote	661	5	6.2	144	2	F64094	ribosomal protein
589	5	6.2	128	1	RGSBI	regulatory protein	662	5	6.2	144	2	C70455	hypothetical prote
590	5	6.2	128	2	B28183	beta-lactamase rep	663	5	6.2	144	2	F75044	hypothetical prote
591	5	6.2	128	2	AE0528	conserved hypotet	664	5	6.2	144	2	AG2568	hypothetical prote
592	5	6.2	128	2	S45230	yaeh protein - Esc	665	5	6.2	144	2	T41544	hypothetical prote
593	5	6.2	128	2	G85500	probable structura	666	5	6.2	145	1	B44798	phosphotransferase
594	5	6.2	128	2	G90649	probable structura	667	5	6.2	145	2	S06307	T-cell receptor ga
595	5	6.2	128	2	H69970	conserved hypotet	668	5	6.2	145	2	B83607	hypothetical prote
596	5	6.2	128	2	F72661	hypothetical prote	669	5	6.2	145	2	D90283	hypothetical prote
597	5	6.2	128	2	I51295	vascular endotheli	670	5	6.2	146	1	C64085	hypothetical prote
598	5	6.2	129	2	B71350	probable ribosomal	671	5	6.2	146	1	T46729	citrate (pro-3S)-1
599	5	6.2	129	2	AE2508	conserved hypotet	672	5	6.2	146	1	G3ZLB	bacterial hemoglob
600	5	6.2	129	2	AE0206	conserved hypotet	673	5	6.2	146	2	G97474	probable asnc-famI
601	5	6.2	130	2	T48771	hypothetical prote	674	5	6.2	146	2	F75280	transglycosylase a
602	5	6.2	130	2	S55141	hypothetical prote	675	5	6.2	146	2	G90201	conserved hypotet
603	5	6.2	130	2	AC2314	hypothetical prote	676	5	6.2	146	2	B29701	hemoglobin beta ch
604	5	6.2	131	2	S08328	Ig heavy chain V r	677	5	6.2	146	2	F83274	conserved hypotet
605	5	6.2	131	2	A81312	hypothetical prote	678	5	6.2	146	2	S60748	phaeoelotoxin synt
606	5	6.2	131	2	G82684	hypothetical prote	679	5	6.2	147	2	A70462	ribosomal protein
607	5	6.2	131	2	A11964	hypothetical prote	680	5	6.2	147	2	AD3081	hypothetical prote
608	5	6.2	132	1	PWPFEL	H+-transporting tw	681	5	6.2	147	2	D98205	hypothetical prote
609	5	6.2	132	2	AB3272	succinate dehydrog	682	5	6.2	147	2	S75758	hypothetical prote
610	5	6.2	132	2	F75510	hypothetical prote	683	5	6.2	147	2	G87278	PTS system, IIA co
611	5	6.2	132	2	G75409	hypothetical prote	684	5	6.2	147	2	D64331	hypothetical prote
612	5	6.2	132	2	B64474	hypothetical prote	685	5	6.2	148	2	A82591	conserved hypotet
613	5	6.2	133	2	JC2003	NADH ubiquinone ox	686	5	6.2	148	2	G82489	hypothetical prote

687	5	6.2	148	2	S73004	hypothetical prote	760	5	6.2	163	2	D64427	hypothetical prote
688	5	6.2	148	2	A71130	hypothetical prote	761	5	6.2	164	2	S60130	H+-exporting ATPas
689	5	6.2	148	2	A71130	hypothetical prote	762	5	6.2	164	2	D84152	hypothetical prote
690	5	6.2	149	1	RSNKE	ribosomal protein	763	5	6.2	164	2	E97061	integrase XerD fam
691	5	6.2	149	2	A90133	translation factor	764	5	6.2	164	2	H97702	H+-transporting tw
692	5	6.2	150	2	S39980	hemoglobin II alph	765	5	6.2	165	1	A40814	H+-exporting ATPas
693	5	6.2	150	2	A87344	chemotaxis protein	766	5	6.2	165	1	RMEC18	primosomal operon
694	5	6.2	150	2	D81314	small protein B ho	767	5	6.2	166	2	S60132	H+-exporting ATPas
695	5	6.2	150	2	S48568	hypothetical prote	768	5	6.2	166	2	S60132	H+-exporting ATPas
696	5	6.2	150	2	S36996	transposase (clone	769	5	6.2	165	2	C86135	probable glycoprot
697	5	6.2	150	2	D97188	uncharacterized pr	770	5	6.2	165	2	H91293	probable glycoprot
698	5	6.2	150	2	G95348	nitric-oxide reduc	771	5	6.2	165	2	C95309	probable ABC sugar
699	5	6.2	150	2	AG3456	coXG protein limpo	772	5	6.2	166	1	B35703	cofilin - chicken
700	5	6.2	151	2	I53929	epididymal secreto	773	5	6.2	166	2	S60131	H+-exporting ATPas
701	5	6.2	151	2	I38365	epididymal secreto	774	5	6.2	166	2	S42783	relaxin 1 precursor
702	5	6.2	151	2	AZ2017	cell wall-binding	775	5	6.2	166	2	S42786	relaxin 2 precursor
703	5	6.2	151	2	D81713	small protein B TC	776	5	6.2	166	2	A53812	cofilin, muscle -
704	5	6.2	151	2	AC2084	phosphonate metabo	777	5	6.2	166	2	E90434	conserved hypothet
705	5	6.2	151	2	H97545	hypothetical prote	778	5	6.2	166	2	A75367	heat shock protein
706	5	6.2	151	2	S65893	overoxidase - se	779	5	6.2	166	2	J70358	hypothetical prote
707	5	6.2	151	2	A83263	thiol:disulfide in	780	5	6.2	166	2	B81435	hypothetical prote
708	5	6.2	152	2	S21826	T-cell receptor be	781	5	6.2	167	2	F97238	probable acetyltra
709	5	6.2	152	2	AZ2961	transcription regu	782	5	6.2	167	2	B89970	signal transductio
710	5	6.2	152	2	AH0368	conserved hypothet	783	5	6.2	168	2	S36294	T-cell receptor ga
711	5	6.2	152	2	T33169	hypothetical prote	784	5	6.2	168	2	F96762	hypothetical prote
712	5	6.2	152	2	H95386	protein (imported	785	5	6.2	169	2	S73136	allophycocyanin be
713	5	6.2	153	2	S66503	hemoglobin I alpha	786	5	6.2	169	2	C75595	hypothetical prote
714	5	6.2	153	2	F46882	ribosomal protein	787	5	6.2	169	2	T38765	probable VBPI/PACI
715	5	6.2	153	2	A1070	probable secreted	788	5	6.2	169	2	D70226	hypothetical prote
716	5	6.2	154	1	F65230	probable PTS syate	789	5	6.2	170	2	T11964	allophycocyanin be
717	5	6.2	154	1	A70792	hypothetical prote	790	5	6.2	170	2	S18064	peroxidase (EC 1.1
718	5	6.2	154	2	T03584	plastocyanin precu	791	5	6.2	170	2	I40045	invasion-associate
719	5	6.2	154	2	A11051	protein-Npi-phosph	792	5	6.2	170	2	T37792	hypothetical prote
720	5	6.2	154	2	C86116	probable PTS syate	793	5	6.2	170	2	B95169	conserved domain p
721	5	6.2	154	2	C91275	probable PTS syate	794	5	6.2	170	2	C98035	hypothetical prote
722	5	6.2	154	2	S76191	hypothetical prote	795	5	6.2	171	2	T49493	hypothetical prote
723	5	6.2	154	2	T34818	hypothetical prote	796	5	6.2	171	2	B96934	molybdopterin bios
724	5	6.2	154	2	G84396	hypothetical prote	797	5	6.2	171	2	A10943	probable membrane
725	5	6.2	154	2	T36601	probable transcrip	798	5	6.2	171	2	T06438	homeobox-leucine z
726	5	6.2	154	2	A62607	transposase homolo	799	5	6.2	172	2	A83628	hypothetical prote
727	5	6.2	154	2	B71149	hypothetical prote	800	5	6.2	172	2	H90003	ATP synthase B cha
728	5	6.2	155	2	T41746	ribosomal protein	801	5	6.2	173	2	T26299	hypothetical prote
729	5	6.2	155	2	B86840	ribosomal protein	802	5	6.2	173	2	G64495	hypothetical prote
730	5	6.2	155	2	D93098	conserved hypothet	803	5	6.2	173	2	T21815	hypothetical prote
731	5	6.2	155	2	A11883	hypothetical prote	804	5	6.2	174	2	T12008	NADH2 dehydrogenas
732	5	6.2	155	2	T21364	hypothetical prote	805	5	6.2	174	2	B69979	hypothetical prote
733	5	6.2	156	2	T47739	hypothetical prote	806	5	6.2	174	2	F64413	probable chorismat
734	5	6.2	156	2	E69196	conserved hypothet	807	5	6.2	174	2	A49616	hypothetical prote
735	5	6.2	157	2	C84271	hypothetical prote	808	5	6.2	175	2	A49616	pancreatitis-assoc
736	5	6.2	157	2	A71137	hypothetical prote	809	5	6.2	175	2	S45905	hypothetical prote
737	5	6.2	158	2	S47140	pathogenesis-relat	810	5	6.2	175	2	A95058	conserved domain p
738	5	6.2	158	2	D70755	hypothetical prote	811	5	6.2	175	2	B97927	hypothetical prote
739	5	6.2	158	2	E90198	hypothetical prote	812	5	6.2	176	2	B70429	conserved hypothet
740	5	6.2	159	2	C95064	conserved hypothet	813	5	6.2	176	2	C82797	hypothetical prote
741	5	6.2	159	2	E97931	conserved hypothet	814	5	6.2	176	2	F95863	probable cytochrom
742	5	6.2	159	2	T48837	hypothetical prote	815	5	6.2	177	2	F84782	60S ribosomal prot
743	5	6.2	159	2	AZ2547	hypothetical prote	816	5	6.2	177	2	C69476	hypothetical prote
744	5	6.2	160	1	C70315	2-amino-4-hydroxy-	817	5	6.2	177	2	T16280	hypothetical prote
745	5	6.2	160	2	C82875	ribosomal protein	818	5	6.2	177	2	T24466	hypothetical prote
746	5	6.2	161	1	APAIB	allophycocyanin be	819	5	6.2	177	2	F64645	conjugal transfer
747	5	6.2	161	2	B27873	allophycocyanin be	820	5	6.2	177	2	B97201	hypothetical prote
748	5	6.2	161	2	S33624	allophycocyanin be	821	5	6.2	178	2	C64168	hypothetical prote
749	5	6.2	161	2	B44462	allophycocyanin be	822	5	6.2	178	2	A64336	hypothetical prote
750	5	6.2	161	2	S73630	ribosomal protein	823	5	6.2	178	2	S36289	hypothetical prote
751	5	6.2	161	2	D82042	transcription elon	824	5	6.2	179	2	A33164	T-cell receptor ga
752	5	6.2	161	2	C36810	hypothetical prote	825	5	6.2	179	2	A33164	hypothetical prote
753	5	6.2	161	2	F69418	ISORF2 homolog ISA	826	5	6.2	179	2	C96853	hypothetical prote
754	5	6.2	162	2	C31385	allophycocyanin 1	827	5	6.2	179	2	H85429	ribosomal protein
755	5	6.2	162	2	A11809	allophycocyanin be	828	5	6.2	179	2	T26744	hypothetical prote
756	5	6.2	162	2	T06178	ribosomal protein	829	5	6.2	180	2	E97355	hypothetical prote
757	5	6.2	162	2	T00651	hypothetical prote	830	5	6.2	180	2	H81343	molybdopterin bios
758	5	6.2	162	2	AB1842	hypothetical prote	831	5	6.2	181	1	RKRPF1	ribulose-bisphosph
759	5	6.2	163	2	T47559	60S ribosomal prot	832	5	6.2	181	1	RKRPS	ribulose-bisphosph

833	5	6.2	181	1	RKRVS	ribulose-bisphosph	906	5	6.2	193	2	G81433	hypothetical prote
834	5	6.2	181	1	B44057	early E3 20.3K gly	907	5	6.2	193	2	E87539	maf protein [impor
835	5	6.2	181	1	ERAD23	early E3 20.3K gly	908	5	6.2	193	2	A85658	robable tellurium
836	5	6.2	181	1	F44057	early E3 20.3K gly	909	5	6.2	193	2	G90797	probable tellurium
837	5	6.2	181	1	S37292	ribulose-bisphosph	910	5	6.2	193	2	T44907	hypothetical prote
838	5	6.2	181	2	S37575	ribulose-bisphosph	911	5	6.2	193	2	AD1221	two-component resp
839	5	6.2	181	2	A64393	hypothetical prote	912	5	6.2	193	2	AG1574	two-component resp
840	5	6.2	181	2	E70209	conserved hypothet	913	5	6.2	193	2	G64074	thymidine kinase (
841	5	6.2	181	2	AI0861	syd protein [impor	914	5	6.2	194	1	MOHUA1	myosin alkali ligh
842	5	6.2	181	2	B24859	legumin B - tick b	915	5	6.2	194	2	G64075	probable ribosomal
843	5	6.2	182	2	T43602	yop targeting prot	916	5	6.2	194	2	AE1195	B. subtilis YjBk p
844	5	6.2	182	2	I59203	gene Hox2.8 protei	917	5	6.2	194	2	H72392	hypothetical prote
845	5	6.2	183	1	TLBP84	tail fiber assembl	918	5	6.2	194	2	G83282	probable sigma-70
846	5	6.2	183	2	AB1821	DNA-3-methyladenin	919	5	6.2	194	2	JC2098	legumin type B bet
847	5	6.2	183	2	C81057	DNA-3-methyladenin	920	5	6.2	195	2	AE2145	hypothetical prote
848	5	6.2	183	2	S13240	tail fiber assembl	921	5	6.2	195	2	AH2774	hypothetical prote
849	5	6.2	183	2	G70596	hypothetical prote	922	5	6.2	195	2	C70928	probable transcrip
850	5	6.2	183	2	AF1883	hypothetical prote	923	5	6.2	195	2	S32123	glycine-rich prote
851	5	6.2	183	2	E69029	hypothetical prote	924	5	6.2	196	2	C75468	gliding motility p
852	5	6.2	184	2	AH3581	alkyl hydroperoxid	925	5	6.2	196	2	B49453	transcription init
853	5	6.2	184	2	AF0622	probable bacteriop	926	5	6.2	196	2	E69042	hypoxanthine phosph
854	5	6.2	184	2	AE0734	probable bacteriop	927	5	6.2	196	2	T49023	hypothetical prote
855	5	6.2	184	2	G86739	teichoic acid bios	928	5	6.2	196	2	S70957	hypothetical prote
856	5	6.2	185	2	S39317	replication initia	929	5	6.2	196	2	F90572	hypothetical prote
857	5	6.2	185	2	S39318	replication initia	930	5	6.2	196	2	C71053	hypothetical prote
858	5	6.2	185	2	JC7369	prenylated Rab acc	931	5	6.2	197	2	H64415	hypothetical prote
859	5	6.2	185	2	F75048	hypothetical prote	932	5	6.2	198	2	S61091	probable GTP-bindi
860	5	6.2	185	2	A64015	hypothetical prote	933	5	6.2	198	2	S44998	coat protein - gra
861	5	6.2	185	2	S77594	type 4 fimbrial bi	934	5	6.2	198	2	E83631	hypothetical prote
862	5	6.2	186	2	S04671	H+-transporting tw	935	5	6.2	198	2	D88098	protein T06D4.5 [i
863	5	6.2	186	2	F63194	GMP synthetase, su	936	5	6.2	198	2	T32025	hypothetical prote
864	5	6.2	186	2	H91252	probable DNA-inver	937	5	6.2	199	2	JC5126	polyU-preferential
865	5	6.2	186	2	G86864	hypothetical prote	938	5	6.2	199	2	T06871	endopeptidase Clp
866	5	6.2	186	2	C71601	probable integral	939	5	6.2	199	2	C84311	hypothetical prote
867	5	6.2	186	2	C71093	hypothetical prote	940	5	6.2	199	2	AH1186	indirect negative
868	5	6.2	187	2	AH0877	conserved hypothet	941	5	6.2	199	2	T40919	probable signal re
869	5	6.2	187	2	G70688	probable lppV prot	942	5	6.2	199	2	T49450	hypothetical prote
870	5	6.2	187	2	F72700	hypothetical prote	943	5	6.2	200	2	A83566	probable bacteriop
871	5	6.2	188	1	G70955	probable 2-amino-4	944	5	6.2	200	2	C75303	MutT/nudix family
872	5	6.2	188	1	F64494	conserved hypothet	945	5	6.2	200	2	D96023	probable C-P (carb
873	5	6.2	188	2	F64496	GMP synthetase (EC	946	5	6.2	201	2	H71655	endopeptidase Clp
874	5	6.2	188	2	A23253	myosin A1 catalyti	947	5	6.2	201	2	H83086	conserved hypothet
875	5	6.2	188	2	AG2351	hypothetical prote	948	5	6.2	201	2	G69340	cobalamin biosynth
876	5	6.2	188	2	B82183	ankB protein VC158	949	5	6.2	201	2	G90385	hypothetical prote
877	5	6.2	189	2	I57590	myosin light chain	950	5	6.2	202	2	S36293	T-cell receptor ga
878	5	6.2	189	2	G64496	hypothetical prote	951	5	6.2	202	2	T08693	hypothetical prote
879	5	6.2	189	2	G96657	hypothetical prote	952	5	6.2	202	2	B87340	transcription regu
880	5	6.2	189	2	C64014	hypothetical prote	953	5	6.2	202	2	A82917	hypothetical prote
881	5	6.2	189	2	E90408	conserved hypothet	954	5	6.2	203	2	AD1326	ribosomal protein
882	5	6.2	189	2	D89966	truncated transpos	955	5	6.2	203	2	AH1080	hypothetical prote
883	5	6.2	190	1	MORTA1	myosin alkali ligh	956	5	6.2	203	2	AD1080	hypothetical prote
884	5	6.2	190	1	VCBVC	coat protein - cow	957	5	6.2	204	2	C75214	hypothetical prote
885	5	6.2	190	2	AG0030	conserved hypothet	958	5	6.2	204	2	G81876	type IV pilus asse
886	5	6.2	190	2	G75207	GTP-binding protei	959	5	6.2	204	2	F81145	probable 60S ribos
887	5	6.2	190	2	C69844	hypothetical prote	960	5	6.2	204	2	F84184	hypothetical prote
888	5	6.2	190	2	G71672	hypothetical prote	961	5	6.2	204	2	G87495	hypothetical prote
889	5	6.2	190	2	D70027	hypothetical prote	962	5	6.2	205	1	B44963	nef protein - huma
890	5	6.2	190	2	F71242	hypothetical prote	963	5	6.2	205	2	C75155	methytransferase
891	5	6.2	191	2	G75299	tellurium resistan	964	5	6.2	205	2	S35029	hypothetical prote
892	5	6.2	191	2	C90284	hypothetical prote	965	5	6.2	205	2	G84204	hypothetical prote
893	5	6.2	191	2	D98218	hypothetical prote	966	5	6.2	206	2	AB2152	transcription regu
894	5	6.2	191	2	AG3068	conserved hypothet	967	5	6.2	206	2	T26418	hypothetical prote
895	5	6.2	192	1	MORBLA	translation elonga	968	5	6.2	206	2	T08285	hypothetical prote
896	5	6.2	192	2	F70126	conserved hypothet	969	5	6.2	206	2	F71450	hypothetical prote
897	5	6.2	192	2	G83096	DNA-directed DNA p	970	5	6.2	206	2	T50439	probable 60S ribos
898	5	6.2	192	2	S41510	hypothetical prote	971	5	6.2	207	1	QQLJND	nef protein - huma
899	5	6.2	192	2	B70352	hypothetical prote	972	5	6.2	207	2	AC2950	transcription regu
900	5	6.2	193	1	F64941	rnd protein - Esch	973	5	6.2	207	2	H75065	hypothetical prote
901	5	6.2	193	2	S01958	heat shock 90K pro	974	5	6.2	207	2	D90526	conserved hypothet
902	5	6.2	193	2	AD0725	probable lipoprote	975	5	6.2	207	2	F87094	conserved hypothet
903	5	6.2	193	2	G85791	probable outer mem	976	5	6.2	208	1	MOHUSA	myosin alkali ligh
904	5	6.2	193	2	C90943	probable outer mem	977	5	6.2	208	2	G81336	uracil phosphoribo
905	5	6.2	193	2	B82554	translation elonga	978	5	6.2	208	2	B86907	signal peptidase I

979 5 6.2 208 2 T34512 hypothetical prote
980 5 6.2 209 2 E90004 uracil phosphoribo
981 5 6.2 209 2 AF726 phosphoglucomutase
982 5 6.2 209 2 T032599 hypothetical prote
983 5 6.2 209 2 T03422 hypothetical prote
984 5 6.2 209 2 AH3243 conjugal transfer
985 5 6.2 209 2 T02177 hypothetical prote
986 5 6.2 210 1 S39662 GTP-pyrophosphokin
987 5 6.2 210 2 S38394 alpha-actinin 2, s
988 5 6.2 210 2 H75361 leu/phe-tRNA-prote
989 5 6.2 210 2 T27471 hypothetical prote
990 5 6.2 210 2 F87493 conserved hypothet
991 5 6.2 211 1 C65080 hypothetical prote
992 5 6.2 211 2 C97223 probable S-adenosyl
993 5 6.2 211 2 H75079 hypothetical prote
994 5 6.2 211 2 H91106 hypothetical prote
995 5 6.2 211 2 C85952 hypothetical prote
996 5 6.2 211 2 A64490 precorrin-6Y methy
997 5 6.2 211 2 B75349 hypothetical prote
998 5 6.2 211 2 F70103 signal peptidase I
999 5 6.2 211 2 T47489 hypothetical prote
1000 5 6.2 212 1 S16542 ribosomal protein

ALIGNMENTS

RESULT 1
A40402
CD9 antigen [validated] - human
N:Alternate names: motility-related protein-1
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1991 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A46123; A40402; JH0555; A39029; S10564
R:Rubinstein, E.; Benoit, P.; Billard, M.; Plessance, S.; Prenant, M.; Uzan, G.; Bouchet
Genomics 16, 132-138, 1993
A:Title: Organization of the human CD9 gene.
A:Reference number: A46123; MUID:93252369; PMID:8486348
A:Accession: A46123
A:Molecule type: DNA
A:Residues: 1-228 <RUB>
A:Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:G300112; PIDN:
A:Experimental source: leukocyte
A>Note: Sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,
R:Rianza, F.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.;
J. Biol. Chem. 266, 10638-10645, 1991
A:Title: CDNA cloning and expression of platelet p24/CD9. Evidence for a new family of m
A:Reference number: A40402; MUID:91244846; PMID:2037603
A:Accession: A40402
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-228 <LAN>
A:Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:G508495; PIDN:AAAS9
A>Note: parts of this sequence, including the amino end of the mature protein, were conf
R:Miyake, M.; Koyana, M.; Seno, M.; Ikeyama, S.
J. Exp. Med. 174, 1347-1354, 1991
A:Title: Identification of the motility-related protein (MRP-1), recognized by monoclonal
A:Reference number: JH0555; MUID:92078843; PMID:1720807
A:Accession: JH0555
A:Molecule type: mRNA
A:Residues: 1-228 <MIY>
A:Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:G34768; PIDN:CAA42708.1; PID:G
A:Experimental source: breast carcinoma
A>Note: This protein has the epitope defined by cell motility-inhibiting monoclonal anti
R:Bouchelx, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uza
J. Biol. Chem. 266, 117-122, 1991
A:Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.
A:Reference number: A39029; MUID:91093112; PMID:1840589
A:Accession: A39029
A:Molecule type: mRNA
A:Residues: 1-8, 'S', 10-66, 'A', 68-193, 195-228 <BOU>
A:Cross-references: UNIPARC:UPI000017414B; GB:M38690
A>Note: parts of this sequence, including the amino end of the mature protein, were conf

R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.
FEBS Lett. 264, 270-274, 1990
A:Title: Purification and partial characterization of CD9 antigen of human platelets.
A:Reference number: S10564; MUID:90292223; PMID:2358073
A:Accession: S10564
A:Molecule type: protein
A:Residues: 2-8, 'X', 10-21 <HIG>
A:Cross-references: UNIPARC:UPI000017414C
C:Genetics:
A:Gene: GDB:CD9; MIC3
A:Cross-references: GDB:120582; OMIM:143030
A:Map position: 12p13-12p13
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status experimental <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQFYKDTYNNKLTQBPQRETLLKAIHYALNCCGLAGGVQFISDTCPKDQV 60
DB 113 HKDEVIKEVQFYKDTYNNKLTQBPQRETLLKAIHYALNCCGLAGGVQFISDTCPKDQV 172
QY 61 LETFTVKSCTPAIKEVFDNK 80
DB 173 LETFTVKSCTPAIKEVFDNK 192

RESULT 2
A42929
CD9 antigen - green monkey
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, Grivet)
C>Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A42929
R:Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
eptors on toxin-sensitive cells.
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-228 <MIT>
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:G218565; PIDN:
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:12-35/Domain: transmembrane #status predicted <CY1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52/53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.5%; Score 38; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.4e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQFYKDTYNKLTKEPQRETLKAIHYAL 38
|||||
Db 113 HKDEVKEVQFYKDTYNKLTKEPQRETLKAIHYAL 150
|||||

RESULT 3
S39262
CD9 antigen - rat
N;Alternate names: platelet cell surface glycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: I56562; S39262
R;Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A;Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed in a variety of tissues.
A;Reference number: I56562; MUID:95123481; PMID:7823164
A;Accession: I56562
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-226 <RES>
A;Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:g434314; PID:149589
C;Genetics:
A;Gene: CD9
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-80/Domain: transmembrane #status predicted <TM2>
F;81-84/Domain: intracellular #status predicted <CY2>
F;85-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CY3>
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 15; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 AGGVEQFISDIPCK 58
|||||
Db 154 AGGVEQFISDIPCK 168
|||||

RESULT 4
JX0221
CD9 antigen - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: JX0221
R;Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell
A;Reference number: JX0221; MUID:93054422; PMID:1339429
A;Accession: JX0221
A;Molecule type: mRNA
A;Residues: 1-226 <MAR>
A;Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:g162820; PIDN:149589
A;Experimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-226/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CY3>

F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 13; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRETLKAIH 35
|||||
Db 133 KDEPQRETLKAIH 145
|||||

RESULT 5
I49589
antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49589
R;Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A;Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A;Reference number: I49589; MUID:94054345; PMID:8236164
A;Accession: I49589
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-226 <RES>
A;Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g388911; PIDN:149589
C;Superfamily: CD9 antigen

Query Match 16.2%; Score 13; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRETLKAIH 35
|||||
Db 133 KDEPQRETLKAIH 145
|||||

RESULT 6
T07054
cysteine proteinase inhibitor (clone R1) - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07054
R;Zhao, Y.; Botella, M.A.; Subramanian, L.; Niu, X.; Nielsen, S.S.; Bressan, R.A.; Hasegawa, A.
submitted to the EMBL Data Library, March 1996
A;Description: Wound-inducible soybean cyteine proteinase inhibitors have greater insecticidal activity than the cyteine proteinase inhibitor.
A;Reference number: Z15886
A;Accession: T07054
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-100 <ZHA>
A;Cross-references: UNIPROT:Q39842; UNIPARC:UPI00000A8C6C; EMBL:U51855; NID:g1277167; PIDN:149589
C;Superfamily: cystatin; cystatin homology
C;Keywords: cysteine proteinase inhibitor

Query Match 8.8%; Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKEVQEF 12
|||||
Db 80 IKEVQEF 86
|||||

RESULT 7
A72276
phosphate ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72276
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: A72276
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <ARN>
A:Cross-references: UNIPROT:Q9X0Y9; UNIPARC:UPI00000D38E4; GB:AE001781; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1262
C:Superfamily: phoW protein

Query Match 8.8%; Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 RETLKAI 34
|||||||
Db 149 RETLKAI 155

RESULT 8
B64551
oligopeptide ABC transporter, ATP-binding protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 05-Oct-2004
C:Accession: B64551
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 398, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64551
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-516 <TOM>
A:Cross-references: UNIPROT:Q25032; UNIPARC:UPI00000D316B; GB:AE000544; GB:AE000511; NID
C:Keywords: ATP; nucleotide binding; P-loop
F:17-222/Domain: ATP-binding cassette homology <ABCI>
F:34-41/Region: nucleotide-binding motif A (P-loop)
F:288-488/Domain: ATP-binding cassette homology <ABC2>
F:305-312/Region: nucleotide-binding motif A (P-loop)

Query Match 8.8%; Score 7; DB 2; Length 516;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 IKEVFDN 79
|||||||
Db 496 IKEVFDN 502

RESULT 9
T00045
cellodextrin phosphorylase - Clostridium thermocellum
C:Species: Clostridium thermocellum
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00045
R:Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M.
J. Ferment. Bioeng. 85, 144-149, 1998
A:Title: Cloning, nucleotide sequence, and expression of the Clostridium thermocellum cellodextrin phosphorylase gene
A:Reference number: Z14077
A:Accession: T00045
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-980 <KAN>
A:Cross-references: UNIPROT:Q24780; UNIPARC:UPI00000B5BEB; EMBL:AB006822; NID:d1117395;
A:Experimental source: ATCC 27405
C:Genetics:
A:Gene: cdp

Query Match 8.8%; Score 7; DB 2; Length 980;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 RETLKAI 34
|||||||
Db 591 RETLKAI 597

RESULT 10
T23236
hypothetical protein K02C4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23236
R:Lightning, J.
submitted to the EMBL Data Library, January 1995
A:Reference number: Z19713
A:Accession: T23236
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1302 <MIL>
A:Cross-references: UNIPROT:Q09931; UNIPARC:UPI0000137A03; EMBL:Z47811; PIDN:CAA87786.1;
A:Experimental source: clone K02C4
C:Genetics:
A:Gene: CESP:K02C4.3
A:Map position: 2
A:Introns: 10/1; 31/3; 84/3; 279/3; 464/1; 745/1; 957/2; 978/3; 1090/2; 1201/3; 1270/3

Query Match 8.8%; Score 7; DB 2; Length 1302;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 EQFISDI 54
|||||||
Db 94 EQFISDI 100

RESULT 11
S03353
plastocyanin - Microcystis aeruginosa (fragment)
C:Species: Microcystis aeruginosa
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03353
R:Tan, S.; Ho, K.K.
Biochim. Biophys. Acta 973, 111-117, 1989
A:Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.
A:Reference number: S03353; MUID:89134784; PMID:2537099
A:Accession: S03353
A:Molecule type: protein
A:Residues: 1-15 <TAN>
A:Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match 7.5%; Score 6; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 ETFTVK 67
|||||||
Db 1 ETFTVK 6

RESULT 12
H35057
MHC class II histocompatibility antigen DO-B beta chain - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 31-Dec-2004
C:Accession: H35057
R:Gyllenstein, U.B.; Lashkari, D.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1835-1839, 1990
A:Title: Allelic diversification at the class II DOB locus of the mammalian major histocompatibility complex
A:Reference number: A35054; MUID:90175391; PMID:2308943

A:Accession: H35057
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-57 <GYL>
A:Cross-references: UNIPROT:Q02712; UNIPROT:Q9TFP4; UNIPARC:UPI0000176FDF
C:Superfamily: immunoglobulin homology

Query Match 7.5%; Score 6; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 KDVLET 63
DB 45 KDVLET 50

RESULT 13
H82927
hypothetical protein UUI51 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: H82927
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: H82927
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60 <GLA>
A:Cross-references: UNIPARC:UPI000139389; GB:AE002115; GB:AF222894; NID:G68999102; PIDN:
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UUI51
A:Genetic code: SGC3

Query Match 7.5%; Score 6; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEVIKE 8
DB 50 DEVIKE 55

RESULT 14
PQ0469
cysteine proteinase inhibitor - potato (fragment)
N:Alternate names: wound-induced protein
C:Species: Solanum tuberosum (potato)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PQ0469; S24768
R:Hildmann, T.; Ebmest, M.; Pena-Cortes, H.; Sanchez-Serrano, J.J.; Willmitzer, L.; Prati
Plant Cell 4, 1157-1170, 1992
A:Title: General roles of abscisic and jasmonic acids in gene activation as a result of
A:Reference number: JQ1692; MUID:93005746; PMID:1392612
A:Accession: PQ0469
A:Molecule type: mRNA
A:Residues: 1-66 <HIL>
A:Cross-references: UNIPROT:Q03196; UNIPARC:UPI0000128D7E; EMBL:X67844; NID:G21440; PIDN:
A:Experimental source: strain desirée
C:Keywords: cysteine proteinase inhibitor
P:18-22/Region: inhibitory

Query Match 7.5%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEP 12
DB 53 KEVQEP 58

RESULT 15

D64538
hypothetical protein HP0148 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: D64538
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: D64538
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-68 <TOM>
A:Cross-references: UNIPROT:O24959; UNIPARC:UPI00000C07EE; GB:AE000536; GB:AE000511; NID:

Query Match 7.5%; Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TLKAIH 35
DB 25 TLKAIH 30

Search completed: January 20, 2006, 17:44:46
Job time : 29.4615 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:34:35 ; Search time 100.769 Seconds
(without alignments)
560.114 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192

Perfect score: 80

Sequence: 1 HKDEVIKEVQEFYKDTYNKL.....LEFTTVKSPDAIKSVFONK 80

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	227	1	CD9_HUMAN
2	80	100.0	228	2	Q5J7W6_HUMAN
3	39	48.8	182	2	Q56CY1_HUMAN
4	38	47.5	227	1	CD9_CERE
5	17	21.2	225	1	CD9_FELCA
6	15	18.8	225	1	CD9_RAT
7	13	16.2	225	1	CD9_BOVIN
8	13	16.2	225	1	CD9_MOUSE
9	13	16.2	225	1	CD9_PIG
10	13	16.2	226	2	Q8MT48_PIG
11	8	10.0	298	2	Q8CSN0_STREP
12	8	10.0	298	2	Q5HPF1_STAEQ
13	8	10.0	410	2	Q5AJ90_CANAL
14	7	8.8	29	2	Q4XUQ5_PLACH
15	7	8.8	91	2	Q6LHC2_PHOPR
16	7	8.8	100	2	Q39842_SOYEN
17	7	8.8	131	2	Q5M0F4_STR11
18	7	8.8	147	2	Q92LY3_RHIME
19	7	8.8	153	2	Q7R639_GIALA
20	7	8.8	154	2	Q8ELW1_OCEIH
21	7	8.8	158	2	Q7VGL4_HELHP
22	7	8.8	171	2	Q975Y2_SULTO
23	7	8.8	196	2	Q4IJ64_GIBZE
24	7	8.8	203	2	Q90B56_HIV1
25	7	8.8	227	2	Q6NWG7_BRARE
26	7	8.8	227	2	Q4REW0_TETNG
27	7	8.8	243	2	Q5PBR2_ANAMM
28	7	8.8	250	2	Q5M501_STR12
29	7	8.8	275	2	Q624R8_CAENH
30	7	8.8	276	2	Q9X0Y9_THEMA
31	7	8.8	290	2	Q7W811_BORPA

32	7	8.8	290	2	Q7WM43_BORBR
33	7	8.8	329	2	Q7RI86_PLAYO
34	7	8.8	331	2	Q7RCP6_PLAYO
35	7	8.8	355	2	Q5N5W9_SYNP6
36	7	8.8	364	2	Q93CU7_SHIBO
37	7	8.8	389	1	MBTK_TREDE
38	7	8.8	393	2	Q6MQQ6_BDEBA
39	7	8.8	414	2	Q5K5K2_9VIRU
40	7	8.8	416	2	Q86IY4_DICDI
41	7	8.8	421	2	Q4FPB4_9RICK
42	7	8.8	474	2	Q65MM0_BACLD
43	7	8.8	482	1	MTTB1_METTE
44	7	8.8	494	1	MTTB1_METAC
45	7	8.8	494	1	MTTB1_METBA
46	7	8.8	495	1	MTTB1_METWA
47	7	8.8	495	1	MTTB2_METAC
48	7	8.8	495	1	MTTB2_METWA
49	7	8.8	516	2	Q25032_HELPY
50	7	8.8	585	2	Q9K5M5_9NOST
51	7	8.8	615	2	Q6NZ26_BRARE
52	7	8.8	624	2	Q8IH03_DROME
53	7	8.8	701	2	Q54XW5_DICDI
54	7	8.8	751	2	Q82QA3_STRAW
55	7	8.8	871	2	Q55GB2_DICDI
56	7	8.8	872	2	Q6CYD6_KLULA
57	7	8.8	896	2	Q5KXY3_GEOKA
58	7	8.8	940	2	Q5R111_DROME
59	7	8.8	968	2	Q6FLE6_CANGA
60	7	8.8	980	2	Q24780_CLOTM
61	7	8.8	984	2	Q9JHT8_CLOTH
62	7	8.8	1056	2	Q5A2L3_CANAL
63	7	8.8	1056	2	Q5A2S3_CANAL
64	7	8.8	1104	1	TRPM8_MOUSE
65	7	8.8	1104	1	TRPM8_RAT
66	7	8.8	1132	2	Q4NT75_9BELT
67	7	8.8	1140	2	Q8SYE5_DROME
68	7	8.8	1140	2	Q9VN25_DROME
69	7	8.8	1193	2	Q9U7N7_PLAFA
70	7	8.8	1193	2	Q76NL8_PLAFA
71	7	8.8	1302	1	UBPY_CABEL
72	7	8.8	1844	2	Q8IE31_PLAFA7
73	7	8.8	2618	2	Q7KTX8_DROME
74	7	8.8	2723	2	Q8I5X3_PLAFA7
75	7	8.8	2738	2	Q8IHU4_PLAFA7
76	6	7.5	15	1	PLAS_MICAR
77	6	7.5	37	2	Q93Y77_4TRBE
78	6	7.5	42	2	Q53412_BACSU
79	6	7.5	48	2	Q4RNP7_TETNG
80	6	7.5	51	2	Q4RNP23_TETNG
81	6	7.5	60	1	Y151_UREPA
82	6	7.5	62	2	Q74EK4_GROSL
83	6	7.5	63	2	Q4FLM6_9RICK
84	6	7.5	66	1	CYT_SOLTU
85	6	7.5	67	2	Q7UUB3_RHOBA
86	6	7.5	68	2	Q24959_HELPY
87	6	7.5	71	2	Q52950_BACSU
88	6	7.5	71	2	Q728A1_DRSVH
89	6	7.5	73	2	Q5BQT7_SCHJA
90	6	7.5	74	2	Q6VXZ3_ECHOL
91	6	7.5	74	2	Q6VXZ4_ECHOL
92	6	7.5	76	2	Q6D6L6_ERWCT
93	6	7.5	79	2	Q7VTU2_BORPE
94	6	7.5	79	2	Q7W4U2_BORPA
95	6	7.5	79	2	Q7WGB9_BORBR
96	6	7.5	82	2	Q5P948_AZOSE
97	6	7.5	82	2	Q5P948_9NCV
98	6	7.5	83	2	Q86549_BHV4
99	6	7.5	84	2	Q54570_STRPY
100	6	7.5	84	2	Q8RHW9_FUSNN
101	6	7.5	85	1	CYC6_FORTE
102	6	7.5	86	2	Q50T58_ENTHI
103	6	7.5	88	2	Q5WGW9_BACSK
104	6	7.5	88	2	Q6NJV4_CORDI

Q7wm43	bordetella
Q7ri86	plasmidium
Q7rcp6	plasmidium
Q5n5w9	synchococc
Q93cu7	shigella bo
Q731r4	treponema d
Q6mqg6	bdellovibri
Q5k5k2	bacterioph
Q86iy4	dictyosteli
Q4fpb4	candidatus
Q65mm0	bacillus li
Q9p955	methanosar
Q8ttac9	methanosar
Q93658	methanosar
P58973	methanosar
Q8t973	methanosar
P58974	methanosar
Q25032	helicobacte
Q9k5m5	anabaena ci
Q6nz26	brachydanio
Q8ih03	drosophila
Q54xw5	dictyosteli
Q82ga3	streptomyce
Q55gb2	dictyosteli
Q6cyd6	klyuveromyc
Q5kxy3	geobacillus
Q95r11	drosophila
Q6fle6	candida gla
Q24780	clostridium
Q93ht8	clostridium
Q5a2l3	candida alb
Q5a2s3	candida alb
Q8r4d5	mus musculu
Q8r455	rattus norv
Q4nt75	anaeromyxob
Q8sy55	drosophila
Q9vn25	drosophila
Q9u7n7	plasmidium
Q76nl8	plasmidium
Q09931	caenorhabdi
Q8ie31	plasmidium
Q7ktx8	drosophila
Q8i5x3	plasmidium
Q8ihu4	plasmidium
P10625	microcystis
Q93y77	atropa bell
Q53412	bacillus su
Q4rnp7	tetraodon n
Q4rnp23	tetraodon n
Q9pqz3	ureaplasma
Q74ek4	geobacter s
Q4flm6	candidatus
Q03196	solanum tub
Q7uub3	rhodopirell
Q24959	helicobacte
Q52950	bacillus su
Q728a1	desulfovibr
Q5bqt7	schistosoma
Q6vxz3	echinococcu
Q6vxz4	echinococcu
Q6d6l6	erwinia car
Q7vtu2	bordetella
Q7w4u2	bordetella
Q7wgb9	bordetella
Q5p948	azocarcus sp
Q9ypk5	encephalomy
Q86549	bovine herp
Q54570	streptococ
Q8rhw9	fusobacteri
F00111	porphyra te
Q50t58	entamoeba h
Q5wgw9	bacillus cl
Q6njv4	corynebacte

105	89	1	HG173 HUMAN	O00479 homo sapien	178	6	7.5	125	2	Q89J73 BRAJA	Q89j73 bradyrhizob
106	89	1	HMG17_BOVIN	P02313 bos taurus	179	6	7.5	126	2	Q8ZMG8_PVRAE	Q8Zwg8 pyrobaculum
107	89	1	HMG17_CANFA	P0711a6 canis famil	180	6	7.5	126	2	Q67412_9ORTO	Q67412 influenza c
108	89	1	HMG17_CHICK	P02314 gallus gall	181	6	7.5	126	2	Q67413_INCNB	Q67413 influenza c
109	89	1	HMG17_GECJA	P04218 gecko japon	182	6	7.5	126	2	Q67414_9ORTO	Q67414 influenza c
110	89	1	HMG17_HUMAN	P05204 homo sapien	183	6	7.5	128	2	Q9NIF7_9INSE	Q9nif7 thermobia d
111	89	1	HMG17_MOUSE	P05204 mus musculus	184	6	7.5	128	2	Q9WXM6_THEMEA	Q9wxm6 thermotoga
112	89	1	HMG17_PIG	P80272 sus scrofa	185	6	7.5	129	2	Q7AFY0_ECO57	Q7afy0 escherichia
113	89	1	HMG17_PONPY	Q5raa0 pongo pygma	186	6	7.5	131	2	Q5BFC1_ENENI	Q5bfc1 aspergillus
114	89	1	HMG17_RAT	P18437 rattus norv	187	6	7.5	131	2	Q8XJX2_CLOPE	Q8xjx2 clostridium
115	90	2	Q6FGI5 HUMAN	Q6fgi5 homo sapien	188	6	7.5	131	2	Q66J17_XENLA	Q66j17 xenopus lae
116	90	2	Q53R27 HUMAN	Q53r27 homo sapien	189	6	7.5	134	2	Q4FLU0_9RICK	Q4flu0 candidatus
117	90	2	Q53XL9 HUMAN	Q53xl9 homo sapien	190	6	7.5	136	2	Q6M004_WETMP	Q6m0g4 methanococc
118	90	2	Q5BL14 MOUSE	Q5bl14 mus musculus	191	6	7.5	136	2	Q75L69_ORYSA	Q75l69 oryza sativ
119	90	2	Q5BES7 MOUSE	Q5be57 mus musculus	192	6	7.5	137	2	Q8FIG3_ECOL6	Q8fig3 escherichia
120	90	2	Q4KLJ0 RAT	Q4klj0 rattus norv	193	6	7.5	137	2	Q8X5D5_ECO57	Q8x5d5 escherichia
121	91	2	Q91987 XENLA	Q91987 xenopus lae	194	6	7.5	138	2	Q86BP6_SCHJA	Q86ep6 schistosoma
122	91	2	Q7SYV7 XENLA	Q7syv7 xenopus lae	195	6	7.5	138	2	Q5JZX4_LACSN	Q5jzx4 lactobacill
123	92	2	Q7M478 TENMO	Q7m478 tenebrio mo	196	6	7.5	139	1	PLAS_PHOLA	PL1883 phormidium
124	92	2	Q8T4K7 9CEST	Q8t4k7 taenia cras	197	6	7.5	140	2	Q64328_BPN15	Q64328 bacterioph
125	92	2	Q5J2R3_9VIRU	Q5j2r3 bacterioph	198	6	7.5	140	2	Q8PRJ8_XANAC	Q8prj8 xanthomonas
126	92	2	Q39840 SOYBN	Q39840 glycine max	199	6	7.5	141	2	Q65HU6_BACLD	Q65hu6 bacillus li
127	92	2	Q5XK38 MOUSE	Q5xk38 mus musculus	200	6	7.5	142	2	Q8KQK2_ANAPH	Q8kqk2 anaplasma p
128	93	2	Q63ZT7 XENTR	Q63zt7 xenopus tro	201	6	7.5	142	2	Q4J4T6_AZOVY	Q4j4t6 azotobacter
129	93	2	Q8CYT4 STRR6	Q8cyt4 streptococc	202	6	7.5	142	2	P73568_SVNY3	P73568 synochocyst
130	93	2	Q37QZ4 STRPN	Q37qz4 streptococc	203	6	7.5	143	2	Q55DJ7_DICDI	Q55dj7 dictyosteli
131	96	2	Q38446_9VIRU	Q38446 bacterioph	204	6	7.5	144	1	VMTT_LAMBD	P03735 bacterioph
132	98	2	Q647G6_ARAHY	Q647g6 arachis hyp	205	6	7.5	144	2	Q6M1B6_HUMAN	Q6mlb6 homo sapien
133	99	2	P72752 SYN3	P72752 synochocyst	206	6	7.5	144	2	Q8FEW7_ECOL6	Q8few7 escherichia
134	101	2	Q9M4Q4 MANES	Q9m4q4 manihot esc	207	6	7.5	144	2	Q8X6X1_ECO57	Q8x6x1 escherichia
135	101	2	Q7ACW6_ECO57	Q7acw6 escherichia	208	6	7.5	145	2	Q93AL4_NODSP	Q93al4 nodularia s
136	102	2	Q687FA_9VIRU	Q687fa bacterioph	209	6	7.5	146	1	CHA3_LYMDI	P43513 lymantria d
137	102	2	Q3ZRP6_CASSA	Q3zrp6 castanea sa	210	6	7.5	146	2	Q59Z16_CANAL	Q59zi6 candida alb
138	102	2	Q9E1B0_ECO57	Q9e1b0 escherichia	211	6	7.5	149	2	Q61ML2_XENLA	Q61ml2 xenopus lae
139	103	2	Q8E1Y9_MACFA	Q8e1y9 macaca fasc	212	6	7.5	150	2	Q9ZE16_BRAJA	Q9zei6 bradyrhizob
140	103	2	Q82726_9VIRU	Q82726 infectious	213	6	7.5	150	2	Q576W7_BRUAB	Q576w7 brucella ab
141	105	2	Q6GQRO HUMAN	Q6gqro homo sapien	214	6	7.5	150	2	Q89QB4_BRAJA	Q89qb4 bradyrhizob
142	105	2	Q50T33_ENTHI	Q50t33 entamoeba h	215	6	7.5	150	2	Q8FX41_BRUSU	Q8fx41 brucella su
143	107	2	Q6K2X1_ORYSA	Q6k2x1 oryza sativ	216	6	7.5	150	2	Q8YBA1_BRUME	Q8yba1 brucella me
144	108	2	Q5YEE3_9PROT	Q5yee3 epsilon pro	217	6	7.5	150	2	Q9D8R4_MOUSE	Q9d8r4 mus musculu
145	109	2	Q50XD9_ENTHI	Q50xd9 entamoeba h	218	6	7.5	152	2	Q52131_ECOLI	Q52131 escherichia
146	109	2	Q572K7_PHYIN	Q572k7 phytophthor	219	6	7.5	152	2	Q85639_ECOLI	Q85639 escherichia
147	110	1	CYC6_PORPY	P51200 porphyra pu	220	6	7.5	152	2	Q5WMB0_ECOLI	Q5wmb0 escherichia
148	110	1	CYC6_PORYE	Q8wkj8 porphyra ye	221	6	7.5	152	2	Q62FW3_BURMA	Q62fw3 burkholderi
149	110	2	Q9AUI9_CABEL	Q9xui9 caenorhabdi	222	6	7.5	152	2	Q7DB60_ECO57	Q7db60 escherichia
150	110	2	Q61ML3 HORSE	Q61ml3 equus cabal	223	6	7.5	154	2	Q97Z29_SULSO	Q97z29 sulfolobus
151	110	2	Q9KN87_VIBCH	Q9kn87 vibrio chol	224	6	7.5	154	2	Q7NJZ3_GLOVI	Q7njz3 gloeobacter
152	110	2	Q6D6K2_ERWCT	Q6d6k2 erwinia car	225	6	7.5	155	2	Q8A8B0_BACTN	Q8a8b0 bacteroides
153	111	2	Q5WQ72_9ZZZZ	Q5wq72 uncultured	226	6	7.5	155	2	Q5QF39_9CAUD	Q5qf39 pseudomonas
154	112	2	Q6W622_9BACT	Q6w622 uncultured	227	6	7.5	156	2	Q9LFA5_ARATH	Q9lfa5 arabidopsis
155	112	2	Q5WQ51_9ZZZZ	Q5wq51 uncultured	228	6	7.5	156	2	Q9SE07_LYCES	Q9se07 lycopersico
156	112	2	Q5WQ62_9ZZZZ	Q5wq62 uncultured	229	6	7.5	156	2	Q4LHW5_9BURK	Q4lhw5 burkholderi
157	112	2	Q5WQ66_9ZZZZ	Q5wq66 uncultured	230	6	7.5	156	2	Q8ZF92_YERPE	Q8zf92 yersinia pe
158	112	2	Q9YW22_MGEPPV	Q9yw22 melanoplus	231	6	7.5	156	2	Q66BS3_YERPS	Q66bs3 yersinia ps
159	112	2	Q4TAH5_TRTNG	Q4tah5 tetraodon n	232	6	7.5	156	2	Q5FBB9_9ORTO	Q5fbb9 influenza c
160	113	2	Q6G9B1_STAAS	Q6g9b1 staphylococ	233	6	7.5	156	2	Q8QZG1_9ORTO	Q8qzg1 influenza c
161	113	2	Q6GGV8_STAAR	Q6ggv8 staphylococ	234	6	7.5	156	2	Q8QZL8_9ORTO	Q8qzl8 influenza c
162	113	2	Q8HFZ2_STAAC	Q8hfx2 staphylococ	235	6	7.5	156	2	Q8QZL9_9ORTO	Q8qzl9 influenza c
163	113	2	Q7A5K7_STAAN	Q7a5k7 staphylococ	236	6	7.5	156	2	Q8QZM0_9ORTO	Q8qzm0 influenza c
164	113	2	Q8NWP4_STAAN	Q8nwp4 staphylococ	237	6	7.5	156	2	Q8QZM1_9ORTO	Q8qzm1 influenza c
165	113	2	Q99U38_STAAM	Q99u38 staphylococ	238	6	7.5	156	2	Q8QZM2_9ORTO	Q8qzm2 influenza c
166	114	2	Q5OY32_ENTHI	Q5oy32 entamoeba h	239	6	7.5	156	2	Q8QZM3_9ORTO	Q8qzm3 influenza c
167	115	2	Q7QFQ3_ANGOA	Q7qfq9 anopheles g	240	6	7.5	156	2	Q8QZM4_9ORTO	Q8qzm4 influenza c
168	116	2	Q9UXM3_SULSO	Q9uxm3 sulfolobus	241	6	7.5	156	2	Q8QZM5_9ORTO	Q8qzm5 influenza c
169	116	2	Q8DEV6_SCHJA	Q8dev6 schistosoma	242	6	7.5	156	2	Q68CC2_9ORTO	Q68cc2 influenza c
170	117	2	Q8DW57_STRMU	Q8dw57 streptococc	243	6	7.5	156	2	Q68CC3_9ORTO	Q68cc3 influenza c
171	118	2	Q9SAC3_ARATH	Q9sac3 arabidopsis	244	6	7.5	156	2	Q68CC4_9ORTO	Q68cc4 influenza c
172	118	2	Q5HKS1_STAEO	Q5hks1 staphylococ	245	6	7.5	156	2	Q68CC5_9ORTO	Q68cc5 influenza c
173	118	2	Q8CQW8_STAEP	Q8cqwh staphylococ	246	6	7.5	156	2	Q68CC6_9ORTO	Q68cc6 influenza c
174	119	1	Y2063_AQUAE	Q67844 aquifex aeo	247	6	7.5	156	2	Q68CC7_9ORTO	Q68cc7 influenza c
175	122	2	Q9AN42_BRAJA	Q9an42 bradyrhizob	248	6	7.5	156	2	Q68CC8_9ORTO	Q68cc8 influenza c
176	124	2	Q4S0A0_TETNG	Q4s0a0 tetraodon n	249	6	7.5	156	2	Q68CC9_9ORTO	Q68cc9 influenza c
177	125	2	Q6N4R8_RHOPA	Q6n4r8 rhodospseudo	250	6	7.5	156	2	Q68CD0_9ORTO	Q68cd0 influenza c

251	6	7.5	156	2	Q68CD1_9ORTO	Q68cd1 influenza c	324	6	7.5	164	2	Q74M85_NANEQ	Q74m85 nanoarchaeu
252	6	7.5	156	2	Q68CD2_9ORTO	Q68cd2 influenza c	325	6	7.5	165	2	P96986_RHIET	P96986 rhizobium e
253	6	7.5	156	2	Q68CD3_9ORTO	Q68cd3 influenza c	326	6	7.5	165	2	Q5L1B7_GEOKA	Q5L1b7 geobacillus
254	6	7.5	156	2	Q68CD4_9ORTO	Q68cd4 influenza c	327	6	7.5	165	2	Q8EPA3_OCEIH	Q8epa3 oceanobacil
255	6	7.5	156	2	Q68CD5_9ORTO	Q68cd5 influenza c	328	6	7.5	166	2	Q5QC24_9CAUD	Q5qc24 enterobacte
256	6	7.5	156	2	Q68CD6_9ORTO	Q68cd6 influenza c	329	6	7.5	167	2	Q4N377_THEPA	Q4n377 theileria p
257	6	7.5	156	2	Q68CD7_9ORTO	Q68cd7 influenza c	330	6	7.5	168	2	Q85255_STRPN	Q85255 streptococc
258	6	7.5	156	2	Q68CD8_9ORTO	Q68cd8 influenza c	331	6	7.5	168	2	Q85258_STRPN	Q85258 streptococc
259	6	7.5	156	2	Q68CD9_9ORTO	Q68cd9 influenza c	332	6	7.5	168	2	Q6J2R9_STRPN	Q6j2r9 streptococc
260	6	7.5	156	2	Q68CE0_9ORTO	Q68ce0 influenza c	333	6	7.5	168	2	Q6J2S1_STRPN	Q6j2s1 streptococc
261	6	7.5	156	2	Q68CE1_9ORTO	Q68ce1 influenza c	334	6	7.5	170	2	Q8RP60_ANAPH	Q8rp60 anaplasma p
262	6	7.5	156	2	Q68CE2_9ORTO	Q68ce2 influenza c	335	6	7.5	170	2	Q8RP63_ANAPH	Q8rp63 anaplasma p
263	6	7.5	156	2	Q68CE3_9ORTO	Q68ce3 influenza c	336	6	7.5	170	2	Q9L719_CAUCR	Q9l719 caulobacter
264	6	7.5	156	2	Q68CE4_9ORTO	Q68ce4 influenza c	337	6	7.5	171	2	Q6MEB4_PARUW	Q6meb4 parachlamyd
265	6	7.5	156	2	Q68CE5_9ORTO	Q68ce5 influenza c	338	6	7.5	172	2	Q4JAT6_SULAC	Q4jat6 sulfolobus
266	6	7.5	156	2	Q68CE6_9ORTO	Q68ce6 influenza c	339	6	7.5	172	2	Q5A5C2_CANAL	Q5a5c2 candida alb
267	6	7.5	156	2	Q91Q60_9ORTO	Q91q60 influenza c	340	6	7.5	172	2	Q8UVI8_CANAL	Q8uvi8 candida alb
268	6	7.5	156	2	Q91Q61_9ORTO	Q91q61 influenza c	341	6	7.5	172	2	Q8H9D7_SOLTU	Q8h9d7 solanum tub
269	6	7.5	156	2	Q9Q221_9ORTO	Q9q221 influenza c	342	6	7.5	172	2	Q9LEC7_SOLTU	Q9lec7 solanum tub
270	6	7.5	156	2	Q9Q224_9ORTO	Q9q224 influenza c	343	6	7.5	172	2	Q9KFV1_BACHD	Q9kfv1 bacillus ha
271	6	7.5	156	2	Q9Q227_9ORTO	Q9q227 influenza c	344	6	7.5	173	2	Q5SKH0_THET8	Q5skh0 thermus the
272	6	7.5	156	2	Q9Q232_9ORTO	Q9q232 influenza c	345	6	7.5	173	2	Q72KL9_THET2	Q72kl9 thermus the
273	6	7.5	156	2	Q9Q235_9ORTO	Q9q235 influenza c	346	6	7.5	176	2	Q8GTI9_9DINO	Q8gti9 symbiodinlu
274	6	7.5	156	2	Q9Q238_9ORTO	Q9q238 influenza c	347	6	7.5	176	2	Q606M4_METCA	Q606m4 methylococc
275	6	7.5	156	2	Q9Q241_9ORTO	Q9q241 influenza c	348	6	7.5	177	2	Q86Y24_HUMAN	Q86y24 homo sapien
276	6	7.5	156	2	Q9Q244_9ORTO	Q9q244 influenza c	349	6	7.5	177	2	Q4XX05_PLACH	Q4xx05 plasmodium
277	6	7.5	156	2	Q9Q247_9ORTO	Q9q247 influenza c	350	6	7.5	179	1	RL5_BUCAK	P46178 buchnera ap
278	6	7.5	156	2	Q9Q250_9ORTO	Q9q250 influenza c	351	6	7.5	181	2	Q5E6G5_ANTLO	Q5e6g5 antonospora
279	6	7.5	156	2	Q9Q253_9ORTO	Q9q253 influenza c	352	6	7.5	181	2	Q4W0J3_9VIRU	Q4w0j3 banana stre
280	6	7.5	156	2	Q8B040_9ORTO	Q8b040 influenza c	353	6	7.5	181	2	Q4W0J4_9VIRU	Q4w0j4 banana stre
281	6	7.5	156	2	Q8B041_9ORTO	Q8b041 influenza c	354	6	7.5	181	2	Q4W0J5_9VIRU	Q4w0j5 banana stre
282	6	7.5	156	2	Q8B042_9ORTO	Q8b042 influenza c	355	6	7.5	181	2	Q4W0J6_9VIRU	Q4w0j6 banana stre
283	6	7.5	156	2	Q8B043_9ORTO	Q8b043 influenza c	356	6	7.5	181	2	Q4W0J7_9VIRU	Q4w0j7 banana stre
284	6	7.5	156	2	Q8B044_9ORTO	Q8b044 influenza c	357	6	7.5	181	2	Q4W0K0_9VIRU	Q4w0k0 banana stre
285	6	7.5	156	2	Q8B045_9ORTO	Q8b045 influenza c	358	6	7.5	181	2	Q4W0K1_9VIRU	Q4w0k1 banana stre
286	6	7.5	156	2	Q8B046_9ORTO	Q8b046 influenza c	359	6	7.5	181	2	Q4W0K2_9VIRU	Q4w0k2 banana stre
287	6	7.5	156	2	Q8B047_9ORTO	Q8b047 influenza c	360	6	7.5	181	2	Q4W0K3_9VIRU	Q4w0k3 banana stre
288	6	7.5	156	2	Q8B048_9ORTO	Q8b048 influenza c	361	6	7.5	181	2	Q4W0K4_9VIRU	Q4w0k4 banana stre
289	6	7.5	156	2	Q8B049_9ORTO	Q8b049 influenza c	362	6	7.5	181	2	Q4W0K5_9VIRU	Q4w0k5 banana stre
290	6	7.5	156	2	Q8B050_9ORTO	Q8b050 influenza c	363	6	7.5	181	2	Q4W0K6_9VIRU	Q4w0k6 banana stre
291	6	7.5	156	2	Q8B051_9ORTO	Q8b051 influenza c	364	6	7.5	181	2	Q4W0K7_9VIRU	Q4w0k7 banana stre
292	6	7.5	156	2	Q8B052_9ORTO	Q8b052 influenza c	365	6	7.5	181	2	Q4W0K8_9VIRU	Q4w0k8 banana stre
293	6	7.5	156	2	Q8B053_9ORTO	Q8b053 influenza c	366	6	7.5	181	2	Q4W0K9_9VIRU	Q4w0k9 banana stre
294	6	7.5	156	2	Q8B054_9ORTO	Q8b054 influenza c	367	6	7.5	182	2	Q8TSA5_METAC	Q8tsa5 methanosarc
295	6	7.5	156	2	Q8B055_9ORTO	Q8b055 influenza c	368	6	7.5	182	2	Q73M40_TREDE	Q73m40 treponema d
296	6	7.5	156	2	Q8B056_9ORTO	Q8b056 influenza c	369	6	7.5	183	1	TBP_METJA	Q57930 methanococc
297	6	7.5	156	2	Q8B057_9ORTO	Q8b057 influenza c	370	6	7.5	183	2	Q97Q14_STRPN	Q97q14 streptococc
298	6	7.5	156	2	Q8B058_9ORTO	Q8b058 influenza c	371	6	7.5	184	2	Q7QN85_ANOGA	Q7qn85 anopheles g
299	6	7.5	156	2	Q8B059_9ORTO	Q8b059 influenza c	372	6	7.5	184	2	Q7VGB0_HBLHP	Q7vgb0 helicobacte
300	6	7.5	156	2	Q8B060_9ORTO	Q8b060 influenza c	373	6	7.5	184	2	Q8DMA4_STRMU	Q8dma4 streptococc
301	6	7.5	156	2	Q8B061_9ORTO	Q8b061 influenza c	374	6	7.5	185	2	Q8TEK8_HUMAN	Q8tek8 homo sapien
302	6	7.5	156	2	Q8B062_9ORTO	Q8b062 influenza c	375	6	7.5	185	2	Q7O9F4_ARATH	Q7o9f4 arabidopsias
303	6	7.5	156	2	Q8B063_9ORTO	Q8b063 influenza c	376	6	7.5	186	2	Q5T981_HUMAN	Q5t981 homo sapien
304	6	7.5	156	2	Q8B064_9ORTO	Q8b064 influenza c	377	6	7.5	186	2	Q57S02_SALCH	Q57s02 salmonella
305	6	7.5	156	2	Q8B065_9ORTO	Q8b065 influenza c	378	6	7.5	186	2	Q5PCD1_SALPA	Q5pcd1 salmonella
306	6	7.5	156	2	Q8B066_9ORTO	Q8b066 influenza c	379	6	7.5	186	2	Q8ZR55_SALTY	Q8zr55 salmonella
307	6	7.5	156	2	Q8B067_9ORTO	Q8b067 influenza c	380	6	7.5	186	2	Q8Z8N1_SALTI	Q8z8n1 salmonella
308	6	7.5	156	2	Q8B068_9ORTO	Q8b068 influenza c	381	6	7.5	186	2	Q8YIF4_PHOLLE	Q8yif4 photorhabdu
309	6	7.5	156	2	Q4U6Y3_9ORTO	Q4u6y3 influenza c	382	6	7.5	187	1	Y1183_PHOLL	Q7y1f6 phocellula me
310	6	7.5	156	2	Q4U6Y4_9ORTO	Q4u6y4 influenza c	383	6	7.5	187	1	Y936_YERPE	Q6thg3 yersinia pe
311	6	7.5	156	2	Q4U6Y5_9ORTO	Q4u6y5 influenza c	384	6	7.5	187	2	Q6TA04_ANAPH	Q6ta04 anaplasma p
312	6	7.5	156	2	Q4U6Y6_9ORTO	Q4u6y6 influenza c	385	6	7.5	187	2	Q666P0_YERPS	Q666p0 yersinia ps
313	6	7.5	157	2	Q9RRJ0_DEIRA	Q9rrj0 deinococcus	386	6	7.5	187	2	Q6D076_ERWCT	Q6d076 erwinia car
314	6	7.5	158	2	Q7RR40_NEUCR	Q7rr40 neurospora	387	6	7.5	188	2	Q71W82_LISMF	Q71w82 listeria mo
315	6	7.5	159	2	Q57AG7_BRUAB	Q57ag7 bruceella ab	388	6	7.5	188	2	Q8Y3Y9_LISMO	Q8y3y9 listeria mo
316	6	7.5	159	2	Q82M14_STRAW	Q82m14 streptomyce	389	6	7.5	188	2	Q927F2_LISIN	Q927f2 listeria in
317	6	7.5	159	2	Q8FY02_BRUSE	Q8fy02 bruceella su	390	6	7.5	189	2	Q8D0B0_YERPE	Q8d0b0 yersinia pe
318	6	7.5	159	2	Q8YE44_BRUME	Q8ye44 brume	391	6	7.5	190	2	Q556D4_DICDI	Q556d4 dictyosteli
319	6	7.5	160	2	Q5TWS3_ANOGA	Q5tws3 anopheles g	392	6	7.5	190	2	Q9G4D4_9STRA	Q9g4d4 chaustocchy
320	6	7.5	161	2	Q4JLK0_LACRE	Q4jlk0 lactobacill	393	6	7.5	191	2	Q6TNR4_BRARE	Q6tnr4 brachydanio
321	6	7.5	161	2	Q9X7P1_STRCO	Q9x7p1 streptomyce	394	6	7.5	191	2	Q4JTV48_CORJK	Q4jtv48 corynebacte
322	6	7.5	162	2	Q8ZUL0_PYRAE	Q8zul0 pyrobaculum	395	6	7.5	192	2	Q54BZ2_DICDI	Q54bz2 dictyosteli
323	6	7.5	163	2	Q63PU3_BURPS	Q63pu3 burkholderi	396	6	7.5	193	2	Q4N084_THEPA	Q4n084 theileria p

397	194	2	Q5B237	EMENI	Q5b237	aspergillus	470	6	7.5	230	2	Q5ZWN4	LEGPH	Q5zwn4	legionella
398	194	2	Q4UV17	XANCP	Q4uv17	xanthomonas	471	6	7.5	233	2	Q7VZ01	BORPE	Q7vz01	bordetella
399	194	2	Q8C702	MOUSE	Q8c702	mus musculus	472	6	7.5	235	2	Q5BYA8	SCHJA	Q5bya8	schistosoma
400	195	2	Q8GTH4	SYMPU	Q8gth4	ymbiodiniu	473	6	7.5	235	2	Q77103	LEITA	Q77103	leishmania
401	195	2	Q71SU8	VIGNU	Q71su8	vigna ungui	474	6	7.5	235	2	Q9AG66	RH1ET	Q9ag66	rhizobium
402	196	2	Q8U4E2	PYRFU	Q8u4e2	pyrococcus	475	6	7.5	236	2	Q9SGX2	ARATH	Q9sgx2	arabidopsis
403	196	2	Q73BM8	BACCL	Q73bm8	bacillus ce	476	6	7.5	236	2	Q7NZ54	CHROV	Q7nz54	chromobacte
404	197	2	Q44195	AGRRH	Q44195	agrobacteri	477	6	7.5	237	2	Q27679	LEIDO	Q27679	leishmania
405	198	2	Q6SX99	BACCE	Q6sxp9	bacillus ce	478	6	7.5	237	2	Q4Q9H8	LEIMA	Q4q9h8	leishmania
406	199	2	Q8GTH2	SYMPU	Q8gth2	ymbiodiniu	479	6	7.5	238	1	Y037	METJA	Q60344	methanococc
407	199	2	Q4JWS2	CORJK	Q4jws2	corynebacte	480	6	7.5	238	2	Q7RUS7	NEUCR	Q7rus7	neurospora
408	200	2	Q86F17	SCHJA	Q86f17	schistosoma	481	6	7.5	241	1	DPM1	DROME	Q9viu7	drosophila
409	200	2	Q4XHD9	PLACH	Q4xhd9	plasmodium	482	6	7.5	242	2	Q4J4Q8	AZOV1	Q4j4q8	azotobacter
410	200	2	Q97GZ6	CLOAB	Q97gz6	clostridium	483	6	7.5	242	2	Q89Y25	BRAJA	Q89y25	bradyrhizob
411	201	2	Q7ZW81	BRARE	Q7zw81	brachydanio	484	6	7.5	242	2	Q9HWJ6	PSEAE	Q9hwj6	pseudomonas
412	202	2	Q6MXK8	SERMA	Q6mxk8	serratia ma	485	6	7.5	243	2	Q75VH8	9BACT	Q75vh8	uncultured
413	203	2	Q6IME7	9STRA	Q6ime7	phytophthor	486	6	7.5	244	1	ADC	CLOAB	P23670	clostridium
414	203	2	Q523K4	NOCPA	Q5z3k4	nocardia fa	487	6	7.5	244	2	Q5ZQT8	ARCVE	Q5zqt8	archaeoglob
415	205	2	Q42ZU7	PLABE	Q42zu7	plasmodium	488	6	7.5	244	2	Q6L469	SOLDE	Q6l469	solanum dem
416	205	2	Q33115	MYCLE	Q33115	mycobacteri	489	6	7.5	245	2	Q23616	ARATH	Q23616	arabidopsis
417	206	2	Q58K99	THET8	Q5skg9	thermus the	490	6	7.5	245	2	Q4FQM0	9GAMM	Q4fqm0	psychrobact
418	206	2	Q72KL8	THET2	Q72kl8	thermus the	491	6	7.5	246	2	Q84LB7	MALDO	Q84lb7	malus domes
419	207	2	Q69YA5	ORYSA	Q69ya5	oryza sativ	492	6	7.5	246	2	Q88Q72	PSEPK	Q88q72	pseudomonas
420	207	2	Q4TLU7	9SPHN	Q4tlu7	erythrobact	493	6	7.5	247	2	Q75VJ0	9BACT	Q75vj0	uncultured
421	208	2	Q9HE35	NEUCR	Q9he35	neurospora	494	6	7.5	248	1	YWQC	BACSU	P96715	bacillus su
422	208	2	Q4HM62	CAMLA	Q4hm62	campylobact	495	6	7.5	248	2	Q5WRZ4	LEGPL	Q5wrz4	legionella
423	210	1	PEM_MOUSE		P52651	mus musculus	496	6	7.5	248	2	Q8D459	VIBVU	Q8d459	vibrio vuln
424	210	2	Q59PA4	CANAL	Q59pa4	candida alb	497	6	7.5	248	2	Q8XXX9	RALSO	Q8xxx9	raistonia s
425	210	2	Q8J2J8	NEOUN	Q8j2j8	neotryphodiu	498	6	7.5	249	2	Q8GTH0	9DINO	Q8gth0	ymbiodiniu
426	210	2	Q7QFW9	ANOCA	Q7qfw9	anopheles g	499	6	7.5	249	2	Q5NF40	FRATT	Q5nf40	francisella
427	210	2	Q9QYR4	MUSSA	Q9qyr4	mus saxicol	500	6	7.5	250	2	Q68E87	AERPU	Q68e87	aeromonas p
428	210	2	Q9QYR5	MUSCR	Q9qyr5	mus caroli	501	6	7.5	251	2	Q74M76	NANEQ	Q74m76	nanorarchaeu
429	210	2	Q4TU88	MOUSE	Q4tu88	mus musculus	502	6	7.5	251	2	Q9HSX5	HUMAN	Q9hsx5	homo sapien
430	210	2	Q7TN91	MOUSE	Q7tn91	mus musculus	503	6	7.5	251	2	Q6V204	9BACT	Q6v204	uncultured
431	212	2	Q8LPCL	PHYPA	Q8lpc1	physcomitre	504	6	7.5	251	2	Q9F5F9	AGRRH	Q9f5f9	agrobacteri
432	212	2	Q6A4H9	CAMJE	Q6a4h9	campylobact	505	6	7.5	251	2	Q7W5U1	BORBR	Q7wgj2	bordetella
433	213	2	Q9EV56	RHIME	Q9ev56	rhizobium m	506	6	7.5	251	2	Q7WGJ2	BORBR	Q7wgj2	bordetella
434	214	2	Q4GZM1	9HIV1	Q4gzv1	human immun	507	6	7.5	253	2	Q98X0	GUILTH	Q98x0	guillardia
435	215	2	Q66KP3	XENLA	Q66kp3	xenopus lae	508	6	7.5	253	2	Q6V1Z8	9BACT	Q6v1z8	uncultured
436	217	2	Q81ZQ0	PLAF7	Q81zq0	plasmodium	509	6	7.5	253	2	Q6V1Z9	9BACT	Q6v1z9	uncultured
437	218	2	Q52217	NOCPA	Q5z217	nocardia fa	510	6	7.5	253	2	Q6V201	9BACT	Q6v201	uncultured
438	219	2	Q98HX1	RHILO	Q98hx1	rhizobium l	511	6	7.5	253	2	Q6V202	9BACT	Q6v202	uncultured
439	220	2	Q57BZ1	BRUAB	Q57bz1	bruceila ab	512	6	7.5	253	2	Q6V203	9BACT	Q6v203	uncultured
440	220	2	Q8FZP8	BRUSU	Q8fzfp8	bruceila su	513	6	7.5	253	2	Q72LA6	THET2	Q72la6	thermus the
441	220	2	Q8XMS4	CLOPE	Q8xms4	clostridium	514	6	7.5	254	2	Q4Z243	PLABE	Q4z243	plasmodium
442	221	1	CAPA_STRAU		P39850	staphylococ	515	6	7.5	254	2	Q82U53	NITEU	Q82u53	nitrosomona
443	221	2	Q6VUV3	9BACT	Q6vuv3	uncultured	516	6	7.5	254	2	Q68FD8	MOUSE	Q68fd8	mus musculus
444	221	2	Q8E039	STRA5	Q8e039	streptococc	517	6	7.5	255	2	Q96HS1	HUMAN	Q96hs1	homo sapien
445	221	2	Q8E5R6	STRA3	Q8e5r6	streptococc	518	6	7.5	255	2	Q7Z368	HUMAN	Q7z368	homo sapien
446	221	2	Q5NHA7	FRATT	Q5nha7	francisella	519	6	7.5	255	2	Q6L407	SOLDE	Q6l407	solanum dem
447	222	1	FLPA_THEVO		Q979p2	thermoplasm	520	6	7.5	258	2	Q6MIM4	BDEBA	Q6mim4	bdellovibri
448	222	2	Q5ZE75	ORYSA	Q5ze75	oryza sativ	521	6	7.5	258	2	Q6LCF0	MOUSE	Q6lcf0	mus musculus
449	223	1	PURQ_RHIME		Q92pi1	rhizobium m	522	6	7.5	259	2	Q5F9V7	NEIG1	Q5f9v7	neisseria g
450	223	2	Q8TUA9	METAC	Q8tua9	methanosarc	523	6	7.5	259	2	Q9JVB4	NEIMA	Q9jvb4	neisseria m
451	223	2	Q54BL9	DICDI	Q54bl9	dictyosteli	524	6	7.5	259	2	Q9K0A8	NEIME	Q9k0a8	neisseria m
452	223	2	Q847V6	VIBPA	Q847v6	vibrio para	525	6	7.5	260	2	Q7QDH5	ANOCA	Q7qdh5	anopheles g
453	224	2	Q87G70	VIBPA	Q87g70	vibrio para	526	6	7.5	262	2	Q525U4	WAGGR	Q525j4	magnaporthe
454	224	2	Q81KJ2	BACAN	Q81kj2	bacillus an	527	6	7.5	264	1	THIG	CHROV	Q7nr14	chromobacte
455	224	2	Q6HCC9	BACHK	Q6hcc9	bacillus th	528	6	7.5	264	2	Q4KI36	PSEF5	Q4ki36	pseudomonas
456	224	2	Q632T9	BACCZ	Q632t9	bacillus ce	529	6	7.5	265	2	Q8WXP4	HUMAN	Q8wxf4	h ras effec
457	224	2	Q91BC9	CHICK	Q91bc9	gallus gall	530	6	7.5	265	2	Q4NG57	9WICC	Q4ng57	arthrobacte
458	225	2	Q8PW93	METMA	Q8pw93	methanosarc	531	6	7.5	265	2	Q8C2E8	MOUSE	Q8c2e8	mus musculus
459	225	2	Q86IU7	DICDI	Q86iu7	dictyosteli	532	6	7.5	266	2	Q8TNX7	METAC	Q8tnx7	methanosarc
460	225	2	Q4V9X0	MOUSE	Q4v9x0	mus musculus	533	6	7.5	266	2	Q6W249	RHIGN	Q6w249	rhizobium s
461	228	2	Q813T0	PLAF7	Q813t0	plasmodium	534	6	7.5	266	2	Q6F272	MESFL	Q6f272	mesoplasma
462	228	2	Q5FI52	LACAC	Q5fi52	lactobacill	535	6	7.5	267	2	Q51X64	WAGGR	Q51x64	magnaporthe
463	228	2	Q74HN2	LACJO	Q74hn2	lactobacill	536	6	7.5	267	2	Q4JL32	SCHJA	Q4jl32	schistosoma
464	228	2	Q6GOE5	XENLA	Q6goe5	xenopus lae	537	6	7.5	267	2	Q8GSK1	9DINO	Q8gsk1	ymbiodiniu
465	229	2	Q33T06	HUMAN	Q33t06	homo sapien	538	6	7.5	267	2	Q8GTH5	9DINO	Q8gth5	ymbiodiniu
466	229	2	Q7QRH5	GIALA	Q7qrh5	giardia lam	539	6	7.5	267	2	Q8GTH6	9DINO	Q8gth6	ymbiodiniu
467	229	2	Q89B84	BRAJA	Q89b84	bradyrhizob	540	6	7.5	267	2	Q8GTH7	9DINO	Q8gth7	ymbiodiniu
468	229	2	Q88T18	LACPL	Q88t18	lactobacill	541	6	7.5	267	2	Q9X919	STRCO	Q9x919	streptomyce
469	230	2	Q5X2Q6	LRGPA	Q5x2q6	legionella	542	6	7.5	268	2	Q60E71	ORYSA	Q60e71	oryza sativ

543	6	7.5	268	2	Q8GT14_9DINO	Q8gti4 symbiodiniu	616	6	7.5	293	2	Q6KAR0_MOUSE	Q6kar0 mus musculu
544	6	7.5	270	2	Q75FT4_LEPIC	Q75ft4 leptospira	617	6	7.5	293	2	Q4RP15_TETNG	Q4rp15 tetraodon n
545	6	7.5	270	2	Q8EXT7_LEPIN	Q8ext7 leptospira	618	6	7.5	294	2	Q5PDW4_SALPA	Q5pdw4 salmonella
546	6	7.5	272	2	Q8GEZ4_SCHJA	Q8geza4 schistosoma	619	6	7.5	294	2	Q8Z5F1_SALTI	Q8z5f1 salmonella
547	6	7.5	273	2	Q9NZQ0_HUMAN	Q9nza0 homo sapien	620	6	7.5	294	2	Q8ZNP7_SALTY	Q8znp7 salmonella
548	6	7.5	273	2	Q5RDE5_PONPY	Q5rde5 pongo pygma	621	6	7.5	294	2	Q834B2_ENTFA	Q834b2 enterococcu
549	6	7.5	273	2	Q61ML7_RAT	Q61ml7 rattus norv	622	6	7.5	294	2	Q8CCX5_MOUSE	Q8ccx5 mus musculu
550	6	7.5	273	2	Q8BX00_MOUSE	Q8bx00 mus musculu	623	6	7.5	295	2	Q8N1A0_HUMAN	Q8n1a0 homo sapien
551	6	7.5	273	2	Q8CFP6_MOUSE	Q8cfp6 mus musculu	624	6	7.5	295	2	Q617J5_CAEBR	Q617j5 caenorhabdi
552	6	7.5	273	2	Q61MM1_CHICK	Q61mm1 gallus gall	625	6	7.5	295	2	Q65U99_MANSI	Q65u99 manhelimia
553	6	7.5	273	2	Q72YF1_XENLA	Q72yf1 xenopus lae	626	6	7.5	296	2	Q96ZJ4_SULTO	Q96zj4 sulfolobus
554	6	7.5	274	2	Q86FD1_SCHJA	Q86fd1 schistosoma	627	6	7.5	296	2	Q5VRP2_ORYSA	Q5vrp2 oryza sativ
555	6	7.5	274	2	Q86LD9_ORYSA	Q86ld9 oryza sativ	628	6	7.5	297	2	Q67PA0_SMYTH	Q67pa0 symbiobacte
556	6	7.5	274	2	Q92310_MOUSE	Q92310 mus musculu	629	6	7.5	297	2	Q91905_XENLA	Q91905 xenopus lae
557	6	7.5	276	2	Q5DMH3_BPT5	Q5dmh3 bacterioph	630	6	7.5	298	2	Q7MSN2_WOLSA	Q7msn2 wolinnella s
558	6	7.5	276	2	Q5M7D1_XENLA	Q5m7d1 xenopus lae	631	6	7.5	298	2	Q6P818_XENTR	Q6p818 xenopus tro
559	6	7.5	278	1	CB1O1_EACHD	Q529j3 bacillus ha	632	6	7.5	298	2	Q4SSB3_TETNG	Q4ssb3 tetraodon n
560	6	7.5	278	2	Q5URP2_HUMAN	Q529j3 bacillus ha	633	6	7.5	299	2	Q4L695_STAHI	Q4l695 staphylococ
561	6	7.5	278	2	Q8VV19_CORGL	Q8vv19 corynebacte	634	6	7.5	299	2	Q9PVL6_CHICK	Q9pvl6 gallus gall
562	6	7.5	278	2	Q63AB0_BACCG	Q63ab0 bacillus ce	635	6	7.5	300	2	Q96DH7_HUMAN	Q96dh7 homo sapien
563	6	7.5	279	1	TVSY_STRMU	Q8dui4 streptococc	636	6	7.5	300	2	Q817G8_ARATH	Q817g8 arabidopsis
564	6	7.5	280	2	Q721E7_TRYCR	Q721e7 trypanosoma	637	6	7.5	300	2	Q7X735_ORYSA	Q7x735 oryza sativ
565	6	7.5	280	2	Q41JBE6_STAHI	Q41jbe6 staphylococ	638	6	7.5	300	2	Q6G9H0_STAAS	Q6g9h0 staphylococ
566	6	7.5	281	2	Q8GVD6_ORYSA	Q8gvd6 oryza sativ	639	6	7.5	300	2	Q6GH17_STAAR	Q6gh17 staphylococ
567	6	7.5	282	2	Q9RGD2_LACCA	Q9rgd2 lactobacill	640	6	7.5	300	2	Q7ASQ1_STAAN	Q7asq1 staphylococ
568	6	7.5	282	2	Q5FHU4_LACAC	Q5fhu4 lactobacill	641	6	7.5	300	2	Q8NWS9_STAAN	Q8nws9 staphylococ
569	6	7.5	282	2	Q6G5E1_BARHE	Q6g5e1 bartonella	642	6	7.5	300	2	Q9U9J3_STAAM	Q9u9j3 staphylococ
570	6	7.5	282	2	Q8OVY8_MOUSE	Q8ovy8 mus musculu	643	6	7.5	300	2	Q5HG23_STAAC	Q5hg23 staphylococ
571	6	7.5	283	2	Q515L5_CHLAB	Q515l5 chlamydophi	644	6	7.5	300	2	Q9PUL9_BRARE	Q9pul9 brachydanio
572	6	7.5	284	2	Q612P7_PICTO	Q612p7 picrophilus	645	6	7.5	301	2	Q9V1P4_PYRAB	Q9v1p4 pyrococcus
573	6	7.5	284	2	Q529K3_HUMAN	Q529k3 homo sapien	646	6	7.5	301	2	Q7NK17_GLOVI	Q7nk17 gloeobacter
574	6	7.5	284	2	Q5K2M2_BACLI	Q5k2m2 bacillus li	647	6	7.5	301	2	Q7NM69_GLOVI	Q7nm69 gloeobacter
575	6	7.5	284	2	Q5UF41_9PROT	Q5uf41 uncultured	648	6	7.5	301	2	Q5QNI0_ORYSA	Q5qni0 oryza sativ
576	6	7.5	285	2	Q86FAL_SCHJA	Q86fal schistosoma	649	6	7.5	302	2	Q832F3_ENTFA	Q832f3 enterococcu
577	6	7.5	285	2	Q4NT19_9DELT	Q4nt19 anaeronyxob	650	6	7.5	302	2	Q73115_SYNY3	Q73115 syntechocyst
578	6	7.5	285	2	Q5LXD8_SILPO	Q5lxd8 silicibacte	651	6	7.5	303	1	MTCH2_BOVIN	Q7n285 bos taurus
579	6	7.5	285	2	Q82R08_STRAW	Q82r08 streptococ	652	6	7.5	303	1	MTCH2_MOUSE	Q7n285 bos taurus
580	6	7.5	286	1	TVSY_STRT2	Q5m0b7 streptococ	653	6	7.5	303	1	MTCH2_MOUSE	Q7n285 bos taurus
581	6	7.5	286	1	TVSY_STRT2	Q5m0b7 streptococ	654	6	7.5	303	1	MTCH2_MOUSE	Q7n285 bos taurus
582	6	7.5	286	2	Q8T83_METAC	Q8t83 methanosarc	655	6	7.5	303	1	MTCH2_MOUSE	Q7n285 bos taurus
583	6	7.5	286	2	Q5KSB6_LOTJA	Q5ksb6 locus japon	656	6	7.5	303	2	Q5G3G4_HUMAN	Q5g3g4 homo sapien
584	6	7.5	286	2	Q4TQM6_9SPHN	Q4tqm6 erythroba	657	6	7.5	304	2	Q9FPC6_ORYSA	Q9fpc6 oryza sativ
585	6	7.5	287	2	Q8VMP2_PSEPU	Q8vmf2 pseudomonas	658	6	7.5	304	2	Q8XKS7_LACPL	Q8xks7 lactobacill
586	6	7.5	287	2	Q8BM78_MOUSE	Q8bm78 m mus muscu	659	6	7.5	305	2	Q9NPP5_HUMAN	Q9npp5 homo sapien
587	6	7.5	288	2	Q8TZJ1_PYRFU	Q8tzj1 pyrococcus	660	6	7.5	305	2	Q9C878_ARATH	Q9c878 arabidopsis
588	6	7.5	288	2	Q6BPJ1_DEBHA	Q6bpj1 debaryomyce	661	6	7.5	306	2	Q67R84_SYMTH	Q67r84 symbiobacte
589	6	7.5	288	2	Q4TYV9_PLABE	Q4tyv9 plasmodium	662	6	7.5	306	2	Q6HCA6_BACHK	Q6hca6 bacillus th
590	6	7.5	288	2	Q8BX10_MOUSE	Q8bx10 mus musculu	663	6	7.5	306	2	Q72YU8_BACCI	Q72yu8 bacillus ce
591	6	7.5	288	2	Q562B5_RAT	Q562b5 rattus norv	664	6	7.5	306	2	Q816Q3_BACCR	Q816q3 bacillus ce
592	6	7.5	289	2	Q8GT12_9DINO	Q8gt12 symbiodiniu	665	6	7.5	306	2	Q8XDX9_RALSO	Q8xxd9 ralestonia s
593	6	7.5	289	2	Q8GT13_9DINO	Q8gt13 symbiodiniu	666	6	7.5	306	2	Q81KH1_BACAN	Q81kh1 bacillus an
594	6	7.5	289	2	Q8GT15_9DINO	Q8gt15 symbiodiniu	667	6	7.5	306	2	Q632R8_BACCC	Q632r8 bacillus ce
595	6	7.5	289	2	Q8GT16_9DINO	Q8gt16 symbiodiniu	668	6	7.5	307	2	Q5VIC2_HALAR	Q5vic2 haloarcula
596	6	7.5	289	2	Q8GT17_9DINO	Q8gt17 symbiodiniu	669	6	7.5	307	2	Q6ASD1_DESPA	Q6aad1 desulfotale
597	6	7.5	289	2	Q8GT18_9DINO	Q8gt18 symbiodiniu	670	6	7.5	308	2	Q7QD97_ANOGA	Q7qgd97 anophelies g
598	6	7.5	289	2	Q85066_9BROM	Q85066 peanut stun	671	6	7.5	308	2	Q61EN4_CAEBR	Q61en4 caenorhabdi
599	6	7.5	290	1	EX05_BPT5	P06229 bacterioph	672	6	7.5	308	2	Q51BW5_ENTHI	Q51bw5 entamoeba h
600	6	7.5	290	2	Q6P8A9_XENTR	Q6p8a9 xenopus tro	673	6	7.5	308	2	Q5RD19_PONPY	Q5rd19 pongo pygma
601	6	7.5	291	2	Q8P193_METNA	Q8py93 methanosarc	674	6	7.5	308	2	P71522_MARHA	P71522 marincoccu
602	6	7.5	291	2	Q66LT5_BPT5	Q66lt5 bacterioph	675	6	7.5	309	2	Q6PJ76_HUMAN	Q6pj76 homo sapien
603	6	7.5	292	1	HCHA_STAAM	P64312 staphylococ	676	6	7.5	310	2	Q50PX2_ENTHI	Q50px2 entamoeba h
604	6	7.5	292	1	HCHA_STAAM	P64313 staphylococ	677	6	7.5	310	2	Q51B62_ENTHI	Q51b62 entamoeba h
605	6	7.5	292	1	HCHA_STAAM	Q8nx22 staphylococ	678	6	7.5	310	2	Q8WQ32_CAEL	Q8wq32 caenorhabdi
606	6	7.5	292	2	Q72R49_LEPIC	Q72r49 leptospira	679	6	7.5	310	2	Q87988_BORBR	Q87988 bordetella
607	6	7.5	292	2	Q6GBT6_STAAS	Q6gbt6 staphylococ	680	6	7.5	310	2	Q7W253_BORPA	Q7w253 bordetella
608	6	7.5	292	2	Q6GJB7_STAAR	Q6gjb7 staphylococ	681	6	7.5	310	2	Q7WGG6_BORBR	Q7wgg6 bordetella
609	6	7.5	292	2	Q5HIC4_STAAC	Q5hic4 staphylococ	682	6	7.5	311	2	Q8C3A0_MOUSE	Q8c3a0 mus musculu
610	6	7.5	292	2	Q5BLC1_BRARE	Q5blc1 brachydanio	683	6	7.5	311	2	Q9H8F7_HUMAN	Q9h8f7 homo sapien
611	6	7.5	293	2	Q6MU03_MYCWS	Q6mu03 mycoplasma	684	6	7.5	311	2	Q5J5N7_HUMAN	Q5j5n7 homo sapien
612	6	7.5	293	2	Q724P2_LISMP	Q724p2 listeria mo	685	6	7.5	311	2	Q5WC88_BACSK	Q5wc88 bacillus cl
613	6	7.5	293	2	Q8YAF9_LISMP	Q8yaf9 listeria mo	686	6	7.5	311	2	Q7URM1_RHOBA	Q7urm1 rhodospirell
614	6	7.5	293	2	Q92F96_LISIN	Q92f96 listeria in	687	6	7.5	312	2	Q9Y9N2_AERPE	Q9y9n2 aeropyrum p
615	6	7.5	293	2	Q69ZE3_MOUSE	Q69ze3 mus musculu	688	6	7.5	312	2	Q7MFN5_VIBVY	Q7mfns vibrio vuln

689	6	7.5	312	2	Q9D050_MOUSE	Q9D050_mus musculus	762	6	7.5	329	2	Q98GR0_RHIL0	Q98gr0 rhizobium 1
690	6	7.5	312	2	Q640V7_XENLA	Q640v7 xenopus lae	763	6	7.5	332	2	Q6FRW9_CANGA	Q6frw9 candida gla
691	6	7.5	313	2	Q421A1_PLABE	Q421a1 plasmodium	764	6	7.5	332	2	Q4MMV1_BACCE	Q4mmv1 bacillus ce
692	6	7.5	313	2	Q7W4Y8_BORPA	Q7w4y8 bordetella	765	6	7.5	332	2	Q4FTF0_9GAMM	Q4ftf0 psychrobact
693	6	7.5	314	2	Q4YH25_PLABE	Q4yh25 plasmodium	766	6	7.5	332	2	Q635H9_BACCZ	Q635h9 bacillus ce
694	6	7.5	314	2	Q6D5T6_ERWCT	Q6d5t6 erwinia car	767	6	7.5	332	2	Q6HEG3_BACHK	Q6he63 bacillus th
695	6	7.5	315	2	Q6ZM20_BRARE	Q6zm20 brachydanio	768	6	7.5	332	2	Q731J5_BACC1	Q731j5 bacillus ce
696	6	7.5	315	2	Q5OSD0_ENTHI	Q5osd0 entamoeba h	769	6	7.5	332	2	Q81MC5_BACAN	Q81mc5 bacillus an
697	6	7.5	316	1	GSEP_BACLD	P80057 bacillus li	770	6	7.5	332	2	Q4VA36_MOUSE	Q4va36 mus musculus
698	6	7.5	316	2	Q9QM44_9VIRU	Q9qm44 parvo-like	771	6	7.5	334	2	Q4P0Z4_USTMA	Q4p0z4 ustilago ma
699	6	7.5	316	2	Q4U3C5_BMDNV	Q4u3c5 bombyx mori	772	6	7.5	334	2	Q4FVS3_9GAMM	Q4fvs3 psychrobact
700	6	7.5	317	2	Q6CGL1_KLULA	Q6cgl1 kluyveromyc	773	6	7.5	335	2	Q6CS23_KLULA	Q6cs23 kluyveromyc
701	6	7.5	317	2	Q8S3G8_PSESJ	Q8s3g8 pseudomonas	774	6	7.5	336	2	Q8WVW9_HUMAN	Q8wvw9 homo sapien
702	6	7.5	318	2	Q5OR23_ENTHI	Q5or23 entamoeba h	775	6	7.5	336	2	Q4NMX0_9DELT	Q4nmx0 anaeromyxob
703	6	7.5	318	2	Q6MSK1_MYCMS	Q6mse1 mycoplasma	776	6	7.5	336	2	Q4NSB0_9DELT	Q4nbs0 anaeromyxob
704	6	7.5	319	2	Q61SE9_CABBR	Q61se9 caenorhabdi	777	6	7.5	337	1	CWC2_KLULA	Q6ct50 kluyveromyc
705	6	7.5	320	2	Q743H7_MYCPA	Q743h7 mycobacteri	778	6	7.5	338	2	Q28757_ARCFU	Q28757 archaeooglob
706	6	7.5	320	2	Q16457_CAEEL	Q16457 caenorhabdi	779	6	7.5	338	2	Q5SUR5_CRYNE	Q5sur5 cryptococcu
707	6	7.5	320	2	Q5CZU2_BRARE	Q5czu2 brachydanio	780	6	7.5	338	2	Q8J0X1_CRYNE	Q8j0x1 cryptococcu
708	6	7.5	321	2	Q61TD9_CABBR	Q61td9 caenorhabdi	781	6	7.5	338	2	Q8J0Y7_CRYNE	Q8j0y7 cryptococcu
709	6	7.5	321	2	Q5OXU1_ENTHI	Q5oxu1 entamoeba h	782	6	7.5	338	2	Q5KHM4_CRYNE	Q5khm4 cryptococcu
710	6	7.5	321	2	Q8DY20_STRAS	Q8dy20 streptococc	783	6	7.5	338	2	Q4Y6H2_PLACH	Q4y6h2 plasmodium
711	6	7.5	321	2	Q5VBD2_9REOV	Q5vbd2 human rotav	784	6	7.5	338	2	Q5LP70_SILPO	Q5lp70 silicibacte
712	6	7.5	321	2	Q6XD89_9REOV	Q6xd89 human rotav	785	6	7.5	338	2	Q7TNQ4_MOUSE	Q7tnq4 mus musculu
713	6	7.5	321	2	Q77NA3_9REOV	Q77na3 human rotav	786	6	7.5	339	2	Q7XFX4_ORISA	Q7xfx4 oryza sativ
714	6	7.5	321	2	Q86192_9REOV	Q86199 human rotav	787	6	7.5	339	2	Q8S841_ORISA	Q8s841 oryza sativ
715	6	7.5	321	2	Q9J454_9REOV	Q9j454 human rotav	788	6	7.5	339	2	Q6M3P6_CORGL	Q6m3p6 corynebacte
716	6	7.5	321	2	Q87697_SIVCZ	Q87697 chimpanzee	789	6	7.5	339	2	Q8F4N3_LEPIN	Q8f4n3 leptospira
717	6	7.5	322	1	DIDH_RAT	P23457 rattus norv	790	6	7.5	340	2	Q8E7C6_9UROC	Q8e7c6 bradyrhizob
718	6	7.5	322	2	Q9RJ06_STRCO	Q9rj06 streptomyc	791	6	7.5	340	2	Q89J65_BRAJA	Q89j65 bradyrhizob
719	6	7.5	322	2	Q5BKCB_RAT	Q5bkcb rattus norv	792	6	7.5	341	2	Q8DGH8_SYNEL	Q8dgh8 synethococc
720	6	7.5	323	1	Y370_MYCSE	P47610 mycoplasma	793	6	7.5	341	2	Q726A3_DESVH	Q726a3 desulfovibr
721	6	7.5	324	1	ODPB_BACSE	P21882 bacillus su	794	6	7.5	341	2	Q9D9A3_MOUSE	Q9d9a3 mus musculu
722	6	7.5	324	1	YHDI_ECOLI	P26646 escherichia	795	6	7.5	342	2	Q6FN43_CANGA	Q6fn43 candida gla
723	6	7.5	324	2	Q4WFN6_ASPFU	Q4wfn6 aspergillus	796	6	7.5	342	2	Q4HB64_9DEIO	Q4hb64 deinococcus
724	6	7.5	324	2	Q57J92_SALCH	Q57j92 salmonella	797	6	7.5	344	1	LPXD_SVNY3	Q55612 synethocyst
725	6	7.5	324	2	Q9RJN8_STRCO	Q9rjn8 streptomyc	798	6	7.5	344	1	Q4NHJ3_9MICC	Q4nhj3 arthrobacte
726	6	7.5	324	2	Q5EJVB_SALPA	Q5ejvb salmonella	799	6	7.5	345	1	KRI_CHV9D	Q45453 cercopithe
727	6	7.5	324	2	Q7CPM2_SALTY	Q7cpm2 salmonella	800	6	7.5	345	1	LPXD2_GLOVI	Q45453 cercopithe
728	6	7.5	324	2	Q83PZ8_SHIFL	Q83pz8 shigella fl	801	6	7.5	345	2	Q727A0_DESVH	Q727a0 gloeobacter
729	6	7.5	324	2	Q8PD42_ECOL6	Q8pd42 escherichia	802	6	7.5	345	2	Q77LR7_SALPH	Q77lr7 desulfovibr
730	6	7.5	324	2	Q8X9C1_ECO57	Q8x9c1 escherichia	803	6	7.5	345	2	Q4T9X3_TETNG	Q4t9x3 cercopithe
731	6	7.5	324	2	Q8XG63_SALTI	Q8xg63 salmonella	804	6	7.5	346	2	Q9AI37_BURMA	Q9ai37 tetradon n
732	6	7.5	324	2	Q7ZUN1_BRARE	Q7zun1 brachydanio	805	6	7.5	346	2	Q6ZHG2_BURMA	Q6zhg2 burkholderi
733	6	7.5	324	2	Q4SMQ7_TETNG	Q4smq7 tetradon n	806	6	7.5	346	2	Q93UJ3_BURPS	Q93uj3 burkholderi
734	6	7.5	325	2	Q5UZQ6_HALMA	Q5uzq6 haloarcula	807	6	7.5	347	2	Q87476_SIVCZ	Q87476 chimpanzee
735	6	7.5	325	2	Q17597_CAEEL	Q17597 caenorhabdi	808	6	7.5	347	2	Q4H2C1_STRGR	Q4h2c1 streptomyc
736	6	7.5	325	2	Q4HBJ4_9DEIO	Q4hbj4 deinococcus	809	6	7.5	348	1	YLM1_CAEEL	Q4h2c1 streptomyc
737	6	7.5	325	2	Q4KBU0_PSEF5	Q4kbu0 pseudomonas	810	6	7.5	348	2	Q26577_METTH	P34404 caenorhabdi
738	6	7.5	325	2	Q665F1_YERPS	Q665f1 yersinia ps	811	6	7.5	348	2	Q60YH9_CABBR	Q60yh9 caenorhabdi
739	6	7.5	325	2	Q6DA18_ERWCT	Q6da18 erwinia car	812	6	7.5	348	2	Q34353_BACSU	Q34353 bacillus su
740	6	7.5	325	2	Q8ZAW8_YERPE	Q8zaw8 yersinia pe	813	6	7.5	349	2	Q8NNK7_CORGL	Q8nnk7 corynebacte
741	6	7.5	325	2	Q65K43_BACLD	Q65k43 bacillus li	814	6	7.5	349	2	Q87696_SIVCZ	Q87696 chimpanzee
742	6	7.5	326	2	Q5YBD0_9CHLO	Q5ybd0 helicospori	815	6	7.5	350	2	Q748P7_GEOSL	Q748p7 geobacter s
743	6	7.5	326	2	Q9K4S7_PSEPU	Q9k4s7 pseudomonas	816	6	7.5	350	2	Q87695_SIVCZ	Q87695 chimpanzee
744	6	7.5	326	2	Q5E8X2_VIBF1	Q5e8x2 vibrio fisc	817	6	7.5	352	2	Q4X872_PLACH	Q4x872 plasmodium
745	6	7.5	326	2	Q6MSE1_MYCMS	Q6mse1 mycoplasma	818	6	7.5	352	2	Q59GG4_HUMAN	Q59gg4 homo sapien
746	6	7.5	326	2	Q81X81_BACAN	Q81x81 bacillus an	819	6	7.5	355	2	Q7S3N7_NEUCR	Q7s3n7 neurospora
747	6	7.5	326	2	Q7VJ94_HELHP	Q7vj94 helicobacte	820	6	7.5	355	2	Q83E04_COXBU	Q83e04 coxiella bu
748	6	7.5	326	2	Q7UHE3_RHOBA	Q7uhe3 rhodopirell	821	6	7.5	355	2	Q7VC86_PROMA	Q7vc86 prochloroco
749	6	7.5	326	2	Q87TP1_VIBPA	Q87tp1 vibrio para	822	6	7.5	356	1	XARG_DRONE	P48610 drosophila
750	6	7.5	326	2	Q8DDK4_VIBVU	Q8ddk4 vibrio vuln	823	6	7.5	356	2	Q8PTS2_METMA	Q8pts2 methanosarc
751	6	7.5	326	2	Q9KW22_VIBCH	Q9kw22 vibrio chol	824	6	7.5	356	2	Q6C018_YARLI	Q6c018 yarrowia li
752	6	7.5	326	2	Q7MQ11_VIBVY	Q7mq11 vibrio vuln	825	6	7.5	356	2	Q9Y4T9_HUMAN	Q9y4t9 homo sapien
753	6	7.5	327	2	Q95J23_MACFA	Q95j23 macaca fasc	826	6	7.5	356	2	Q8H1K4_9DINO	Q8h1k4 symbiodiniu
754	6	7.5	327	2	Q6V4X1_VIGUN	Q6v4x1 vigna ungui	827	6	7.5	356	2	Q6F973_ACTAD	Q6f973 acinetobact
755	6	7.5	327	2	Q8G4Z2_BIFLO	Q8g4z2 bifidobacte	828	6	7.5	356	2	Q5LW08_PROPR	Q5lw08 photobacter
756	6	7.5	327	2	Q9KAW1_BACHD	Q9kaw1 bacillus ha	829	6	7.5	357	2	Q7ZZT2_BRARE	Q7zzt2 brachydanio
757	6	7.5	328	2	Q516U2_ENTHI	Q516u2 entamoeba h	830	6	7.5	357	2	Q87681_SIVCZ	Q87681 chimpanzee
758	6	7.5	328	2	Q6N0V2_RHOPA	Q6n0v2 rhodospseudo	831	6	7.5	357	2	Q87682_SIVCZ	Q87682 chimpanzee
759	6	7.5	329	2	Q54NY5_DICDI	Q54ny5 dictyosteli	832	6	7.5	357	2	Q87683_SIVCZ	Q87683 chimpanzee
760	6	7.5	329	2	Q7VD49_PROMA	Q7vd49 prochloroco	833	6	7.5	357	2	Q87684_SIVCZ	Q87684 chimpanzee
761	6	7.5	329	2	Q89HS0_BRAJA	Q89hs0 bradyrhizob	834	6	7.5	357	2	Q87686_SIVCZ	Q87686 chimpanzee

835	6	7.5	357	2	Q87689_SIVCZ	Q87689 chimpanzee	908	6	7.5	371	2	Q87692_SIVCZ	Q87692 chimpanzee
836	6	7.5	358	2	Q8HD78_BRANA	Q8hd78 brassica na	909	6	7.5	371	2	Q87647_SIVCZ	Q87647 chimpanzee
837	6	7.5	358	2	Q4JU24_CORJK	Q4ju24 corynebacte	910	6	7.5	371	2	Q87648_SIVCZ	Q87648 chimpanzee
838	6	7.5	358	2	Q87688_SIVCZ	Q87688 chimpanzee	911	6	7.5	371	2	Q87649_SIVCZ	Q87649 chimpanzee
839	6	7.5	358	2	Q87690_SIVCZ	Q87690 chimpanzee	912	6	7.5	371	2	Q87650_SIVCZ	Q87650 chimpanzee
840	6	7.5	360	2	Q7PPK6_ANOGA	Q7ppk6 anopheles g	913	6	7.5	371	2	Q87651_SIVCZ	Q87651 chimpanzee
841	6	7.5	360	2	Q91UR2_92ZZZ	Q91ur2 plasmid pb	914	6	7.5	371	2	Q87652_SIVCZ	Q87652 chimpanzee
842	6	7.5	360	2	Q91UX1_92ZZZ	Q91ux1 plasmid pip	915	6	7.5	371	2	Q87654_SIVCZ	Q87654 chimpanzee
843	6	7.5	360	2	Q4K695_PSBPF5	Q4k695 pseudomonas	916	6	7.5	371	2	Q87656_SIVCZ	Q87656 chimpanzee
844	6	7.5	361	2	Q4HSG9_CAMUP	Q4hsg9 campylobact	917	6	7.5	372	2	Q4IEQ5_GIBZE	Q4ieq5 gibberella
845	6	7.5	362	2	Q9EUI1_SALET	Q9eui1 salmonella	918	6	7.5	372	2	Q624P6_CABBR	Q624p6 caenorhabdi
846	6	7.5	362	2	Q74E10_GEOSL	Q74e10 geobacter s	919	6	7.5	372	2	Q97EN7_CIOAB	Q97en7 clostridium
847	6	7.5	364	2	Q8DL75_SYNEL	Q8dl75 synechococ	920	6	7.5	372	2	Q7ZR92_SIVCZ	Q7zr92 chimpanzee
848	6	7.5	365	1	PCP_SYNSP	P51874 symbiodiniu	921	6	7.5	372	2	Q7ZR91_SIVCZ	Q7zr91 chimpanzee
849	6	7.5	365	2	Q5DHJ2_SCHJA	Q5dhj2 schistosoma	922	6	7.5	372	2	Q7ZR95_SIVCZ	Q7zr95 chimpanzee
850	6	7.5	365	2	Q7QB44_ANOGA	Q7qby4 anopheles g	923	6	7.5	373	2	Q93651_ARCPR	Q93651 archaeglob
851	6	7.5	365	2	Q8H110_SYMKA	Q8h110 symbiodiniu	924	6	7.5	373	2	Q53048_9LACO	Q53048 lactobacill
852	6	7.5	365	2	Q8H111_SYMKA	Q8h111 symbiodiniu	925	6	7.5	373	2	Q7ZR89_SIVCZ	Q7zr89 chimpanzee
853	6	7.5	365	2	Q8H113_SYMKA	Q8h113 symbiodiniu	926	6	7.5	373	2	Q7ZR91_SIVCZ	Q7zr91 chimpanzee
854	6	7.5	365	2	Q8H114_SYMKA	Q8h114 symbiodiniu	927	6	7.5	373	2	Q7ZR93_SIVCZ	Q7zr93 chimpanzee
855	6	7.5	365	2	Q8H115_SYMKA	Q8h115 symbiodiniu	928	6	7.5	373	2	Q7ZRF2_SIVCZ	Q7zrf2 chimpanzee
856	6	7.5	365	2	Q8H118_SYMKA	Q8h118 symbiodiniu	929	6	7.5	373	2	Q7ZRH6_SIVCZ	Q7zrh6 chimpanzee
857	6	7.5	365	2	Q8H119_SYMKA	Q8h119 symbiodiniu	930	6	7.5	373	2	Q87653_SIVCZ	Q87653 chimpanzee
858	6	7.5	365	2	Q8HLJ6_9DINO	Q8hlj6 symbiodiniu	931	6	7.5	374	2	Q8A706_BACTN	Q8a706 bacteroides
859	6	7.5	365	2	Q8HLJ7_9DINO	Q8hlj7 symbiodiniu	932	6	7.5	374	2	Q87711_SIVCZ	Q87711 chimpanzee
860	6	7.5	365	2	Q8HLJ8_9DINO	Q8hlj8 symbiodiniu	933	6	7.5	374	2	Q7ZR82_SIVCZ	Q7zr82 chimpanzee
861	6	7.5	365	2	Q8HLJ9_9DINO	Q8hlj9 symbiodiniu	934	6	7.5	374	2	Q87694_SIVCZ	Q87694 chimpanzee
862	6	7.5	365	2	Q8HLK0_9DINO	Q8h1k0 symbiodiniu	935	6	7.5	374	2	Q87712_SIVCZ	Q87712 chimpanzee
863	6	7.5	365	2	Q8HLK1_9DINO	Q8h1k1 symbiodiniu	936	6	7.5	374	2	Q87713_SIVCZ	Q87713 chimpanzee
864	6	7.5	365	2	Q8HLK2_9DINO	Q8h1k2 symbiodiniu	937	6	7.5	374	2	Q87737_SIVCZ	Q87737 chimpanzee
865	6	7.5	365	2	Q8HLK3_9DINO	Q8h1k3 symbiodiniu	938	6	7.5	374	2	Q87738_SIVCZ	Q87738 chimpanzee
866	6	7.5	365	2	Q8HLK5_9DINO	Q8h1k5 symbiodiniu	939	6	7.5	374	2	Q87739_SIVCZ	Q87739 chimpanzee
867	6	7.5	365	2	Q88151_SIVCZ	Q88151 chimpanzee	940	6	7.5	375	1	NUC1_YEAST	P32451 saccharomyc
868	6	7.5	365	2	Q04478_SIVCZ	Q04478 chimpanzee	941	6	7.5	375	1	BIO1_CAEEL	Q17778 caenorhabdi
869	6	7.5	365	2	Q04479_SIVCZ	Q04479 chimpanzee	942	6	7.5	375	2	Q60WQ5_CABBR	Q60wq5 caenorhabdi
870	6	7.5	365	2	Q04480_SIVCZ	Q04480 chimpanzee	943	6	7.5	375	2	Q17039_CAEEL	Q17039 caenorhabdi
871	6	7.5	365	2	Q4U283_SIVCZ	Q4u283 chimpanzee	944	6	7.5	375	2	Q7XWH9_ORISA	Q7xwh9 oryza sativ
872	6	7.5	365	2	Q4U2E0_SIVCZ	Q4u2e0 chimpanzee	945	6	7.5	375	2	Q7ZR88_SIVCZ	Q7zr88 chimpanzee
873	6	7.5	366	2	Q6V587_CRILLO	Q6v587 cricetulus	946	6	7.5	375	2	Q7ZRF3_SIVCZ	Q7zrf3 chimpanzee
874	6	7.5	366	2	Q5BJX5_RAT	Q5bjx5 rattus norv	947	6	7.5	375	2	Q7ZRF4_SIVCZ	Q7zrf4 chimpanzee
875	6	7.5	366	2	Q8C739_MOUSE	Q8c739 mus musculu	948	6	7.5	375	2	Q7ZRF6_SIVCZ	Q7zrf6 chimpanzee
876	6	7.5	367	2	Q8SOV7_ORISA	Q8sov7 oryza sativ	949	6	7.5	375	2	Q7ZRF7_SIVCZ	Q7zrf7 chimpanzee
877	6	7.5	367	2	Q6PFV6_AC1AD	Q6ffv6 acinetobact	950	6	7.5	375	2	Q7ZRF8_SIVCZ	Q7zrf8 chimpanzee
878	6	7.5	367	2	Q74P27_GEOSL	Q74f27 geobacter s	951	6	7.5	375	2	Q7ZRF9_SIVCZ	Q7zrf9 chimpanzee
879	6	7.5	367	2	Q8R346_MOUSE	Q8r346 mus musculu	952	6	7.5	375	2	Q7ZRL1_SIVCZ	Q7zrl1 chimpanzee
880	6	7.5	368	2	Q53VZ4_THET8	Q53vz4 thermus the	953	6	7.5	375	2	Q87691_SIVCZ	Q87691 chimpanzee
881	6	7.5	369	2	Q9C6B1_ARATH	Q9c6b1 arabidopsis	954	6	7.5	375	2	Q87693_SIVCZ	Q87693 chimpanzee
882	6	7.5	369	2	Q4G057_RAT	Q4g057 rattus norv	955	6	7.5	376	2	Q7ZR83_SIVCZ	Q7zr83 chimpanzee
883	6	7.5	369	2	Q4SRE5_TETNG	Q4sre5 tetraodon n	956	6	7.5	376	2	Q7ZR84_SIVCZ	Q7zr84 chimpanzee
884	6	7.5	369	2	Q87671_SIVCZ	Q87671 chimpanzee	957	6	7.5	376	2	Q7ZR85_SIVCZ	Q7zr85 chimpanzee
885	6	7.5	370	2	Q9NUZ1_HUMAN	Q9nuz1 homo sapien	958	6	7.5	376	2	Q7ZR86_SIVCZ	Q7zr86 chimpanzee
886	6	7.5	370	2	Q4UQN2_XANCP	Q4uqn2 xanthomonas	959	6	7.5	376	2	Q7ZR87_SIVCZ	Q7zr87 chimpanzee
887	6	7.5	370	2	Q8PCF7_XANCP	Q8pcf7 xanthomonas	960	6	7.5	376	2	Q7ZR94_SIVCZ	Q7zr94 chimpanzee
888	6	7.5	370	2	Q8FPG6_XANCP	Q8fpg6 xanthomonas	961	6	7.5	376	2	Q7ZR95_SIVCZ	Q7zr95 chimpanzee
889	6	7.5	370	2	Q7ZR90_SIVCZ	Q7zr90 chimpanzee	962	6	7.5	376	2	Q7ZR96_SIVCZ	Q7zr96 chimpanzee
890	6	7.5	370	2	Q7ZRD3_SIVCZ	Q7zrd3 chimpanzee	963	6	7.5	376	2	Q7ZR97_SIVCZ	Q7zr97 chimpanzee
891	6	7.5	370	2	Q7ZRD4_SIVCZ	Q7zrd4 chimpanzee	964	6	7.5	376	2	Q7ZR98_SIVCZ	Q7zr98 chimpanzee
892	6	7.5	370	2	Q7ZRD8_SIVCZ	Q7zrd8 chimpanzee	965	6	7.5	376	2	Q7ZR99_SIVCZ	Q7zr99 chimpanzee
893	6	7.5	370	2	Q87657_SIVCZ	Q87657 chimpanzee	966	6	7.5	376	2	Q7ZRA0_SIVCZ	Q7zra0 chimpanzee
894	6	7.5	370	2	Q87659_SIVCZ	Q87659 chimpanzee	967	6	7.5	376	2	Q7ZRA1_SIVCZ	Q7zra1 chimpanzee
895	6	7.5	370	2	Q87660_SIVCZ	Q87660 chimpanzee	968	6	7.5	376	2	Q7ZRA2_SIVCZ	Q7zra2 chimpanzee
896	6	7.5	370	2	Q87662_SIVCZ	Q87662 chimpanzee	969	6	7.5	376	2	Q7ZRA3_SIVCZ	Q7zra3 chimpanzee
897	6	7.5	370	2	Q87663_SIVCZ	Q87663 chimpanzee	970	6	7.5	376	2	Q7ZRL2_SIVCZ	Q7zrl2 chimpanzee
898	6	7.5	370	2	Q87664_SIVCZ	Q87664 chimpanzee	971	6	7.5	376	2	Q7ZRL3_SIVCZ	Q7zrl3 chimpanzee
899	6	7.5	370	2	Q87665_SIVCZ	Q87665 chimpanzee	972	6	7.5	376	2	Q7ZRL4_SIVCZ	Q7zrl4 chimpanzee
900	6	7.5	370	2	Q87666_SIVCZ	Q87666 chimpanzee	973	6	7.5	376	2	Q7ZRL5_SIVCZ	Q7zrl5 chimpanzee
901	6	7.5	370	2	Q87672_SIVCZ	Q87672 chimpanzee	974	6	7.5	377	2	Q7XVB1_ORISA	Q7xvb1 oryza sativ
902	6	7.5	370	2	Q87674_SIVCZ	Q87674 chimpanzee	975	6	7.5	377	2	Q8LME2_ORISA	Q8lme2 oryza sativ
903	6	7.5	370	2	Q87675_SIVCZ	Q87675 chimpanzee	976	6	7.5	377	2	Q60DR0_ORISA	Q60dr0 oryza sativ
904	6	7.5	370	2	Q87676_SIVCZ	Q87676 chimpanzee	977	6	7.5	377	2	Q67U18_ORISA	Q67u18 oryza sativ
905	6	7.5	370	2	Q87678_SIVCZ	Q87678 chimpanzee	978	6	7.5	377	2	Q6F2X7_ORISA	Q6f2x7 oryza sativ
906	6	7.5	370	2	Q87679_SIVCZ	Q87679 chimpanzee	979	6	7.5	377	2	Q615J4_ORISA	Q615j4 oryza sativ
907	6	7.5	371	2	Q7ZRH7_SIVCZ	Q7zrh7 chimpanzee	980	6	7.5	377	2	Q9HYK4_PSEAE	Q9hyk4 pseudomonas

981 6 7.5 377 2 Q728G8 DESVH
 982 6 7.5 377 2 Q72RF5_SIVCZ
 983 6 7.5 378 2 Q66B9_YARLOWIA LI
 984 6 7.5 378 2 Q51E56_BACFN
 985 6 7.5 378 2 Q9F764_BACFR
 986 6 7.5 378 2 Q56768_HCMV
 987 6 7.5 379 2 Q29504_ARCFU
 988 6 7.5 379 2 Q6C5N1_YARLI
 989 6 7.5 379 2 Q9X0Z7_THEMA
 990 6 7.5 379 2 Q6Q128_RAT
 991 6 7.5 380 1 Y079_METJA
 992 6 7.5 381 2 Q55JD9_CRYNE
 993 6 7.5 381 2 Q5CMP3_KLULA
 994 6 7.5 381 2 Q5KCC0_CRYNE
 995 6 7.5 381 2 Q61510_ORYSA
 996 6 7.5 381 2 Q414D2_STAHOJ
 997 6 7.5 382 2 Q8H2C3_PERA
 998 6 7.5 382 2 Q835Q8_ENTFA
 999 6 7.5 382 2 Q7MT14_PORGI
 1000 6 7.5 382 2 Q7VU27_BORPE

ALIGNMENTS

RESULT 1

CD9_HUMAN
 AC P21926; Q96ES4; STANDARD; PRT; 227 AA.
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)
 DE (MRP-1) (Tetraspanin-29) (TSPAN-29).
 GN Name=CD9; Synonyms=MIC3, TSPAN29;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.
 RX MEDLINE=91093112; PubMed=1840589;
 RA Boucheix J., Benoit P., Frachet P., Billard M., Worthington R.E.,
 RA Gagnon J., Uzan G.;
 RT "Molecular cloning of the CD9 antigen. A new family of cell surface
 RT proteins.";
 RL J. Biol. Chem. 266:117-122(1991).
 [2]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
 RX MEDLINE=91244846; PubMed=2037603;
 RA Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A.,
 RA Coughlin S.R., Phillips D.R., Jennings L.K.;
 RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new
 RT family of multiple membrane-spanning proteins.";
 RL J. Biol. Chem. 266:10638-10645(1991).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;
 RA Miyake M., Koyama M., Seno M., Ikegawa S.;
 RT "Identification of the motility-related protein (MRP-1), recognized by
 RT monoclonal antibody M31-15, which inhibits cell motility.";
 RL J. Exp. Med. 174:1347-1354(1991).
 [4]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC TISSUE=Leukocyte;
 RX MEDLINE=93252369; PubMed=8486348;
 RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,
 RA Uzan G., Boucheix C.;
 RT "Organization of the human CD9 gene.";
 RL Genomics 16:132-138(1993).
 [5]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Rajkumar N., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-
 RT FHCR, Seattle, WA [URL: http://pga.gs.washington.edu].";
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Ovary;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [7]
 RP PROTEIN SEQUENCE OF 1-20.
 RC TISSUE=Platelet;
 RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;
 RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;
 RT "Purification and partial characterization of CD9 antigen of human
 RT platelets.";
 RL FEBS Lett. 264:270-274(1990).
 [8]
 RP ROLE IN CELL MOTILITY AND METASTASIS.
 RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;
 RA Ikegawa S., Koyama M., Yamaoka M., Sasada R., Miyake M.;
 RT "Suppression of cell motility and metastasis by transfection with
 RT human motility-related protein (MRP-1/CD9) DNA.";
 RL J. Exp. Med. 177:1231-1237(1993).
 [9]
 RP ROLE IN CELL ADHESION.
 RX PubMed=7511626;
 RA Masellis-Smith A., Shaw A.R.;
 RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B
 RT cell adhesion to bone marrow fibroblasts through de novo recognition
 RT of fibronectin.";
 RL J. Immunol. 152:2768-2777(1994).
 [10]
 RP ROLE IN GAMETE FUSION.
 RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;
 RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,
 RA Partridge L.J., Monk P.N.;
 RT "Structural requirements for the inhibitory action of the CD9 large
 RT extracellular domain in sperm/oocyte binding and fusion.";
 RL Biochem. Biophys. Res. Commun. 311:208-214(2003).
 [11]
 RP SUBUNIT.
 RX PubMed=14556650; DOI=10.1042/BJ20031037;
 RA Kovalenko O.V., Yang X., Kolesnikova T.V., Hemler M.B.;
 RT "Evidence for specific tetraspanin homodimers: inhibition of
 RT palmitoylation makes cysteine residues available for cross-linking.";
 RL Biochem. J. 377:407-417(2004).
 [12]
 RP PHOSPHORYLATION.
 RX MEDLINE=93327758; PubMed=7687539;
 RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,
 RA Aruffo A., Ledbetter J.A.;
 RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";

EMBO J. 12:2691-2696(1993).
[13]
RN PALMITOYLATION, AND MUTAGENESIS OF CYS-8; CYS-77; CYS-78; CYS-86;
RP CYS-217 AND CYS-218.
RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;
RA Charin S., Manie S., Oualid M., Billard M., Bouchaix C.,
RA Rubinstein E.;
RT "Differential stability of tetraspanin/tetraspanin interactions: role
RT of palmitoylation.";
RL FEBS Lett. 516:139-144(2002).
RN [14]
RN INTERACTION WITH PTGFRN.
RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;
RA Charin S., Le Naour F., Oualid M., Billard M., Faure G., Hanash S.M.,
RA Bouchaix C., Rubinstein E.;
RT "The major CD9 and CD81 complexes.";
RT characterization of the complexes.";
RL J. Biol. Chem. 276:14329-14337(2001).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis.
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with
CC PTGFRN/CD9p1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and
CC epithelial cells.
CC -!- PTM: Protein exists in three forms with molecular masses between
CC 22 and 27 kDa, and is known to carry covalently linked fatty
CC acids.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; S60489; AAC60586.1; -; Genomic DNA.
DR EMBL; S60462; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60463; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60464; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60700; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60699; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60465; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60472; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; M38690; AAA80320.1; -; mRNA.
DR EMBL; L34068; AAA59982.1; -; mRNA.
DR EMBL; X50111; CAA42708.1; -; mRNA.
DR EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; L08119; AAA51954.1; ALT SEQ; Genomic DNA.
DR EMBL; L08120; AAA51955.1; ALT SEQ; Genomic DNA.
DR EMBL; L08121; AAA51956.1; -; Genomic DNA.
DR EMBL; L08122; AAA51957.1; -; Genomic DNA.
DR EMBL; L08123; AAA51958.1; -; Genomic DNA.
DR EMBL; L08124; AAA51959.1; -; Genomic DNA.
DR EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; AY422198; AAQ87878.1; -; Genomic DNA.
DR EMBL; BC011988; AAH11988.1; -; mRNA.
DR PIR; A46123; A40420.
DR Ensembl; ENSG0000010278; Homo sapiens.
DR HGNC; HGNC:1709; CD9.
DR H-InvDB; HIX0010357; -.
DR Reactome; P21926; -.
DR MIM; 143030; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0006928; P:cell motility; IDA.

DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030169; P:platelet activation; NAS.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; I.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;
Query Match 100.0%; Score 80; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.8e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTKEPQRETLLKAIHYALNCCGLAGGVQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNKLTKEPQRETLLKAIHYALNCCGLAGGVQFISDIPCCKDV 171
QY 61 LETFTVKSCPDPAIKEVFDNK 80
Db 172 LETFTVKSCPDPAIKEVFDNK 191
RESULT 2
Q5J7W6_HUMAN
ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.
AC Q5J7W6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Growth-inhibiting gene 2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Kim J.W.;
RA "Identification of a human growth inhibition gene 2 (GIG2).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY423720; AAS00483.1; -; mRNA.
DR EMBL; 228 AA; 25416 MW; F68333E0C20611D8 CRC64;
Query Match 100.0%; Score 80; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.8e-75;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HKDEVIKEVQEFYKDTYNKLTKEPQRETLLKAIHYALNCCGLAGGVQFISDIPCCKDV 60
Db 113 HKDEVIKEVQEFYKDTYNKLTKEPQRETLLKAIHYALNCCGLAGGVQFISDIPCCKDV 172
QY 61 LETFTVKSCPDPAIKEVFDNK 80
Db 173 LETFTVKSCPDPAIKEVFDNK 192
RESULT 3
Q56CY1_HUMAN
ID Q56CY1 HUMAN PRELIMINARY; PRT; 182 AA.
AC Q56CY1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Bladder cancer related CD9 variant.
GN Name=BTCC-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Tissue=Bladder;
RC

RA Ma F., Wang H., Wang X., Chang J.;
 RT "The full-length cloning of a differentially expressed EST sequence in
 RT a bladder cancer subtractive cDNA library.";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY966455; AAX78197.1; -; mRNA.
 SQ SEQUENCE 182 AA; 20750 MW; C26F856F584AADEE CRC64;

Query Match 48.8%; Score 39; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 3.2e-32;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEQVFYKDTYTKLTKDEPQRETLLKAIHYALN 39
 |||||
 DB 113 HKDEVKEQVFYKDTYTKLTKDEPQRETLLKAIHYALN 151
 |||||

RESULT 4
 CD9_CERAE
 ID CD9_CERAE STANDARD; PRT; 227 AA.
 AC P30409;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein)
 DE (DRAP27).
 GN Name=CD9;
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;
 RA Mitamura T., Iwanoto R., Umata T., Yomo T., Tsuneoka M.,
 RA Mekada E.;
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from
 RT vero cells is the monkey homologue of human CD9 antigen: expression of
 RT DRAP27 elevates the number of diphtheria toxin receptors on toxin-
 RT sensitive cells.";
 RL J. Cell Biol. 118:1389-1399(1992).
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis (By similarity).
 CC -!- FUNCTION: Expression of DRAP27 elevates the number of diphtheria
 CC toxin receptors on toxin-sensitive cells.
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; D10726; BAA01569.1; -; mRNA.
 DR F01; A42929; A42929.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0007155; P:cell adhesion; ISS.
 DR GO; GO:0006928; P:cell motility; ISS.
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
 DR GO; GO:0030913; P:paranodal junction formation; ISS.
 DR GO; GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; I.

DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
 KW Palmitate; Phosphorylation; Transmembrane.
 FT INIT MET 0
 FT TOPO_DOM 1 11
 FT TRANSMEM 12 32
 FT TOPO_DOM 33 54
 FT TRANSMEM 55 75
 FT TOPO_DOM 76 86
 FT TRANSMEM 87 110
 FT TOPO_DOM 111 194
 FT TRANSMEM 195 220
 FT TOPO_DOM 221 227
 FT LIPID 8 8
 FT LIPID 77 77
 FT LIPID 78 78
 FT LIPID 86 86
 FT LIPID 217 217
 FT LIPID 218 218
 FT CARBOHYD 51 51
 FT CARBOHYD 52 52
 SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;

Query Match 47.5%; Score 38; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 4.2e-31;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEQVFYKDTYTKLTKDEPQRETLLKAIHYAL 38
 |||||
 DB 112 HKDEVKEQVFYKDTYTKLTKDEPQRETLLKAIHYAL 149
 |||||

RESULT 5
 CD9_FELCA
 ID CD9_FELCA STANDARD; PRT; 225 AA.
 AC P40239;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE CD9 antigen.
 GN Name=CD9;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;
 RA Willett B.J., Neil J.C.;
 RT "cDNA cloning and eukaryotic expression of feline CD9.";
 RL Mol. Immunol. 32:417-423(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Morikawa S.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis (By similarity).
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; D10726; BAA01569.1; -; mRNA.
 DR F01; A42929; A42929.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0007155; P:cell adhesion; ISS.
 DR GO; GO:0006928; P:cell motility; ISS.
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
 DR GO; GO:0030913; P:paranodal junction formation; ISS.
 DR GO; GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; I.

CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; L35275; AAA92867.1; -; mRNA.
 CC EMBL; D30786; BAA06452.1; -; mRNA.
 CC GO; GO:0005887; C:integral to plasma membrane; ISS.
 CC GO; GO:0005515; F:protein binding; ISS.
 CC GO; GO:0007155; P:cell adhesion; ISS.
 CC GO; GO:0006928; P:cell motility; ISS.
 CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
 CC GO; GO:0030913; P:paranodal junction formation; ISS.
 CC GO; GO:0030168; P:platelet activation; ISS.
 CC InterPro; IPR000301; Transmem 4.
 CC Pfam; PF00335; Tetraepanin; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4 1; 1.
 CC Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
 KW Phosphorylation; Transmembrane.
 FT INIT_MET 0 0 By similarity.
 FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT TOPO_DOM 74 84 Cytoplasmic (Potential).
 FT TRANSMEM 85 108 Potential.
 FT TOPO_DOM 109 192 Extracellular (Potential).
 FT TRANSMEM 193 218 Potential.
 FT TOPO_DOM 219 225 Cytoplasmic (Potential).
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
 FT CONFLICT 82 82 S -> Y (in Ref. 2).
 SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 21.2%; Score 17; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCGAGGVEQFISDIPC 56
 |||||
 Db 149 CCGAGGVEQFISDIPC 165

RESULT 6

CD9_RAT ID CD9_RAT STANDARD; PRT; 225 AA.
 AC P40241;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen.
 GN Name=CD9;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
 RX MEDLINE=95123481; PubMed=7823164;
 RA Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;
 RT "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen
 RT and is expressed in the nervous system.";
 RL J. Neurosci. 15:562-573 (1995).
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis (By similarity).
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher

CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; X76489; CAA54027.1; -; mRNA.
 CC PIR; I56562; S39262.
 CC Ensembl; ENSRNOG00000019556; Rattus norvegicus.
 CC RGD; 2318; Cd9.
 CC GO; GO:0009986; C:cell surface; IDA.
 CC GO; GO:0005887; C:integral to plasma membrane; ISS.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0007155; P:cell adhesion; ISS.
 CC GO; GO:0006928; P:cell motility; ISS.
 CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
 CC GO; GO:0030913; P:paranodal junction formation; ISS.
 CC GO; GO:0030168; P:platelet activation; ISS.
 CC InterPro; IPR000301; Transmem 4.
 CC Pfam; PF00335; Tetraepanin; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4 1; 1.
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
 KW Palmitate; Phosphorylation; Transmembrane.
 FT INIT_MET 0 0 By similarity.
 FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT TOPO_DOM 74 84 Cytoplasmic (Potential).
 FT TRANSMEM 85 108 Potential.
 FT TOPO_DOM 109 192 Extracellular (Potential).
 FT TRANSMEM 193 218 Potential.
 FT TOPO_DOM 219 225 Cytoplasmic (Potential).
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 225 AA; 25084 MW; 7889619F99A59C9D CRC64;

Query Match 18.8%; Score 15; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 AGGVEQFISDIPC 58
 |||||
 Db 153 AGGVEQFISDIPC 167

RESULT 7

CD9_BOVIN ID CD9_BOVIN STANDARD; PRT; 225 AA.
 AC P30932;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen.
 GN Name=CD9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP ROLE IN GAMETE FUSION.
RX PubMed:10700183; DOI=10.1038/73502;
RA Kaji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,
RA Tada N., Miyazaki S., Kudo A.;
RT "The gamete fusion process is defective in eggs of Cd9-deficient
mice.";
RL Nat. Genet. 24:279-282(2000).
RN [5]
RP ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.
RX PubMed:14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;
RA Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,
RA Baba H.;
RT "Tetraspanin protein CD9 is a novel paranodal component regulating
paranodal junctional formation.";
RL J. Neurosci. 24:96-102(2004).
RN [6]
RP FUNCTION AS RECEPTOR FOR PSG17.
RX PubMed:11805154; DOI=10.1084/jem.20011741;
RA Waterhouse R., Ha C., Dveksler G.S.;
RT "Murine CD9 is the receptor for pregnancy-specific glycoprotein 17.";
RL J. Exp. Med. 195:277-282(2002).
RN [7]
RP FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
fusion. Involved in cell adhesion, cell motility and tumor
metastasis. Acts as a receptor for PSG17.
CC -! SUBUNIT: Forms both disulfide-linked homodimers and higher
homooligomers as well as heterooligomers with other members of the
tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
(By similarity).
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: Expressed predominantly in the peripheral
nervous system.
CC -! PTM: Phosphorylated on tyrosine following B-cell activation (By
similarity).
CC -! SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; L08115; AAA37405.1; -; mRNA.
CC EMBL; AK002251; BAB21965.1; -; mRNA.
CC EMBL; AK012793; BAB28473.1; -; mRNA.
CC EMBL; BC070474; AAB70474.1; -; mRNA.
CC PIR; I49589; I49589.
CC Ensembl; ENSMUSG0000030342; Mus musculus.
CC MGI; MGI:88348; Cd9.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
CC GO; GO:0030913; P:paranodal junction formation; IDA.
CC GO; GO:0030168; P:platelet activation; ISS.
CC InterPro; IPR00301; Transmem 4.
CC Pfam; PF00335; Tetraspanin 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1; 1.
CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.

FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 25127 MW; 2BBE40B8D7C31BC0 CRC64;
Query Match 16.2%; Score 13; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 KDEPQRETLKAIH 35
DB 132 KDEPQRETLKAIH 144
RESULT 9
ID CD9_PIG STANDARD; PRT; 225 AA.
AC Q8WMQ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Smooth muscle;
RX PubMed:14610355; DOI=10.1159/000074170;
RA Yubero N., Jimenez-Marín A., Yerle M., Morena L., Barbancho M.J.,
RA Llanes D., Garrido J.J.;
RT "Molecular cloning, expression pattern and chromosomal mapping of pig
CD9 antigen.";
RL Cytogenet. Genome Res. 101:143-146(2003).
CC -! FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
fusion. Involved in cell adhesion, cell motility and tumor
metastasis (By similarity).
CC -! SUBUNIT: Forms both disulfide-linked homodimers and higher
homooligomers as well as heterooligomers with other members of the
tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
(By similarity).
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! PTM: Phosphorylated on tyrosine following B-cell activation (By
similarity).
CC -! SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; AY072785; AAL68966.1; -; mRNA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; F:protein binding; ISS.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.

Qy	Db	Query Match	Best Local Similarity	Matches	Score	DB 1; Length	DB 2; Length	Mismatches	Indels	Gaps
DR	DR	InterPro; IPR000301; Transmem_4.	16.2%;	Score 13; DB 1; Length 225;	0;					
DR	DR	Pfam; PF00335; Tetraspannin; 1.	100.0%;	Pred. No. 5.4e-05;	0;					
DR	DR	PRINTS; PR00259; TMFOUR.	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
DR	DR	PROSITE; PS00421; TM4_1; 1.								
KW	KW	Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;								
KW	KW	Palmitate; Phosphorylation; Transmembrane.								
FT	FT	INIT_MET 0 0								
FT	FT	TOPO_DOM 1 11								
FT	FT	TRANSMEM 12 32								
FT	FT	TOPO_DOM 33 52								
FT	FT	TRANSMEM 53 73								
FT	FT	TOPO_DOM 74 84								
FT	FT	TRANSMEM 85 108								
FT	FT	TOPO_DOM 109 192								
FT	FT	TRANSMEM 193 218								
FT	FT	TOPO_DOM 219 225								
FT	FT	LIPID 8 8								
FT	FT	LIPID 75 75								
FT	FT	LIPID 76 76								
FT	FT	LIPID 84 84								
FT	FT	LIPID 215 215								
FT	FT	LIPID 216 216								
FT	FT	CARBOHYD 49 49								
FT	FT	CARBOHYD 50 50								
FT	FT	SEQUENCE 225 AA; 25070 MW; PF280FE39BC11545 CRC64;								
Qy	26	PORETLKAIHYAL 38								
Db	135	PORETLKAIHYAL 147								
RESULT 10										
ID	Q8MJ48	PIG PRELIMINARY;								
AC	Q8MJ48;	PRT; 226 AA.								
DT	01-OCT-2002	(TrEMBLrel. 22, Created)								
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)								
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)								
DE		Transmembrane protein CD9.								
GN		Name=CD9;								
OS		Sus scrofa (Pig).								
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC		Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;								
OC		Sus.								
NCBI_TaxID=9823;										
[1]										
RP		NUCLEOTIDE SEQUENCE.								
RA	Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,									
RA	Kurilla-Nahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,									
RA	Down J.D., Sachs D.H., Goodell M.A.;									
RT	"Use of CD9 Expression to Enrich for Porcine Hematopoietic									
RT	Progenitors.";									
RL	Exp. Hematol. 0:0-0(2002).									
DR	EMBL; AF525029; AAM81376.1; -; mRNA.									
DR	HSSP; P60033; IG8Q.									
GO	GO:0016021; C:integral to membrane; IEA.									
DR	InterPro; IPR000301; Transmem 4.									
DR	Pfam; PF00335; Tetraspannin; 1.									
DR	PRINTS; PR00259; TMFOUR.									
DR	PROSITE; PS00421; TM4_1; 1.									
KW	Transmembrane.									
Qy	26	PORETLKAIHYAL 38								
Db	135	PORETLKAIHYAL 147								
Query Match										
Best Local Similarity										

Query Match 10.0%; Score 8; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIKSVF 77
| | | | | | | |
Db 252 PDAIKSVF 259

RESULT 13

Q5AJ90 CANAL PRELIMINARY; PRT; 410 AA.
AC Q5AJ90;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Potential peroxisomal 3-ketoacyl-CoA thiolase.
GN Name=PO2; ORFNames=CaO19.1704, CaO19.9271;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S.;
RA "The diploid genome sequence of Candida albicans.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;
RA "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000014; EAL02864.1; -; Genomic_DNA.
DR EMBL; AACQ01000013; EAL02993.1; -; Genomic_DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Acyltransferase; Transferase.
SQ SEQUENCE 410 AA; 43877 MW; 65CBEC99E39B4692 CRC64;

Query Match 10.0%; Score 8; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CGLAGGVE 48
| | | | | | | |
Db 121 CGLAGGVE 128

RESULT 14

Q4XU05 PLACH PRELIMINARY; PRT; 29 AA.
AC Q4XU05;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC105993.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A., Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K., James K., Rutherford K., Harris B., Harris D., Churcher C.,

Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C., Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; CAAJ01003007; CAH79356.1; -; Genomic_DNA.
DR Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 29 AA; 3541 MW; A386F2C2D29442CC CRC64;

Query Match 8.8%; Score 7; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YNKLKTK 23
| | | | | | | |
Db 2 YNKLKTK 8

RESULT 15

Q6LHC2 PROPR PRELIMINARY; PRT; 91 AA.
AC Q6LHC2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PBPRB1442;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N., Romualdi C., Bartlett D.H., Valle G.;
RA "Life at depth: Photobacterium profundum genome sequence and expression analysis.";
RL Science 307:1459-1461(2005).
DR EMBL; CR378679; CAG33308.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 91 AA; 11346 MW; 47435EB3848A1126 CRC64;

Query Match 8.8%; Score 7; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRE 29
| | | | | | | |
Db 29 KDEPQRE 35

Search completed: January 20, 2006, 17:44:43
Job time : 129.769 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:33:55 ; Search time 35.0769 Seconds
(without alignments)
300.628 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24
Sequence: 1 LRPDSQTKSIFRQETNNNSFPYT 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	95	3	Aag01570 Human sec
2	24	100.0	209	4	Aag76051 Human col
3	24	100.0	227	2	Aar86834 Human CD9
4	24	100.0	227	5	Abb78366 Amino aci
5	24	100.0	227	5	Aae14636 Human CD9
6	24	100.0	227	6	Abu05057 Human exp
7	24	100.0	227	6	Abu05060 Human exp
8	24	100.0	227	7	Abw00436 Human CD9
9	24	100.0	227	7	Adk69862 Human CD9
10	24	100.0	227	8	Adl19366 Human CD9
11	24	100.0	227	9	Aea89005 Human CD9
12	24	100.0	228	4	Abb44581 Human wou
13	24	100.0	228	6	Abu05059 Human exp
14	24	100.0	228	6	Abu05052 Human exp
15	24	100.0	228	6	Abu05048 Human exp
16	24	100.0	228	6	Abu05049 Human exp
17	24	100.0	228	6	Abu05050 Human exp
18	24	100.0	228	6	Abu05053 Human exp
19	24	100.0	228	7	Abw01519 Protein #
20	24	100.0	228	7	Adk89037 TAT278. 1
21	24	100.0	228	7	Adg32002 Human hom
22	24	100.0	228	8	Adj57558 Human CD9
23	24	100.0	228	8	Adl26782 Human CD9
24	24	100.0	228	8	Adl82853 Human PRO

98	6	25.0	203	8	ADT58596	Adt58596 Plant pol	171	6	25.0	398	4	ABB70325	Abb70325 Drosophil
99	6	25.0	214	4	ABB70772	Abb70772 Drosophil	172	6	25.0	402	4	ABB70534	Abb70534 Drosophil
100	6	25.0	221	4	ABB64291	Abb64291 Drosophil	173	6	25.0	402	7	ABO77783	AbO77783 Pseudomon
101	6	25.0	228	4	ABB62497	Abb62497 Drosophil	174	6	25.0	405	3	AAG49723	Aag49723 Arabidops
102	6	25.0	236	2	AAW9456	Aaw9456 Amino aci	175	6	25.0	405	8	ADS24369	AdS24369 Bacterial
103	6	25.0	236	5	AAE19800	Aae19800 Candida a	176	6	25.0	406	8	ADN47627	Adn47627 Thermococ
104	6	25.0	236	7	ADM33265	Adm33265 Candida a	177	6	25.0	409	6	ABR40849	Abr40849 Momordica
105	6	25.0	242	7	ADD30644	Add30644 Plant yie	178	6	25.0	410	9	ABE40766	Aeb40766 L. pneumo
106	6	25.0	242	8	ADI43685	Adi43685 Plant tra	179	6	25.0	411	3	AAG35679	Aag35679 Arabidops
107	6	25.0	242	8	ADO03477	Ado03477 Thalecres	180	6	25.0	416	4	ABB59251	Abb59251 Drosophil
108	6	25.0	242	8	ADO63011	Ado63011 Transcrip	181	6	25.0	417	9	ABE37451	Aeb37451 L. pneumo
109	6	25.0	242	8	ADX66575	Adx66575 Plant ful	182	6	25.0	426	4	ABB67253	Abb67253 Drosophil
110	6	25.0	242	9	AEA26613	Aea26613 Stress to	183	6	25.0	431	6	ABR53542	Abr53542 Protein s
111	6	25.0	244	4	ABB65539	Abb65539 Drosophil	184	6	25.0	431	7	ADK64408	Adk64408 Disease t
112	6	25.0	249	4	ABM60887	Abm60887 Drosophil	185	6	25.0	431	8	ADT87238	Adt87238 Yeast Str
113	6	25.0	252	6	ADA15537	Ada15537 A. thalia	186	6	25.0	437	4	ABB62782	Abb62782 Drosophil
114	6	25.0	252	7	ADB31901	Adb31901 Plant (A.	187	6	25.0	440	3	AAB18146	Aab18146 Plaasmodiu
115	6	25.0	252	7	ADC46655	Adc46655 Thalecres	188	6	25.0	440	4	ABB72014	Abb72014 Drosophil
116	6	25.0	252	8	ADO02097	Ado02097 Thalecres	189	6	25.0	443	4	ABB65770	Abb65770 Drosophil
117	6	25.0	270	4	ABB66659	Abb66659 Drosophil	190	6	25.0	445	3	AAB00060	Aab00060 VRN2 poly
118	6	25.0	272	2	AKR05876	Akr05876 Merozite	191	6	25.0	447	4	AAG70714	Aag70714 S cerevis
119	6	25.0	272	3	AB18202	Ab18202 Plasmodiu	192	6	25.0	467	3	RAY54602	Ray54602 AV37 anti
120	6	25.0	274	3	AAG48240	Aag48240 Arabidops	193	6	25.0	477	4	ABB66931	Abb66931 Drosophil
121	6	25.0	274	3	AAG14699	Aag14699 Arabidops	194	6	25.0	478	3	RAA42226	Raa42226 Human ORF
122	6	25.0	275	3	AAG48239	Aag48239 Arabidops	195	6	25.0	478	3	RAY57603	Ray57603 Human pro
123	6	25.0	275	3	AG14598	Agl14598 Arabidops	196	6	25.0	478	7	ADJ68892	Adj68892 Human hea
124	6	25.0	276	3	AG165378	Agl65378 S. mansoni	197	6	25.0	479	6	ABR53846	Abr53846 Protein s
125	6	25.0	278	4	ABB69939	Abb69939 Drosophil	198	6	25.0	479	7	ADK64948	Adk64948 Disease t
126	6	25.0	280	4	ABB65783	Abb65783 Drosophil	199	6	25.0	480	4	ABB69134	Abb69134 Drosophil
127	6	25.0	284	4	ABB69768	Abb69768 Drosophil	200	6	25.0	480	8	ADU69147	Adu69147 Fruit fly
128	6	25.0	287	2	AAK05877	Aak05877 Merozite	201	6	25.0	482	8	ADJ49010	Adj49010 Oil-assoc
129	6	25.0	287	2	AAK88002	Aak88002 Delta-end	202	6	25.0	483	8	ADJ50397	Adj50397 Oil-assoc
130	6	25.0	287	8	AXG66164	Axg66164 Plant ful	203	6	25.0	483	8	ADJ49009	Adj49009 Oil-assoc
131	6	25.0	288	3	AG14697	Agl14697 Arabidops	204	6	25.0	485	8	ADJ91353	Adj91353 Plant ful
132	6	25.0	288	3	AAG48238	Aag48238 Arabidops	205	6	25.0	490	8	ADJ50209	Adj50209 Oil-assoc
133	6	25.0	293	8	ADT58681	Adt58681 Plant pol	206	6	25.0	493	4	ABB71880	Abb71880 Drosophil
134	6	25.0	298	7	ADC46637	Adc46637 Thalecres	207	6	25.0	495	8	ADG76671	Adg76671 Phospholi
135	6	25.0	298	7	ADJ55830	Adj55830 Thalecres	208	6	25.0	498	3	RAG54168	Rag54168 Arabidops
136	6	25.0	298	8	ADI61459	Adi61459 A. thalia	209	6	25.0	500	3	AAG21939	Aag21939 Arabidops
137	6	25.0	298	8	ADO02451	Ado02451 Thalecres	210	6	25.0	506	4	AAG78226	Aag78226 Lepomis c
138	6	25.0	300	2	AAK05878	Aak05878 Merozite	211	6	25.0	508	4	ABB71345	Abb71345 Arabidops
139	6	25.0	304	8	ADT57907	Adt57907 Plant pol	212	6	25.0	509	8	ADT77459	Adt77459 Human nuc
140	6	25.0	313	8	ADK89567	Adk89567 Plant ful	213	6	25.0	512	5	ABP29785	Abp29785 Streptoco
141	6	25.0	323	4	ABM60025	Abm60025 Drosophil	214	6	25.0	512	5	ABP27229	Abp27229 Streptoco
142	6	25.0	337	8	ADK69102	Adk69102 Plant ful	215	6	25.0	512	8	ADV89570	Adv89570 Streptoco
143	6	25.0	339	3	AG54170	Ags54170 Arabidops	216	6	25.0	512	8	ADV82977	Adv82977 Streptoco
144	6	25.0	341	8	ADK66275	Adk66275 Plant ful	217	6	25.0	512	8	ADV80823	Adv80823 Streptoco
145	6	25.0	351	5	ABG79591	Abg79591 Candida g	218	6	25.0	513	3	AAV91276	Aav91276 Group B S
146	6	25.0	354	4	ABB30793	Abb30793 Amino aci	219	6	25.0	520	8	ADK68098	Adk68098 Plant ful
147	6	25.0	355	8	AX95777	Ax95777 Plant ful	220	6	25.0	526	4	ABB67142	Abb67142 Drosophil
148	6	25.0	367	3	AG54169	Ags54169 Arabidops	221	6	25.0	526	4	ABB68634	Abb68634 Drosophil
149	6	25.0	368	4	ABB58030	Abb58030 Drosophil	222	6	25.0	533	5	ABB54316	Abb54316 Lactococc
150	6	25.0	368	4	ABG96585	Abg96585 Putative	223	6	25.0	535	4	ABB58915	Abb58915 Drosophil
151	6	25.0	368	5	ABG93036	Abg93036 S. cerevi	224	6	25.0	561	4	ABB67878	Abb67878 Drosophil
152	6	25.0	368	8	ADS43197	Ads43197 Bacterial	225	6	25.0	570	4	ABB64692	Abb64692 Drosophil
153	6	25.0	369	7	ADD30364	Add30364 Plant yie	226	6	25.0	575	3	RAG21938	Rag21938 Arabidops
154	6	25.0	369	8	ADI44287	Adi44287 Plant tra	227	6	25.0	578	6	ABU30855	Abu30855 Protein e
155	6	25.0	370	5	ABP11368	Abp11368 Human ORF	228	6	25.0	578	8	ADU05598	Adu05598 H. pylori
156	6	25.0	372	5	ABB93414	Abb93414 Herbicida	229	6	25.0	581	7	ADB37538	Adb37538 Neural th
157	6	25.0	374	3	ABG35680	Abg35680 Arabidops	230	6	25.0	582	4	AAG78227	Aag78227 Lepomis c
158	6	25.0	375	8	ADN19891	Adn19891 Bacterial	231	6	25.0	592	4	ABM82297	Abm82297 Arabidops
159	6	25.0	378	4	ABB68211	Abb68211 Drosophil	232	6	25.0	592	4	ABM82296	Abm82296 Arabidops
160	6	25.0	381	8	ADI42928	Adi42928 Plant tra	233	6	25.0	592	5	ABP99405	Abp99405 Arabidops
161	6	25.0	384	3	AG13903	Agl13903 Arabidops	234	6	25.0	592	8	ADM98799	Adm98799 HMG-CoA r
162	6	25.0	386	4	ABB70630	Abb70630 Drosophil	235	6	25.0	592	8	ADM98789	Adm98789 HMG-CoA r
163	6	25.0	388	3	ABG49725	Abg49725 Arabidops	236	6	25.0	592	8	ADM98937	Adm98937 HMG-CoA r
164	6	25.0	388	3	AG133902	Agl133902 Arabidops	237	6	25.0	592	8	ADM98827	Adm98827 HMG-CoA r
165	6	25.0	390	8	ADX73219	Adx73219 Plant ful	238	6	25.0	592	9	ADY52924	Ady52924 Thale cre
166	6	25.0	391	6	ABM68619	Abm68619 Photornab	239	6	25.0	592	9	ADY52374	Ady52374 Novel ket
167	6	25.0	392	9	ABE53803	Aeb53803 Drosophil	240	6	25.0	592	9	ADY51371	Ady51371 Arabidops
168	6	25.0	396	3	AG13901	Agl13901 Arabidops	241	6	25.0	593	9	ADW18652	Adw18652 Pinus rad
169	6	25.0	396	3	AAG49724	Aag49724 Arabidops	242	6	25.0	598	3	AAG21937	Aag21937 Arabidops
170	6	25.0	398	3	AAG29336	Aag29336 Arabidops	243	6	25.0	601	4	ABB61643	Abb61643 Drosophil

244	6	25.0	602	7	ADP30578	Adi1669 Plant tra	317	6	25.0	960	7	ADK11471	Adk11471 Drosophil
245	6	25.0	602	8	AD141669	Adi1669 Plant tra	318	6	25.0	960	7	ADK11488	Adk11488 Drosophil
246	6	25.0	602	8	AD161491	Adi161491 A. thalia	319	6	25.0	968	8	ADO01020	ADO01020 Fruit fly
247	6	25.0	602	8	ADO02005	Thalecres	320	6	25.0	998	4	ABB60423	ABB60423 Drosophil
248	6	25.0	603	6	ADA89359	Adi89359 Drosophil	321	6	25.0	1001	6	ABU30822	ABU30822 Protein e
249	6	25.0	605	8	ADS43386	Adi43386 Bacterial	322	6	25.0	1023	6	ABP97078	ABP97078 Human G p
250	6	25.0	608	4	AAH82298	Arabidops	323	6	25.0	1046	4	ABB59307	ABB59307 Drosophil
251	6	25.0	610	4	ABE71317	Adi71317 Drosophil	324	6	25.0	1058	4	AAH68341	AAH68341 A human d
252	6	25.0	610	9	ADZ07750	HIV CON-S	325	6	25.0	1080	7	ABM85355	ABM85355 Human pro
253	6	25.0	613	4	ABB65716	Drosophil	326	6	25.0	1100	8	ADP99064	ADP99064 C. albica
254	6	25.0	623	3	AG411366	Arabidops	327	6	25.0	1111	7	ADB67097	ADB67097 Kinesin-1
255	6	25.0	627	3	AG411365	Arabidops	328	6	25.0	1111	8	ADL99368	ADL99368 Nanostruc
256	6	25.0	628	2	AAH88424	Arabidops	329	6	25.0	1111	8	ADN18760	ADN18760 Bacterial
257	6	25.0	628	3	AG411364	Arabidops	330	6	25.0	1113	6	ABR53293	ABR53293 Protein s
258	6	25.0	628	4	AAE01936	Arabidops	331	6	25.0	1113	7	ADK63560	ADK63560 Disease t
259	6	25.0	628	5	AAU93141	Arabidops	332	6	25.0	1138	2	AAH06461	AAH06461 BtPGS1245
260	6	25.0	628	7	ADP15138	Thale cre	333	6	25.0	1138	2	AAH37214	AAH37214 B. t. toxl
261	6	25.0	628	7	ADH86843	Arabidops	334	6	25.0	1138	2	AAH46226	AAH46226 Bacillus
262	6	25.0	628	8	ADN73205	Thale cre	335	6	25.0	1138	9	ADR89429	ADR89429 cry7Aa. 1
263	6	25.0	645	4	ABB61545	Adi61545 Drosophil	336	6	25.0	1138	9	ADY59864	ADY59864 Bacillus
264	6	25.0	649	7	ADD25125	Drosophil	337	6	25.0	1164	4	ABB61495	ABB61495 Drosophil
265	6	25.0	653	7	ABU03135	Alpha amy	338	6	25.0	1169	4	ABB71663	ABB71663 Drosophil
266	6	25.0	653	8	ADU07484	Amino aci	339	6	25.0	1173	4	ABB62245	ABB62245 Drosophil
267	6	25.0	659	4	ABB64863	Drosophil	340	6	25.0	1173	4	ABB59646	ABB59646 Drosophil
268	6	25.0	660	4	ABB68167	Drosophil	341	6	25.0	1194	4	ABB59646	ABB59646 Drosophil
269	6	25.0	669	4	ABB59622	Drosophil	342	6	25.0	1195	4	ABB63694	ABB63694 Drosophil
270	6	25.0	674	7	ADK62474	Disease t	343	6	25.0	1234	8	ADP25437	ADP25437 Plasmodi
271	6	25.0	675	2	AAW00136	Drosophil	344	6	25.0	1234	8	ADN20779	ADN20779 Bacterial
272	6	25.0	676	5	ABG93314	Adi93314 S. cerevi	345	6	25.0	1244	6	ABR53280	ABR53280 Protein s
273	6	25.0	688	5	ABP74039	Candida a	346	6	25.0	1244	7	ADK63590	ADK63590 Disease t
274	6	25.0	704	2	AAW11843	Full leng	347	6	25.0	1244	8	ADN18772	ADN18772 Bacterial
275	6	25.0	706	4	ABR59652	Drosophil	348	6	25.0	1266	7	ADB70308	ADB70308 C. neofo
276	6	25.0	713	7	ADK11383	Drosophil	349	6	25.0	1266	7	ADP74638	ADP74638 Amino aci
277	6	25.0	716	4	ABR71960	Drosophil	350	6	25.0	1288	8	ADP61833	ADP61833 P. falcip
278	6	25.0	720	8	ADU23416	Bacterial	351	6	25.0	1314	6	ABR53132	ABR53132 Protein s
279	6	25.0	722	6	ABU23638	Drosophil	352	6	25.0	1314	7	ADN22849	ADN22849 Bacterial
280	6	25.0	732	4	ABB65450	Protein e	353	6	25.0	1402	8	ADN22849	ADN22849 Bacterial
281	6	25.0	742	8	ADP99099	C. albica	354	6	25.0	1420	9	ABM92747	ABM92747 M. xanthu
282	6	25.0	761	4	ABR71561	Drosophil	355	6	25.0	1423	4	ABM71866	ABM71866 Drosophil
283	6	25.0	764	5	ABP73760	Candida a	356	6	25.0	1436	3	ABR18199	ABR18199 Plasmodi
284	6	25.0	765	4	ABR70099	Drosophil	357	6	25.0	1436	8	ABM82922	ABM82922 Human dia
285	6	25.0	790	4	ABR60771	Drosophil	358	6	25.0	1447	8	ADQ89646	ADQ89646 Antagonis
286	6	25.0	814	4	ABB68374	Drosophil	359	6	25.0	1464	4	ABB61199	ABB61199 Drosophil
287	6	25.0	837	6	AAW063527	Maliganat	360	6	25.0	1476	4	ABR58706	ABR58706 Drosophil
288	6	25.0	842	2	AAW00137	Drosophil	361	6	25.0	1487	7	ABM88950	ABM88950 Rice abio
289	6	25.0	844	5	ABR65418	Drosophil	362	6	25.0	1491	8	ABM82920	ABM82920 Human dia
290	6	25.0	848	5	ABR53982	Drosophil	363	6	25.0	1491	8	ABM82921	ABM82921 Human dia
291	6	25.0	848	8	ADS29320	Bacterial	364	6	25.0	1501	5	AAU76762	AAU76762 Plasmodi
292	6	25.0	849	9	ABE10634	Clade C e	365	6	25.0	1504	8	ADN19818	ADN19818 Bacterial
293	6	25.0	852	9	ADZ07734	HIV CON-S	366	6	25.0	1518	9	AEA23186	AEA23186 GPCR prot
294	6	25.0	856	4	ABB68808	Drosophil	367	6	25.0	1520	8	ADN22943	ADN22943 Bacterial
295	6	25.0	856	4	ABR60983	Drosophil	368	6	25.0	1520	8	ADN22944	ADN22944 Bacterial
296	6	25.0	856	7	ADJ37949	Drosophil	369	6	25.0	1523	8	ABM84812	ABM84812 Human dia
297	6	25.0	865	7	ADH99075	Drosophil	370	6	25.0	1526	7	ADN22943	ADN22943 Bacterial
298	6	25.0	916	4	ABR63615	Drosophil	371	6	25.0	1526	7	ADN22943	ADN22943 Bacterial
299	6	25.0	916	8	ADO01008	Fruit fly	372	6	25.0	1530	7	ADN22943	ADN22943 Bacterial
300	6	25.0	916	8	ADH96718	Drosophil	373	6	25.0	1531	5	ABP67994	ABP67994 Human col
301	6	25.0	920	4	ABR62023	Drosophil	374	6	25.0	1531	5	AAO18890	AAO18890 Human ova
302	6	25.0	921	8	ADH99074	LRP5-rela	375	6	25.0	1531	5	ABR60433	ABR60433 Ant1-huma
303	6	25.0	921	8	ADJ49846	Oil-assoc	376	6	25.0	1531	6	ABU56492	ABU56492 Lung canc
304	6	25.0	922	8	ADJ49844	Oil-assoc	377	6	25.0	1531	6	ABR92156	ABR92156 Human cer
305	6	25.0	924	8	ADJ49847	Oil-assoc	378	6	25.0	1531	7	ADN22943	ADN22943 Bacterial
306	6	25.0	924	8	ADJ49845	Oil-assoc	379	6	25.0	1531	7	ADN22943	ADN22943 Bacterial
307	6	25.0	938	4	ABR60562	Drosophil	380	6	25.0	1531	8	ADH13197	ADH13197 Human mal
308	6	25.0	941	4	ABG25801	Novel hum	381	6	25.0	1531	8	ADL12474	ADL12474 Human etc
309	6	25.0	941	5	ABP74093	Candida a	382	6	25.0	1531	8	ADL70599	ADL70599 Cervical
310	6	25.0	943	4	ABR62085	Drosophil	383	6	25.0	1531	8	ADL26776	ADL26776 Human Top
311	6	25.0	950	2	AAH06376	Product o	384	6	25.0	1531	8	ADN03718	ADN03718 Antipsori
312	6	25.0	950	4	ABR71271	Drosophil	385	6	25.0	1531	8	ADQ19281	ADQ19281 Human sof
313	6	25.0	950	8	ADU43488	Bacterial	386	6	25.0	1531	8	ADQ89838	ADQ89838 Antagonis
314	6	25.0	959	3	ABR18194	Plasmodi	387	6	25.0	1531	9	ADK05548	ADK05548 Cyclin-de
315	6	25.0	960	4	ABR58434	Drosophil	388	6	25.0	1531	9	ADY14470	ADY14470 PRO poly
316	6	25.0	960	7	ADK11469	Drosophil	389	6	25.0	1531	9	ADY14468	ADY14468 PRO poly

390	6	25.0	1531	9	AE15084	Human pol	463	5	20.8	9	5	AAE31351	Aae31351 Human tyr
391	6	25.0	1540	8	ABM84811	Human dia	464	5	20.8	9	5	AAE31352	Aae31352 Human tyr
392	6	25.0	1545	8	AD10988	Human the	465	5	20.8	9	6	ABJ20142	Adj20142 MHC bindi
393	6	25.0	1562	8	ABM82919	Human dia	466	5	20.8	9	8	ADP25771	Adp25771 Plaemodiu
394	6	25.0	1568	6	ABP70152	Amino aci	467	5	20.8	9	8	ADP25547	Adp25547 Plaemodiu
395	6	25.0	1572	2	AAW99301	Human BAI	468	5	20.8	9	8	ADT40166	Adt40166 hSARS vir
396	6	25.0	1576	6	ABP81929	Human bra	469	5	20.8	9	8	ADT79583	Adt79583 SARS viru
397	6	25.0	1572	8	ADQ29004	Human nov	470	5	20.8	9	8	ADT37696	Adt37696 hSARS vir
398	6	25.0	1572	8	ADQ05172	Human G p	471	5	20.8	9	9	ADZ50678	Adz50678 Y. pestis
399	6	25.0	1573	7	ADC86417	Human GPC	472	5	20.8	10	4	AAAG86662	AAg86662 Saccharom
400	6	25.0	1591	8	ADO29005	Mouse nov	473	5	20.8	10	4	AAAG86800	AAg86800 Saccharom
401	6	25.0	1609	8	ADM90833	Human pha	474	5	20.8	10	4	ABP12285	Abp12285 HIV A02 s
402	6	25.0	1613	6	ABR41134	Human LRP	475	5	20.8	10	4	ABP14839	Abp14839 CTL epito
403	6	25.0	1613	7	ADQ98801	Human LRP	476	5	20.8	10	5	ABB95132	Abb95132 CTL epito
404	6	25.0	1613	8	ADI27182	Mouse LRP	477	5	20.8	12	5	ABG93666	Abg93666 Human Mit
405	6	25.0	1613	8	ADI27183	Human LRP	478	5	20.8	12	5	ABG93725	Abg93725 Human Mit
406	6	25.0	1613	9	ADX06321	Cyclin-de	479	5	20.8	14	7	ADF71051	Adf71051 Saccharom
407	6	25.0	1621	4	AAZ25646	Human pro	480	5	20.8	15	8	ADM36120	Adm36120 RTN3 pept
408	6	25.0	1621	8	ABM80429	Tumour-as	481	5	20.8	16	4	AAW99487	AAw99487 Vaccine r
409	6	25.0	1621	8	ADS12217	Human the	482	5	20.8	16	5	AAE17169	AAe17169 Meningoco
410	6	25.0	1626	7	ADJ71211	Human hea	483	5	20.8	17	2	AAW17549	AAw17549 Beta-B2-c
411	6	25.0	1626	8	AQ89840	Antagonis	484	5	20.8	17	5	AAU89944	AAu89944 Insulin/i
412	6	25.0	1664	2	AAW99462	C.albican	485	5	20.8	17	5	AAE43954	AAe43954 Anti-TPO
413	6	25.0	1664	5	AAE19799	Antigen	486	5	20.8	17	9	AEA43960	AEA43960 Anti-TPO
414	6	25.0	1664	5	AAU79331	Candida a	487	5	20.8	18	6	ABP82477	Abp82477 G protein
415	6	25.0	1664	7	ADC73265	Yeast Int	488	5	20.8	18	6	ABP82915	Abp82915 G protein
416	6	25.0	1664	7	ADM33264	Candida a	489	5	20.8	20	8	ADH16103	Adh16103 Gliadin r
417	6	25.0	1665	4	ABM64010	Drosophil	490	5	20.8	20	8	ADH16104	Adh16104 Gliadin r
418	6	25.0	1677	8	ADO17159	Novel exp	491	5	20.8	20	8	ADH15373	Adh15373 Gliadin r
419	6	25.0	1703	4	ABB66223	Drosophil	492	5	20.8	20	8	ADH15374	Adh15374 Gliadin r
420	6	25.0	1778	4	ABB60081	Drosophil	493	5	20.8	20	8	ADM36164	Adm36164 Human RTN
421	6	25.0	1805	4	ABB65262	Drosophil	494	5	20.8	21	5	AAU89040	AAu89040 Insulin/i
422	6	25.0	1810	7	ADF70505	Orphan re	495	5	20.8	21	6	ADA03870	Ada03870 Insulin r
423	6	25.0	1893	4	ABM59829	Drosophil	496	5	20.8	21	7	ADH95083	Adh95083 Insulin r
424	6	25.0	1926	4	AAAG84915	Shrimp wh	497	5	20.8	21	7	ADW35382	Adw35382 HLA bindi
425	6	25.0	1954	4	ABB59197	Drosophil	498	5	20.8	21	7	ADW34149	Adw34149 HLA bindi
426	6	25.0	1980	4	ABB67589	Drosophil	499	5	20.8	21	8	ADL67774	Adl67774 IGF-1R/IR
427	6	25.0	1987	4	ABB61083	Drosophil	500	5	20.8	21	8	ADM37619	Adm37619 Anti-IR f
428	6	25.0	2000	6	ABR52731	Protein s	501	5	20.8	21	9	ADX85960	Adx85960 HIV gp120
429	6	25.0	2000	7	ADK61970	Disease t	502	5	20.8	22	2	AAAR06590	AAr06590 Interleuk
430	6	25.0	2006	4	ABJ71277	Drosophil	503	5	20.8	22	9	ADV55048	Adv55048 G protein
431	6	25.0	2006	8	ADU96448	Drosophil	504	5	20.8	22	9	ADV54935	Adv54935 G protein
432	6	25.0	2023	4	ABB63487	Drosophil	505	5	20.8	22	9	ADV55154	Adv55154 G protein
433	6	25.0	2053	4	AAW69135	M. catarr	506	5	20.8	23	2	AAW82478	AAw82478 Neurospor
434	6	25.0	2071	3	AAW84686	Amino aci	507	5	20.8	23	5	AAE22579	AAe22579 Drosophil
435	6	25.0	2071	3	AAW84686	Amino aci	508	5	20.8	23	5	ADO55733	Ado55733 Neurospor
436	6	25.0	2071	3	AAW84686	Amino aci	509	5	20.8	24	2	AAAR06593	AAr06593 Interleuk
437	6	25.0	2150	5	AAO22566	Wooden le	510	5	20.8	25	2	AAAR06594	AAr06594 Eubacteri
438	6	25.0	2167	8	ADN19120	Bacterial	511	5	20.8	25	5	ABG62549	Abg62549 Interleuk
439	6	25.0	2175	4	ABB65698	Drosophil	512	5	20.8	26	2	AAAR06595	AAr06595 Interleuk
440	6	25.0	2280	4	ABB61650	Drosophil	513	5	20.8	27	2	AAAR06596	AAr06596 Interleuk
441	6	25.0	2406	4	ABB60250	Drosophil	514	5	20.8	28	2	AAAR06597	AAr06597 Interleuk
442	6	25.0	3056	8	ADR43499	CSA-bind	515	5	20.8	28	6	ABR81914	ABr81914 Human int
443	6	25.0	3190	4	AAW84634	Amino aci	516	5	20.8	28	9	ADZ36485	Adz36485 Human int
444	6	25.0	3275	4	ABB70437	Drosophil	517	5	20.8	30	4	AAW22035	AAw22035 Peptide #
445	6	25.0	3275	7	ADK11301	Drosophil	518	5	20.8	30	4	ABB44421	Abb44421 Peptide #
446	6	25.0	3536	4	ABB65480	Drosophil	519	5	20.8	30	4	AAW38408	AAw38408 Peptide #
447	6	25.0	3614	4	ABB62664	Drosophil	520	5	20.8	30	4	ABB27268	Abb27268 Protein #
448	6	25.0	3973	3	AAW18253	Plaemodiu	521	5	20.8	30	4	AAW78163	AAw78163 Human bon
449	5	20.8	5	2	AAW00431	Interleuk	522	5	20.8	30	4	AAW65501	AAw65501 Human bra
450	5	20.8	7	1	AAW71426	Immunomod	523	5	20.8	30	4	ABG59809	ABg59809 Human liv
451	5	20.8	8	2	AAW11529	Interleuk	524	5	20.8	30	5	ABG47175	ABg47175 Human pep
452	5	20.8	9	2	AAW11528	Interleuk	525	5	20.8	30	5	AAU84914	AAu84914 Human Tyr
453	5	20.8	9	2	AAW47083	Immunogen	526	5	20.8	30	5	AAU84915	AAu84915 Human tyr
454	5	20.8	9	4	ABP12131	HIV A02 s	527	5	20.8	31	9	ABM95343	ABm95343 M. xanthu
455	5	20.8	9	5	ABB94781	CTL epito	528	5	20.8	31	3	AAW56606	AAw56606 Arabidops
456	5	20.8	9	5	ABB94781	CTL epito	529	5	20.8	33	3	AAW56606	AAw56606 Arabidops
457	5	20.8	9	5	ABB94780	CTL epito	530	5	20.8	35	3	ADX91570	Adx91570 Plant ful
458	5	20.8	9	5	ABB94512	CTL epito	531	5	20.8	37	3	AAW55191	AAw55191 Arabidops
459	5	20.8	9	5	ABB95000	CTL epito	532	5	20.8	37	6	ABP59758	Abp59758 HIV immun
460	5	20.8	9	5	ABB94602	CTL epito	533	5	20.8	37	6	ADR58083	Adr58083 Novel ant
461	5	20.8	9	5	ABB95087	CTL epito	534	5	20.8	37	8	ADR58140	Adr58140 Novel ant
462	5	20.8	9	5	AAE31350	Human tyr	535	5	20.8	37	9	ADX85928	Adx85928 HIV gp120

536	5	20.8	37	9	ADXB5770	Adx85770 HIV clade	609	5	20.8	66	7	ADII5883	Adii5883 Human pp
537	5	20.8	39	3	AGS59863	Ags59863 Arabidops	610	5	20.8	67	5	AAO22532	Aao22532 Small aci
538	5	20.8	39	8	ADH12867	Adh12867 Francisel	611	5	20.8	67	5	AAO22524	Aao22524 Small aci
539	5	20.8	40	8	ABO57415	Abos7415 Human gen	612	5	20.8	67	9	ADVB6780	Advb6780 Alpha/bet
540	5	20.8	41	4	ABBA0366	Abba0366 Peptide #	613	5	20.8	67	9	ADVB6772	Advb6772 Alpha/bet
541	5	20.8	41	4	AAW34072	Aam34072 Peptide #	614	5	20.8	68	5	AAO22518	Aao22518 Small aci
542	5	20.8	41	4	AAW33890	Aam33890 Human bon	615	5	20.8	68	5	ADKB6086	Adkb6086 Novel hum
543	5	20.8	41	4	AAW61175	Aam61175 Human bra	616	5	20.8	68	5	ABO63943	Abos63943 Klebsiell
544	5	20.8	41	4	ABG55641	Abg55641 Human liv	617	5	20.8	68	9	ADVB6766	Advb6766 Alpha/bet
545	5	20.8	41	4	ABG19605	Abg19605 Novel hum	618	5	20.8	69	4	ABBE2675	Abbe2675 Drosophil
546	5	20.8	41	5	ABG43778	Abg43778 Human pep	619	5	20.8	69	5	AAO22513	Aao22513 Small aci
547	5	20.8	42	5	AAU17733	Aau17733 Novel hum	620	5	20.8	69	5	AAO22506	Aao22506 Small aci
548	5	20.8	42	7	ADG41113	Adg41113 Human res	621	5	20.8	69	9	ADVB6761	Advb6761 Alpha/bet
549	5	20.8	42	9	ADP196887	Adp196887 Human res	622	5	20.8	69	9	ADVB6753	Advb6753 Alpha/bet
550	5	20.8	42	9	AEBA3263	Aeb43263 Human LRP	623	5	20.8	70	5	AAO22525	Aao22525 Small aci
551	5	20.8	44	6	AAE30231	Aae30231 Human Lp2	624	5	20.8	70	9	ADVB6773	Advb6773 Alpha/bet
552	5	20.8	44	6	AAE30243	Aae30243 Human Lp2	625	5	20.8	71	5	ABP00056	Abp00056 Human ORF
553	5	20.8	44	8	ADS06191	Ads06191 Staphyloc	626	5	20.8	72	5	AAO22530	Aao22530 Small aci
554	5	20.8	46	4	AAW18239	Aam18239 Peptide #	627	5	20.8	72	9	ADVB6778	Advb6778 Alpha/bet
555	5	20.8	46	4	ABE37270	Abb37270 Peptide #	628	5	20.8	73	9	AABS8205	Aabs8205 Lung canc
556	5	20.8	46	4	AAW30730	Aam30730 Peptide #	629	5	20.8	73	4	AAW85561	Aam85561 Human imm
557	5	20.8	46	4	ABB32018	Abb32018 Peptide #	630	5	20.8	73	4	ABGS5908	Abgs5908 Human liv
558	5	20.8	46	4	ABB22559	Abb22559 Protein #	631	5	20.8	73	5	ABP03388	Abp03388 Human ORF
559	5	20.8	46	4	AAW70400	Aam70400 Human bon	632	5	20.8	74	5	AAO22044	Aao22044 Human ORF
560	5	20.8	46	4	AAW57970	Aam57970 Human bra	633	5	20.8	74	5	ABP02044	Abp02044 Human ORF
561	5	20.8	46	4	ABGS2092	Abgs2092 Human liv	634	5	20.8	74	5	ABP03426	Abp03426 Human ORF
562	5	20.8	46	5	ABG40041	Abg40041 Human pep	635	5	20.8	74	5	ABP07318	Abp07318 Human ORF
563	5	20.8	46	9	AEA32754	Aea32754 HTH AraC	636	5	20.8	75	4	ABB70429	Abb70429 Drosophil
564	5	20.8	49	4	AAO80066	Aao80066 Chemokine	637	5	20.8	75	5	ABP11033	Abp11033 Human ORF
565	5	20.8	49	4	AAO05160	Aao05160 Human pol	638	5	20.8	75	8	ADO41438	Ado41438 Therapeut
566	5	20.8	50	5	ABP09330	Abp09330 Human ORF	639	5	20.8	75	8	ADP96016	Adp96016 Human bin
567	5	20.8	51	3	AAO39100	Aao39100 Human sec	640	5	20.8	77	5	ABB97784	Abb97784 Human sec
568	5	20.8	51	4	ABB69142	Abb69142 Drosophil	641	5	20.8	77	7	ADC00298	Adc00298 Enterohae
569	5	20.8	52	6	ABP79893	Abp79893 N. gonorr	642	5	20.8	78	2	AAV36173	Aay36173 Human sec
570	5	20.8	52	7	ADC21299	Adc21299 Mouse MHC	643	5	20.8	78	2	AAV36220	Aay36220 Human sec
571	5	20.8	52	7	ADC21298	Adc21298 Mouse MHC	644	5	20.8	78	7	ADJ45978	Adj45978 Novel hum
572	5	20.8	52	7	ADC21298	Adc21298 Mouse MHC	645	5	20.8	78	7	ADJ46072	Adj46072 Novel hum
573	5	20.8	52	8	ADO41426	Ado41426 Therapeut	646	5	20.8	78	8	ADP19481	Adp19481 Human sec
574	5	20.8	52	8	ADO41424	Ado41424 Therapeut	647	5	20.8	78	8	ADP19481	Adp19481 Human sec
575	5	20.8	52	8	ADP96004	Adp96004 Human bin	648	5	20.8	79	3	AAAG57366	Aags57366 Arabidops
576	5	20.8	52	8	ADP96002	Adp96002 Human bin	649	5	20.8	79	4	AAW82427	Aam82427 Human imm
577	5	20.8	54	3	AAO21293	Aao21293 Human sec	650	5	20.8	79	4	AAW94524	Aam94524 Human rep
578	5	20.8	54	7	ADBA6138	Adb46138 Plasmodi	651	5	20.8	79	4	ABB10848	Abb10848 Human ova
579	5	20.8	54	8	ADSO7766	Adso7766 Staphyloc	652	5	20.8	80	2	AAAR13397	Aar13397 HLA-DRw12
580	5	20.8	55	4	AAO11300	Aao11300 Human pol	653	5	20.8	80	2	AAAR13396	Aar13396 HLA-DRw12
581	5	20.8	56	2	AAV05437	Aay05437 Staphyloc	654	5	20.8	80	5	ADH32781	Adh32781 Yeast smo
582	5	20.8	56	2	AAV60476	Aay60476 Human nor	655	5	20.8	82	3	AAAG24089	Aag24089 Arabidops
583	5	20.8	56	4	ABB15194	Abb15194 Human ner	656	5	20.8	82	7	ABO83381	Abos83381 Pseudomon
584	5	20.8	56	5	ABP10450	Abp10450 Human ORF	657	5	20.8	82	8	ADY24612	Ady24612 Plant ful
585	5	20.8	56	6	ABP31848	Abp31848 Human ORF	658	5	20.8	83	5	ABP34141	Abp34141 Human DNA
586	5	20.8	56	6	ABP80177	Abp80177 N. gonorr	659	5	20.8	83	6	ABU32019	Abu32019 Protein e
587	5	20.8	56	6	ADA95369	Ada95369 Protein d	660	5	20.8	83	7	ADH87090	Adh87090 Enterococ
588	5	20.8	57	5	ABP07846	Abp07846 Human ORF	661	5	20.8	83	8	ADK99934	Adk99934 Streptoco
589	5	20.8	58	2	AAAR10753	Aar10753 Non-A non	662	5	20.8	84	8	ADK99932	Adk99932 Streptoco
590	5	20.8	58	2	AAAR10756	Aar10756 Non-A non	663	5	20.8	84	8	ADK99932	Adk99932 Streptoco
591	5	20.8	59	2	AAV12736	Aay12736 Human 5'	664	5	20.8	85	8	ADK99929	Adk99929 Streptoco
592	5	20.8	59	4	ABB17799	Abb17799 Human ner	665	5	20.8	85	8	ADK99930	Adk99930 Streptoco
593	5	20.8	60	3	AAAG19825	Aag19825 Arabidops	666	5	20.8	85	8	ADK99927	Adk99927 Streptoco
594	5	20.8	60	4	AAO05547	Aao05547 Human pol	667	5	20.8	85	8	ADK99931	Adk99931 Streptoco
595	5	20.8	61	4	AAU52950	Aau52950 Propionib	668	5	20.8	85	8	ADK99933	Adk99933 Streptoco
596	5	20.8	61	5	ABP10643	Abp10643 Human ORF	669	5	20.8	86	3	AAAG57365	Aags57365 Arabidops
597	5	20.8	61	6	ABM49469	Abm49469 Propionib	670	5	20.8	86	3	AAAG61489	Aag61489 Arabidops
598	5	20.8	63	3	AAO20818	Aao20818 Human sec	671	5	20.8	86	8	ADK99928	Adk99928 Streptoco
599	5	20.8	63	7	ADBA6137	Adb46137 Plasmodi	672	5	20.8	86	8	ADK99935	Adk99935 Streptoco
600	5	20.8	63	7	ADC96482	Adc96482 E. faeciu	673	5	20.8	88	6	ABO14007	Abos14007 Novel hum
601	5	20.8	63	8	ADJ06020	Adj06020 M. catarr	674	5	20.8	88	6	ADN60704	Adn60704 Human sec
602	5	20.8	64	4	AAW88153	Aam88153 Human imm	675	5	20.8	89	2	AAV14301	Aay14301 Protein e
603	5	20.8	64	4	AAU44970	Aau44970 Propionib	676	5	20.8	89	2	AAV14306	Aay14306 Protein e
604	5	20.8	64	6	ABW41489	Abw41489 Propionib	677	5	20.8	89	2	AAV14336	Aay14336 Protein e
605	5	20.8	65	4	ABG05578	Abg05578 Novel hum	678	5	20.8	89	2	AAV14307	Aay14307 Protein e
606	5	20.8	65	7	ADF06501	Adf06501 Bacterial	679	5	20.8	89	2	AAV27602	Aay27602 Human sec
607	5	20.8	66	2	AAR97241	Aar97241 Mutant fo	680	5	20.8	89	3	AAAG61072	Aag61072 Arabidops
608	5	20.8	66	7	ADD22416	Add22416 HLA-B*6 T	681	5	20.8	89	3	AAAG44502	Aag44502 Arabidops

682	5	20.8	89	4	ABB68584	Abb68584 Drosophil	755	5	20.8	103	8	ADM32932	Adm32932 Amino aci
683	5	20.8	89	4	ABE87848	AbB87848 Protein e	756	5	20.8	104	4	AAO00241	Aao00241 Human pol
684	5	20.8	89	4	ABE87868	Aab87868 Protein e	757	5	20.8	104	5	ABP08659	Abp08659 Human ORF
685	5	20.8	89	4	ABAB87849	Aab87849 Protein e	758	5	20.8	104	6	ABU02257	Abu02257 S. pneumo
686	5	20.8	89	4	ABAB87875	Aab87875 Protein e	759	5	20.8	104	6	ABP81634	Abp81634 Streptoco
687	5	20.8	89	8	ADG78413	Adg78413 Human sec	760	5	20.8	104	8	ADK46563	Adk46563 Streptoco
688	5	20.8	90	4	AAm18336	Aam18336 Peptide #	761	5	20.8	105	4	AAU20778	Aau20778 Human nov
689	5	20.8	90	4	ABB37369	Abb37369 Peptide #	762	5	20.8	105	8	ADX71269	Adx71269 Plant ful
690	5	20.8	90	4	AAW30822	Aam30822 Peptide #	763	5	20.8	106	4	AAg75279	AAg75279 Human col
691	5	20.8	90	4	ABB32118	Abb32118 Peptide #	764	5	20.8	106	4	AAO13415	Aao13415 Human pol
692	5	20.8	90	4	ABB22659	Abb22659 Protein #	765	5	20.8	107	9	AEb38713	Aeb38713 L. pneumo
693	5	20.8	90	4	AAW70499	Aam70499 Human bon	766	5	20.8	108	4	ABb62825	Abb62825 Drosophil
694	5	20.8	90	4	AAW58059	Aam58059 Human bra	767	5	20.8	108	4	AAU69511	Aau69511 Human pur
695	5	20.8	90	4	AGS52181	AgS52181 Human liv	768	5	20.8	108	5	ABP26894	Abp26894 Streptoco
696	5	20.8	90	4	AAO05942	Aam05942 Peptide #	769	5	20.8	108	5	AAU83193	AAu83193 Novel sec
697	5	20.8	90	4	ABG04097	Abg04097 Novel hum	770	5	20.8	108	6	ABU46750	Abu46750 Protein e
698	5	20.8	90	5	ABG40139	Abg40139 Human pep	771	5	20.8	108	7	ADB65292	AdB65292 Human pro
699	5	20.8	91	2	AAW10494	Aaw10494 Beta1 reg	772	5	20.8	109	5	ABP60792	Abp60792 Synchocy
700	5	20.8	91	2	AAW10501	Aaw10501 Beta1 reg	773	5	20.8	109	5	ABP60836	Abp60836 Synchocy
701	5	20.8	91	5	ABP06601	Abp06601 Human ORF	774	5	20.8	109	6	ABU00723	Abu00723 S. pneumo
702	5	20.8	91	8	ADO59295	Ado59295 TRAC*01 g	775	5	20.8	109	7	ADF58816	Adf58816 Human pol
703	5	20.8	92	2	AAW74820	Aaw74820 Human sec	776	5	20.8	109	8	ADK47455	Adk47455 Streptoco
704	5	20.8	92	2	AAy13124	Aay13124 Human sec	777	5	20.8	110	4	ABB70506	Abb70506 Drosophil
705	5	20.8	92	3	AAg19824	Ag19824 Arabidops	778	5	20.8	110	5	ABg64921	Abg64921 Human alb
706	5	20.8	92	5	ABG95271	Abg95271 Human nov	779	5	20.8	110	5	ABG64923	Abg64923 Human alb
707	5	20.8	92	6	ABO34465	AbO34465 Region of	780	5	20.8	110	5	ABB77008	Abb77008 Human pro
708	5	20.8	92	7	AD123126	Ad123126 Novel hum	781	5	20.8	110	5	ABB77030	Abb77030 Human pro
709	5	20.8	92	8	ADH74128	Adh74128 Human sec	782	5	20.8	110	6	ADAS4138	Ada54138 Human pro
710	5	20.8	93	4	ABB56498	Abb56498 Murine si	783	5	20.8	110	8	ADL78190	AdL78190 Albumin f
711	5	20.8	94	3	AAE52507	Aae52507 Helicobac	784	5	20.8	110	8	ADL78188	Adl78188 Albumin f
712	5	20.8	95	3	AAE24088	Aae24088 Arabidops	785	5	20.8	111	3	AB323917	Ab323917 Pinus rad
713	5	20.8	95	4	AAO04476	Aao04476 Human pol	786	5	20.8	111	6	ADB09627	AdB09627 Alloiococ
714	5	20.8	96	4	AAU18132	Aau18132 Novel hum	787	5	20.8	111	7	ABM87142	Abm87142 Rice abio
715	5	20.8	96	4	AAU17045	Aau17045 Human nov	788	5	20.8	111	8	ADT56893	Adt56893 Plant pol
716	5	20.8	96	4	ABB10351	Abb10351 Human cDN	789	5	20.8	112	2	AAW36112	Aaw36112 Human T-c
717	5	20.8	96	4	AAU19897	Aau19897 Novel hum	790	5	20.8	112	3	AAg61071	Ag61071 Arabidops
718	5	20.8	96	5	ABJ05759	Abj05759 Novel hum	791	5	20.8	112	5	ABP41468	Abp41468 Human ova
719	5	20.8	96	5	ABP69338	Abp69338 Human pol	792	5	20.8	112	6	ABU44610	Abu44610 Protein e
720	5	20.8	97	2	AAW72386	Aaw72386 Pathogen	793	5	20.8	113	2	AAW36108	Aaw36108 Human T-c
721	5	20.8	97	3	AAg61700	Ag61700 Arabidops	794	5	20.8	113	3	AB333318	Ab333318 Pinus rad
722	5	20.8	97	4	AAm14490	Aam14490 Peptide #	795	5	20.8	113	3	AAg58716	Ag58716 Arabidops
723	5	20.8	97	4	AAg62689	Ag62689 Human sac	796	5	20.8	113	3	AAg59230	Ag59230 Arabidops
724	5	20.8	97	4	AB333438	Ab333438 Peptide #	797	5	20.8	113	4	AAU37831	Aau37831 Streptoco
725	5	20.8	97	4	AAm26903	Aam26903 Peptide #	798	5	20.8	113	6	ABP81549	Abp81549 Streptoco
726	5	20.8	97	4	ABB28263	Abb28263 Human pep	799	5	20.8	113	6	ABU45863	Abu45863 Protein e
727	5	20.8	97	4	ABB18897	Abb18897 Protein #	800	5	20.8	113	7	ABO61614	Abo61614 Klebsiell
728	5	20.8	97	4	AAm66617	Aam66617 Human bon	801	5	20.8	114	6	ABP79241	Abp79241 N. gonorr
729	5	20.8	97	4	AAW54223	Aaw54223 Human bra	802	5	20.8	114	8	ADR94295	Adr94295 Novel S.
730	5	20.8	97	4	ABG48285	Abg48285 Human liv	803	5	20.8	114	9	AEA58165	Aea58165 Streptoco
731	5	20.8	97	4	AAW02217	Aaw02217 Peptide #	804	5	20.8	115	4	AAW91128	Aaw91128 Human imm
732	5	20.8	97	5	ABG36269	Abg36269 Human pep	805	5	20.8	115	8	ADY24879	Ady24879 Plant ful
733	5	20.8	97	9	ADW97159	Adw97159 Human IL-	806	5	20.8	116	8	AAy11126	Aay11126 S. pneumo
734	5	20.8	98	6	ADA41194	Ada41194 Human sec	807	5	20.8	117	2	AAU21852	Aau21852 Human car
735	5	20.8	98	7	ADC74396	Adc74396 Human sec	808	5	20.8	118	4	AAU21852	Aau21852 Human car
736	5	20.8	98	8	ADX94498	Adx94498 Plant ful	809	5	20.8	118	6	ADB09625	AdB09625 Alloiococ
737	5	20.8	99	3	AAg19823	Ag19823 Arabidops	810	5	20.8	118	7	ADE45820	Ade45820 Human car
738	5	20.8	99	3	AA383893	Aa383893 Human sec	811	5	20.8	118	7	ABO66138	Abo66138 Klebsiell
739	5	20.8	99	9	AEA32810	Aea32810 HTH Arac	812	5	20.8	118	8	ADJ07238	Adj07238 Human car
740	5	20.8	99	9	AEA32637	Aea32637 AraC-XylS	813	5	20.8	118	9	AEA89797	Aea89797 Antibody
741	5	20.8	102	3	AAg15648	Ag15648 Arabidops	814	5	20.8	118	9	AEA89796	Aea89796 Antibody
742	5	20.8	102	4	AAm14940	Aam14940 Peptide #	815	5	20.8	118	9	AEA44069	Aea44069 Anti-TPO
743	5	20.8	102	4	ABB33909	Abb33909 Peptide #	816	5	20.8	118	9	AEA44073	Aea44073 Anti-TPO
744	5	20.8	102	4	AAW27370	Aam27370 Peptide #	817	5	20.8	119	3	AAO20095	Aao20095 Protein e
745	5	20.8	102	4	ABB28730	Abb28730 Peptide #	818	5	20.8	119	4	AAO10522	Aao10522 Human pol
746	5	20.8	102	4	ABB19350	Abb19350 Protein #	819	5	20.8	119	9	AAg91781	Aag91781 C. glutami
747	5	20.8	102	4	AAW67078	Aam67078 Human bon	820	5	20.8	119	9	ABE41904	Aeb41904 L. pneumo
748	5	20.8	102	4	AAW54676	Aam54676 Human bra	821	5	20.8	120	3	AAg00209	Aag00209 Human sec
749	5	20.8	102	4	ABG48744	Abg48744 Human liv	822	5	20.8	121	3	AAg24879	Ag24879 Arabidops
750	5	20.8	102	4	AAW02668	Aam02668 Peptide #	823	5	20.8	121	3	AAp90402	Aap90402 Plasmodiu
751	5	20.8	102	5	ABG36737	Abg36737 Human pep	824	5	20.8	122	3	AAg57502	Ag57502 Arabidops
752	5	20.8	102	8	ADY12921	Ady12921 Plant ful	825	5	20.8	122	8	ADX90625	Adx90625 Plant ful
753	5	20.8	103	5	ABP60775	Abp60775 Listeria	826	5	20.8	123	2	AAy20151	Aay20151 B. burgdo
754	5	20.8	103	5	ABB48334	Abb48334 Listeria	827	5	20.8	124	8	ADx91889	Adx91889 Plant ful

828	5	20.8	125	2	AAY20107	Aay20107 B. burgdo	901	5	20.8	149	3	AAG37353	Aag37353 Arabidops
829	5	20.8	125	4	AAW19366	Aam19366 Peptide #	902	5	20.8	149	4	ABG05579	Abg05579 Novel hum
830	5	20.8	125	4	ABR38735	Abb38735 Peptide #	903	5	20.8	150	3	ABG49726	Abg49726 Arabidops
831	5	20.8	125	4	AAM32205	Aam32205 Peptide #	904	5	20.8	150	3	ABG36567	Abg36567 Arabidops
832	5	20.8	125	4	ABR32789	Abb32789 Protein #	905	5	20.8	150	4	ABG01651	Abg01651 Novel hum
833	5	20.8	125	4	AAW71924	Aam71924 Human bon	906	5	20.8	150	8	ADL05811	Adl05811 M. catar
834	5	20.8	125	4	AAW59369	Aam59369 Human bra	907	5	20.8	150	8	ABO58682	AbO58682 Human gen
835	5	20.8	125	4	ABG41738	Abg41738 Human pep	908	5	20.8	151	2	AAW20106	Aay20106 B. burgdo
836	5	20.8	125	7	ABO60903	AbO60903 Klebiell	909	5	20.8	151	5	ABP29660	Abp29660 Streptoco
837	5	20.8	125	5	ABP29336	Abp29336 Streptoco	910	5	20.8	151	5	ABP25611	Abp25611 Streptoco
838	5	20.8	126	5	AAU59789	Aau59789 Propionib	911	5	20.8	151	6	ABU00970	Abu00970 S. pneumo
839	5	20.8	127	4	AAU18313	Aau18313 Human end	912	5	20.8	151	6	ADA35142	Ada35142 Acinetoba
840	5	20.8	127	4	ABM56308	Abm56308 Propionib	913	5	20.8	151	8	ADK99925	Adk99925 Streptoco
841	5	20.8	127	6	ADH88549	Adh88549 Enterococ	914	5	20.8	151	9	ADM92108	Adm92108 S. pneumon
842	5	20.8	127	4	ABR68828	Abb68828 Drosophil	915	5	20.8	151	8	ADM42569	Adm42569 Human his
843	5	20.8	129	4	ABR68828	Abb68828 Drosophil	916	5	20.8	151	9	ADM42562	Adm42562 Human his
844	5	20.8	129	4	AAW78794	Aag78794 Human myo	917	5	20.8	152	3	AAG36405	Aag36405 Arabidops
845	5	20.8	130	4	AAO07135	Aao07135 Human pol	918	5	20.8	152	3	AAG16329	Aag16329 Arabidops
846	5	20.8	131	3	ABG32337	Aag32337 Arabidops	919	5	20.8	152	4	ABG64818	Abg64818 Drosophil
847	5	20.8	131	5	ABP25806	Abp25806 Streptoco	920	5	20.8	152	4	ABG75026	Abg75026 Soluble A
848	5	20.8	131	8	ADH89511	Adh89511 Streptoco	921	5	20.8	153	4	ABG63555	Abg63555 Drosophil
849	5	20.8	131	8	ADH89511	Adh89511 Streptoco	922	5	20.8	153	4	ABG63555	Abg63555 Drosophil
850	5	20.8	131	8	ADH89511	Adh89511 Streptoco	923	5	20.8	153	4	ABG63555	Abg63555 Drosophil
851	5	20.8	132	6	ABU58165	Abu58165 Soybean s	924	5	20.8	153	4	AAW74161	Aam74161 Human bon
852	5	20.8	133	4	ABG05986	Abg05986 Novel hum	925	5	20.8	153	4	AAW74161	Aam74161 Human bon
853	5	20.8	133	7	ADP60242	Adp60242 Human con	926	5	20.8	153	4	ABG55944	Abg55944 Human liv
854	5	20.8	134	3	AAG58005	Aag58005 Arabidops	927	5	20.8	153	5	ABG44094	Abg44094 Human pep
855	5	20.8	134	3	AAG16331	Aag16331 Arabidops	928	5	20.8	153	8	ADU02769	Adu02769 Novel hum
856	5	20.8	134	5	ABU51077	Abu51077 Helicobac	929	5	20.8	153	8	ADU02769	Adu02769 Novel hum
857	5	20.8	134	8	ADQ97797	Adq97797 Mouse can	930	5	20.8	153	8	ADU02769	Adu02769 Novel hum
858	5	20.8	135	3	AAG16330	Aag16330 Arabidops	931	5	20.8	153	8	ADU02769	Adu02769 Novel hum
859	5	20.8	136	9	ABR38671	Abb38671 L. pneumo	932	5	20.8	155	2	AAV41230	Aay41230 H. pylori
860	5	20.8	138	3	AAG57501	Aag57501 Arabidops	933	5	20.8	155	4	ABR70923	AbR70923 Drosophil
861	5	20.8	138	3	AAG11796	Aag11796 Arabidops	934	5	20.8	155	4	ABR70923	AbR70923 Drosophil
862	5	20.8	138	9	AEA19872	Aea19872 Novel hum	935	5	20.8	155	4	ABR70923	AbR70923 Drosophil
863	5	20.8	139	3	AAW16371	Aaw16371 Eucalyptu	936	5	20.8	155	4	ABR70923	AbR70923 Drosophil
864	5	20.8	139	3	AAW57364	Aaw57364 Arabidops	937	5	20.8	155	8	ADT49815	Adt49815 Human CAM
865	5	20.8	139	3	AAW57364	Aaw57364 Arabidops	938	5	20.8	156	2	AAW20891	Aaw20891 H. pylori
866	5	20.8	139	7	ADP41547	Adp41547 Diphenol	939	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
867	5	20.8	139	9	ADP41547	Adp41547 Diphenol	940	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
868	5	20.8	140	6	ABO15030	AbO15030 Human NOV	941	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
869	5	20.8	140	6	ABO15030	AbO15030 Human NOV	942	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
870	5	20.8	140	6	ABO15030	AbO15030 Human NOV	943	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
871	5	20.8	140	8	ADQ97800	Adq97800 Human can	944	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
872	5	20.8	141	3	ABG49727	Abg49727 Arabidops	945	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
873	5	20.8	141	3	ABG49727	Abg49727 Arabidops	946	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
874	5	20.8	141	3	ABG49727	Abg49727 Arabidops	947	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
875	5	20.8	141	4	ABR70473	Abb70473 Drosophil	948	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
876	5	20.8	141	5	ABP07896	Abp07896 Human ORF	949	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
877	5	20.8	142	3	AAW24087	Aag24087 Arabidops	950	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
878	5	20.8	142	3	AAW24087	Aag24087 Arabidops	951	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
879	5	20.8	142	3	AAW24087	Aag24087 Arabidops	952	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
880	5	20.8	143	4	ABR71001	Abb71001 Drosophil	953	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
881	5	20.8	144	2	AAW35239	Aay35239 Chlamydia	954	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
882	5	20.8	145	3	AAW47273	Aag47273 Arabidops	955	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
883	5	20.8	145	4	ABG14559	Abg14559 Novel hum	956	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
884	5	20.8	145	7	ADT21616	Adt21616 Novel hum	957	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
885	5	20.8	146	3	AAW32631	Aag32631 Eucalyptu	958	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
886	5	20.8	147	3	AAW32631	Aag32631 Eucalyptu	959	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
887	5	20.8	147	3	AAW32631	Aag32631 Eucalyptu	960	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
888	5	20.8	147	3	AAW32631	Aag32631 Eucalyptu	961	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
889	5	20.8	147	8	ADT55945	Adt55945 Plant pol	962	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
890	5	20.8	148	4	AAW18157	Aam18157 Peptide #	963	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
891	5	20.8	148	4	ABR37189	Abb37189 Peptide #	964	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
892	5	20.8	148	4	AAW30658	Aam30658 Peptide #	965	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
893	5	20.8	148	4	ABR31951	Abb31951 Peptide #	966	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
894	5	20.8	148	4	ABR31951	Abb31951 Peptide #	967	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
895	5	20.8	148	4	AAW70318	Aam70318 Human bon	968	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
896	5	20.8	148	4	AAW57900	Aam57900 Human bra	969	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
897	5	20.8	148	4	ABG52018	Abg52018 Human liv	970	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
898	5	20.8	148	4	AAW05781	Aam05781 Peptide #	971	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
899	5	20.8	148	5	ABG39964	Abg39964 Human pep	972	5	20.8	156	3	AAW20891	Aaw20891 H. pylori
900	5	20.8	149	2	AAW20150	Aay20150 B. burgdo	973	5	20.8	156	3	AAW20891	Aaw20891 H. pylori

974 5 20.8 169 3 AAG36205 Arabidops
975 5 20.8 170 3 AAG37351 Arabidops
976 5 20.8 170 5 ABP73269 Candida a
977 5 20.8 171 3 AAB40227 Gene 36 h
978 5 20.8 171 3 AAB40228 Human sec
979 5 20.8 171 3 AAG40004 Arabidops
980 5 20.8 171 3 AAG36565 Arabidops
981 5 20.8 172 3 AAG17218 Arabidops
982 5 20.8 172 3 AAG10709 Arabidops
983 5 20.8 172 3 AAG47688 Arabidops
984 5 20.8 172 8 ADX87709 Plant ful
985 5 20.8 172 2 AAY06803 Peptide S
986 5 20.8 174 6 AAE33453 Mouse i-E
987 5 20.8 175 3 AAG20202 Arabidops
988 5 20.8 175 4 AAU23698 Novel hum
989 5 20.8 176 5 ABB55408 Lactococc
990 5 20.8 176 5 ABB54197 Lactococc
991 5 20.8 177 2 AAY50043 Pseudomon
992 5 20.8 177 3 AAG58004 Arabidops
993 5 20.8 177 3 AAG36404 Arabidops
994 5 20.8 177 5 ABP27025 Streptoco
995 5 20.8 177 6 ABU41559 Protein e
996 5 20.8 178 5 ABP28585 Streptoco
997 5 20.8 178 6 ABU46406 Protein e
998 5 20.8 178 9 ADX57001 Streptoco
999 5 20.8 178 9 ADX57003 Streptoco
1000 5 20.8 178 9 ADX57005 Streptoco

ALIGNMENTS

RESULT 1
AAG01570
ID AAG01570 standard; protein; 95 AA.
AC AAG01570;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 5651.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GBST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
DR N-PSDB; AAC01576.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 5651; 71pp + Sequence Listing; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 95 AA;
Query Match 100.0%; Score 24; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 24; Conservative - 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 LRFDSTQKSIPEQETNNNSFFYT 24
|||||
Db 35 LRFDSTQKSIPEQETNNNSFFYT 58
RESULT 2
AAG76051
ID AAG76051 standard; protein; 209 AA.
XX
AC AAG76051;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6815.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 12.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR N-PSDB; AAH35456.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 8267-8270; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027


```
CC to 1052, 7921 and 7922
XX Sequence 209 AA;
SQ Sequence 209 AA;

Query Match      100.0%; Score 24; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 9.8e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSKIFQEQTNNNSSFYT 24
Db 73 LRFDSQTSKIFQEQTNNNSSFYT 96

RESULT 3
ID AAR86834 standard; protein; 227 AA.
XX AAR86834;
AC AAR86834;
XX 12-JUL-1996 (first entry)
XX Human CD9 sequence.
XX CD9 antigen; stimulated T cell; antibody; ligand; proliferation;
KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;
KW immune response; cancer; infectious disease; growth factor.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 51
FT /note= "Potential N-linked glycosylation site"
FT Modified-site 52
FT /note= "Potential N-linked glycosylation site"
FT Domain 111..194
FT /note= "Extracellular domain"
FT Domain 195..220
FT /note= "Transmembrane domain"
FT Domain 221..227
FT /note= "Cytoplasmic domain"
XX WO9533823-A1.
XX 14-DEC-1995.
XX 01-DEC-1994; 94WO-US013782.
XX 03-JUN-1994; 94US-00253751.
XX 03-JUN-1994; 94US-00253964.
XX (USNA ) US SEC OF NAVY.
XX (UNMI ) UNIV MICHIGAN.
XX (REPK ) REPLIGEN CORP.
XX (DAND ) DANA FARBER CANCER INST INC.
XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;
XX WPI; 1996-040230/04.
XX Selectively inducing CD8 positive T cell proliferation - by activating
PT the T cells and stimulating CD9 cell surface ligand, useful for
PT immuno:therapy of, e.g. cancer.
XX Example 10; Page 38-39; 79pp; English.
XX This sequence represents CD9 from the surface of stimulated T cells. The
CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an
CC antibody or other ligand to stimulate the T cell population to
CC proliferate and expand leading to a 100- to 10000-fold increase in cell
CC number compared to the original population. The antigenic sequence fits
CC the generic sequence given in AAR86827. This epitope is recognised by the
CC monoclonal antibody (MAB) ES5.2D8. CD9 is a 27 kD accessory protein found
CC on activated T cells. The epitope was recognised by screening a phage
```

```
CC display library. Selective proliferation of an antigen-specific T cell
CC population is useful in cases where the immune response is to be up
CC regulated, e.g. in the treatment of cancer or infectious diseases. By
CC causing proliferation of the T cell population by stimulating T cell
CC epitope removes the need for exogenous growth factors or accessory cells
XX Sequence 227 AA;
SQ Sequence 227 AA;

Query Match      100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSKIFQEQTNNNSSFYT 24
Db 34 LRFDSQTSKIFQEQTNNNSSFYT 57

RESULT 4
ID ABB78366 standard; protein; 227 AA.
XX ABB78366;
AC ABB78366;
XX 16-DEC-2002 (first entry)
XX Amino acid sequence of CD9.
DE Amino acid sequence of CD9.
XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;
KW immunotherapy; CD9.
XX Homo sapiens.
XX US2002115214-A1.
XX 22-AUG-2002.
XX 26-JAN-1996; 96US-00592711.
XX 23-NOV-1988; 88US-00275433.
XX 07-APR-1992; 92US-00864805.
XX 07-APR-1992; 92US-00864807.
XX 07-APR-1992; 92US-00864866.
XX 04-JUN-1993; 93US-00073223.
XX 03-JUN-1994; 94US-00253964.
XX 10-MAR-1995; 95US-00403253.
XX 04-MAY-1995; 95US-00435816.
XX (JUNE/) JUNE C H.
XX (THOM/) THOMPSON C B.
XX (NABE/) NABEL G J.
XX (GRAY/) GRAY G S.
XX (RENN/) RENNERT P D.
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2002-712476/77.
XX Inducing a population of T cells to proliferate, by activating population
PT of T cells and stimulating an accessory molecule on the surface of the T
PT cells with a ligand which binds the accessory molecule.
XX Example 10; Page 25; 80pp; English.
XX The specification describes method for inducing a population of T cells
CC to proliferate. The method involves activating population of T cells,
CC stimulating an accessory molecule on T cell surface with a ligand
CC (protein) which binds the molecule, to induce proliferation of T cells,
CC monitoring proliferation of T cells in response to continuing exposure to
CC the ligand, and reactivating and restimulating T cells when rate of
CC proliferation has decreased to induce further proliferation of the cells.
CC The method is useful for inducing proliferation of T cells, for use in
CC treatment of infectious disease, cancer and immunotherapy. The method
CC allows for the expansion of a population of T cells in numbers sufficient
```

CC to reconstitute an individuals's total CD4+ or CD8+ T cell population.
CC The resulting T cell population can be genetically transduced and used
CC for immunotherapy or can be used in methods of in vitro analyses of
CC infectious agents. A population of tumour-infiltrating lymphocytes can be
CC obtained from an individual afflicted with cancer and the T cells
CC stimulated to proliferate to sufficient numbers. The resulting T cell
CC population can be genetically transduced to express tumour necrosis
CC factor (TNF) or other factor and restored to the individual. CD4+ T cells
CC expanded by this method are useful in the treatment of HIV infection in
CC an individual. The present sequence represents CD9, an antigen present on
CC the surface of activated T cells
XX
SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPEQTNNNSFYT 24
Db 34 LRFDSQTKSIFPEQTNNNSFYT 57

RESULT 5

ID AAE14636 standard; protein; 227 AA.

AC AAE14636;

DT 16-JUL-2002 (first entry)

DE Human CD9 antigen.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;
KW human; CD9 antigen.

OS Homo sapiens.

PN US6352694-B1.

PD 05-MAR-2002.

XX 10-MAR-1995; 95US-00403253.

PR 03-JUN-1994; 94US-00253964.

XX (GENY) GENETICS INST INC.

PA (UNMI) UNIV MICHIGAN.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

PI WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,
PT comprises activating T cells by contacting T cells in vitro with
PT immobilized anti-CD3 antibody and stimulating accessory molecule on T
PT cell surface.

PS Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to
CC proliferate for use in therapy comprising activating T cells by
CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
CC on solid phase surface, and stimulating accessory molecule on T cell
CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural
CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a
CC population of T cells to proliferate in sufficient numbers for use in
CC therapy e.g., for treating cancer or an infectious disease. The method
CC can be used to selectively expand the population of CD28⁺, CD4⁺, CD8⁺,
CC CD28RA⁺ or CD28RO⁺ T cells for immunotherapy. The T cell population
CC resulting by the method can be genetically transduced and used for
CC immunotherapy or can be used for in vitro analysis of infectious agents

CC such as human immunodeficiency virus (HIV). Proliferation of a population
CC of CD4⁺ T cells obtained from an individual infected with HIV can be
CC achieved and the cells rendered resistant to HIV infection. Following the
CC expansion of the T cells to sufficient numbers, the expanded T cells are
CC restored to the individual. Also CD4⁺ T cells expanded by the above
CC mentioned is useful for treating HIV infection in an individual. A
CC population of tumour-infiltrating lymphocytes can be obtained from an
CC individual afflicted with cancer and the T cells stimulated to
CC proliferate to sufficient numbers and restored to the individual. The
CC supernatants from cultures of T cells expanded from above mentioned
CC method are useful as a rich source of cytokines and can be used to
CC sustain T cells in vivo or ex vivo. Stimulating and expanding a
CC population of antigen specific T cells are useful in therapeutic
CC conditions where it is desirable to upregulate an immune response. The T
CC cell proliferation occurs in the absence of exogenous growth factors or
CC accessory cells. The present sequence is human CD9 antigen which is
XX expressed on surface of activated T cells
SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPEQTNNNSFYT 24
Db 34 LRFDSQTKSIFPEQTNNNSFYT 57

RESULT 6

ABU05057

ID ABU05057 standard; protein; 227 AA.

AC ABU05057;

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1723.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

PN WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

PS Example 2; SEQ ID NO 1723; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPEQETNNNSFYT 24
 |||||
 Db 34 LRFDSQTKSIFPEQETNNNSFYT 57

RESULT 7
 ABU05060
 ID ABU05060 standard; protein; 227 AA.

AC ABU05060;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1726.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

PN 10-OCT-2002.

PD 28-MAR-2002; 2002WO-US009671.

PF 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0338780P.

PR 20-FEB-2002; 2002US-0359885P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX Example 2; SEQ ID NO 1726; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPEQETNNNSFYT 24
 |||||
 Db 34 LRFDSQTKSIFPEQETNNNSFYT 57

RESULT 8
 ABW00436

ID ABW00436 standard; protein; 227 AA.

AC ABW00436;

DT 15-JAN-2004 (first entry)

DE Human CD9 antigenic protein.

KW HIV infection; human immunodeficiency virus; therapy; antigen; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 111..194

FT Domain /note= "Extracellular domain"

FT Domain 195..220

FT Domain /note= "Transmembrane domain"

FT Domain 221..227

FT Domain /note= "Cytoplasmic domain"

PN US2003099643-A1.

PD 29-MAY-2003.

PF 08-JUL-1999; 99US-00350202.

PR 23-NOV-1988; 88US-00275433.

PR 22-NOV-1989; 89WO-US005304.

PR 07-APR-1992; 92US-00864805.

PR 07-APR-1992; 92US-00864807.

PR 07-APR-1992; 92US-00864866.

PR 04-JUN-1993; 93US-00073223.

PR 03-JUN-1994; 94US-00253694.

PR 10-MAR-1995; 95US-00403253.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABEL/) NABEL G J.

XX (GRAY/) GRAY G S.

XX (RENN/) RENNERT P D.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2003-801206/75.
XX Treating HIV infection in individual by isolating T cells from
PT leukocytes, contacting T cells with anti-CD3 antibody for T cell
PT proliferation, separating antibody from T cells, monitoring proliferation
PT of T cells.
XX
XX Example 10; Page 23; Opp; English.
XX
XX The present invention relates to a novel method of treating human
CC immunodeficiency virus (HIV) infection in an individual. The method
CC involves isolating population of CD4 T cells from leukocytes, contacting
CC population of CD4+ T cells with an anti-CD3 antibody for stimulating T
CC cell proliferation, separating antibody from T cells, monitoring
CC proliferation of T cells, restimulating T cells with antibody and
CC restoring T cells to individual. The present sequence is human CD9
CC antigenic protein. This sequence is used to illustrate the method of the
CC invention
XX
XX Sequence 227 AA;
SQ
Query Match 100.0%; Score 24; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRFDSTQKSIPEQETNNNSFYT 24
DB 34 LRFDSTQKSIPEQETNNNSFYT 57
RESULT 9
ADK69862
ID ADK69862 standard; protein; 227 AA.
XX
AC ADK69862;
DT 06-MAY-2004 (first entry)
XX
DE Human CD9 protein.
XX
KW CD28-associated signal; immunotherapy; infectious disease; cancer;
KW leukopenia; human.
XX
OS Homo sapiens.
XX
PN US6534055-B1.
XX
PD 18-MAR-2003.
XX
PF 04-MAY-1995; 95US-00435816.
XX
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864856.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253964.
PR 10-MAR-1995; 95US-00403253.
XX
XX (GEMV) GENETICS INST INC.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2003-531074/50.
XX
XX Expanding T cell populations, useful for preparing renewable sources of T
PT cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28
PT -associated signal on the surface of the cells with an anti-CD28
PT antibody, B7-1 or B7-2.
XX
XX Example 10; SEQ ID NO 6; 82pp; English.
XX
XX The invention relates to a method for expanding a population of T cells
CC

CC to about 100-100000-fold over the original T cell population, or to about
CC 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-
CC associated signal on the surface of the T cells with agent comprising an
CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a
CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T
CC cells) to proliferate. The method is particularly useful for preparing a
CC renewable source of CD4+ T cells. The expanded T cell population can be
CC genetically transduced, and used for immunotherapy to treat a variety of
CC human diseases (e.g. infectious diseases or cancer), or used in
CC diagnostic protocols. T cells were obtained from leukopheresis of a
CC normal donor, and purified with FICOLL density gradient centrifugation,
CC followed by magnetic immunobead sorting. The present sequence is CD9 used
CC in the exemplification of the invention.
XX
XX Sequence 227 AA;
SQ
Query Match 100.0%; Score 24; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRFDSTQKSIPEQETNNNSFYT 24
DB 34 LRFDSTQKSIPEQETNNNSFYT 57
RESULT 10
ADI19366
ID ADI19366 standard; protein; 227 AA.
XX
AC ADI19366;
XX
DT 15-APR-2004 (first entry)
XX
DE Human CD9 protein.
XX
KW T cell; immunotherapy; therapy; HIV infection; cancer;
KW infectious disease; cytostatic; antimicrobial; human.
XX
OS Homo sapiens.
XX
PN US2004001829-A1.
XX
PD 01-JAN-2004.
XX
PF 17-MAR-2003; 2003US-00390330.
XX
PR 23-NOV-1988; 88US-00275433.
PR 22-NOV-1989; 89WO-US005304.
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253964.
PR 10-MAR-1995; 95US-00403253.
PR 04-MAY-1995; 95US-00435816.
XX
XX (JUNE/) JUNE C H.
XX (THOM/) THOMPSON C B.
XX (NABEL/) NABEL G J.
XX (GRAY/) GRAY G S.
XX (RENN/) RENNERT P D.
XX
XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX WPI; 2004-061648/06.
XX
XX Inducing a population of T cells to proliferate, for immunotherapy or
PT treating HIV infection, cancer or infectious disease, comprises
PT activating a population of T cells and stimulating an accessory molecule
PT on the surface of the T cells.
XX
XX Example 10; SEQ ID NO 6; 80pp; English.
XX

CC The invention relates to a method for inducing a population of T cells to
CC proliferate. The method comprising activating a population of T cells,
CC and stimulating an accessory molecule on the surface of the T cells with
CC a ligand that binds the accessory molecule. The invention is useful for
CC immunotherapy, for treating HIV infection, cancer or infectious disease,
CC or in diagnostic applications. The present sequence is human CD9 protein.
SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 8; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 LRFDSQTSIFQEQTNNNSSFT 24
DB 34 LRFDSQTSIFQEQTNNNSSFT 57
|||||

RESULT 11
AEA89005
ID AEA89005 standard; protein; 227 AA.

XX AEA89005;

DT 25-AUG-2005 (first entry)

DE Human CD9 antigenic protein, SEQ ID NO: 6.

KW Cell therapy; immune stimulation; immunotherapy; diagnosis;
KW infectious disease; antimicrobial; infection; cancer; cytostatic;
KW neoplasm; CD9; antigen.

OS Homo sapiens.

PN US6905681-B1.

PD 14-JUN-2005.

PF 08-JUL-1999; 99US-00349915.

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

XX (GEMY) GENETICS INST INC.

PA (UNMI) UNIV MICHIGAN.

XX (USNA) US SEC OF NAVY.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2005-46477/47.

DR Ex vivo proliferation of T cell population for use in therapy, involves
XX contacting population of T cells with surface having anti-CD3 antibody
PT and anti-CD28 antibody for activating T cells and stimulating activated T
PT cells, respectively.

PS Example 10; SEQ ID NO 6; 76pp; English.

XX The present invention relates to a method of including ex vivo
CC proliferation of a population of T cells to sufficient numbers for use in
CC therapy. The method involves contacting population of T cells with
CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T
CC cells and stimulating activated T cells, respectively. The invention is
CC useful for treating cancer and infectious disease and also useful in cell
CC therapy. The present sequence is the human CD9 antigenic protein. This
CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used
CC to stimulate a CD8+ T cell population.

SQ Sequence 227 AA;

Query Match 100.0%; Score 24; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSIFQEQTNNNSSFT 24
DB 34 LRFDSQTSIFQEQTNNNSSFT 57
|||||

RESULT 12
ABB44581

XX ID ABB44581 standard; protein; 228 AA.

AC ABB44581;

DT 25-JAN-2002 (first entry)

DE Human wound healing related polypeptide SEQ ID NO 38.

KW Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.

OS Homo sapiens.

PN CA2325226-A1.

PD 17-MAY-2001.

PF 16-NOV-2000; 2000CA-02325226.

PR 17-NOV-1999; 99DE-01055349.

PR 17-DEC-1999; 99US-0172511P.

PR 20-JUN-2000; 2000DE-01030149.

XX (SWIT-) SWITCH BIOTECH AG.

XX Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;

XX WPI; 2001-433142/47.

DR Use of novel polypeptide or its variant or nucleic acid encoding the
XX polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances.

PS Disclosure; Page 193-194; 265pp; English.

XX The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-
CC ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological
CC activity for the diagnosis, prevention and treatment of skin disorders
CC and treatment in wound healing or for the identification of
CC pharmacologically active substances. The nucleic acids are useful in gene
CC therapy. Note: The printed sequence listing for this specification was
CC incomplete, terminating part way through SEQ ID NO 106. The remaining
CC data was obtained from EPO data for an equivalent patent (Epl114862)

XX Sequence 228 AA;

Query Match 100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTSIFQEQTNNNSSFT 24
DB 35 LRFDSQTSIFQEQTNNNSSFT 58
|||||

RESULT 13
ABU05059

ID ABU05059 standard; protein; 228 AA.

XX ABU05059;

XX 29-JAN-2003 (first entry)

XX

```
DE Human expressed protein tag (BPT) #1725.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1725; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor.
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRFDSTQKSIPEQETNNNSSFT 24
DB 35 LRFDSTQKSIPEQETNNNSSFT 58

RESULT 14
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX
XX ABU05052;
AC
XX
XX 29-JAN-2003 (first entry)
DT
XX
```

```
DE Human expressed protein tag (BPT) #1718.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1718; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor.
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
SQ
Query Match 100.0%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LRFDSTQKSIPEQETNNNSSFT 24
DB 35 LRFDSTQKSIPEQETNNNSSFT 58

RESULT 15
ABU05048
ID ABU05048 standard; protein; 228 AA.
XX
XX ABU05048;
AC
XX
XX 29-JAN-2003 (first entry)
DT
XX
```

DE Human expressed protein tag (EPT) #1714.
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX Homo sapiens.
 XX OS
 XX PN WO200278524-A2.
 XX PD 10-OCT-2002.
 XX PF 28-MAR-2002; 2002WO-US009671.
 XX PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX (ZYCO-) ZYCO INC.
 XX PA
 XX PI Chicx RM, Tomlinson AJ, Urban RG;
 XX WPI; 2003-040607/03.
 XX DR
 XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX PS
 PS Example 2; SEQ ID NO 1714; 134pp; English.
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 228 AA;

Query Match 100.0%; Score 24; DB 6; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.1e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTKSIFQETNNNSSFYT 24
 DB 35 LRPDSQTKSIFQETNNNSSFYT 58

Search completed: January 20, 2006, 17:42:00
 Job time : 69.0769 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:38:26 ; Search time 8.76923 Seconds
(without alignments)
226.270 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24
Sequence: 1 LRFDSQTSIFQETNNNSPYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	95	2	US-09-513-999C-5651
2	24	100.0	227	1	US-08-254-493-1
3	24	100.0	227	1	US-08-253-751-6
4	24	100.0	227	1	US-08-453-925-6
5	24	100.0	227	2	US-08-403-253A-6
6	24	100.0	227	2	US-08-435-818A-6
7	24	100.0	227	2	US-09-350-202-6
8	24	100.0	227	2	US-08-592-711-6
9	24	100.0	227	2	US-09-349-915B-6
10	24	100.0	228	1	US-08-408-222B-1
11	23	95.8	26	1	US-08-254-493-7
12	23	95.8	26	1	US-08-408-222B-7
13	7	29.2	153	2	US-09-270-767-41112
14	7	29.2	153	2	US-09-270-767-56328
15	6	25.0	23	1	US-08-642-846-4
16	6	25.0	23	2	US-09-264-604-4
17	6	25.0	23	2	US-09-978-343-4
18	6	25.0	23	5	US-09-599-652-4
19	6	25.0	29	2	US-09-270-767-60339
20	6	25.0	63	2	US-09-248-796A-21641
21	6	25.0	101	2	US-09-248-796A-23557
22	6	25.0	107	2	US-09-538-092-92
23	6	25.0	111	2	US-09-270-767-44871
24	6	25.0	123	2	US-09-270-767-58078
25	6	25.0	146	2	US-09-270-767-33561
26	6	25.0	146	2	US-09-270-767-48778
27	6	25.0	148	2	US-09-270-767-31975

28	6	25.0	148	2	US-09-270-767-47192	Sequence 47192, A
29	6	25.0	154	2	US-09-248-796A-27970	Sequence 27970, A
30	6	25.0	158	2	US-09-248-796A-32805	Sequence 32805, A
31	6	25.0	169	2	US-09-134-001C-4590	Sequence 4590, Ap
32	6	25.0	171	2	US-09-270-767-38172	Sequence 38172, A
33	6	25.0	171	2	US-09-270-767-53389	Sequence 53389, A
34	6	25.0	180	2	US-09-248-796A-21013	Sequence 21013, A
35	6	25.0	200	2	US-09-248-796A-14576	Sequence 14576, A
36	6	25.0	236	1	US-08-642-846-3	Sequence 3, Appli
37	6	25.0	236	2	US-09-264-604-3	Sequence 3, Appli
38	6	25.0	236	2	US-09-978-343-3	Sequence 3, Appli
39	6	25.0	236	5	US-09-599-652-3	Sequence 3, Appli
40	6	25.0	256	2	US-09-248-796A-20626	Sequence 20626, A
41	6	25.0	259	2	US-09-248-796A-20465	Sequence 20465, A
42	6	25.0	260	2	US-09-270-767-58646	Sequence 58646, A
43	6	25.0	278	2	US-09-248-796A-19983	Sequence 19983, A
44	6	25.0	287	1	US-08-433-783-37	Sequence 37, Appl
45	6	25.0	287	1	US-08-337-358-37	Sequence 37, Appl
46	6	25.0	287	2	US-09-270-767-32196	Sequence 32196, A
47	6	25.0	287	2	US-09-270-767-47413	Sequence 47413, A
48	6	25.0	287	4	PCT-US95-07537A-37	Sequence 37, Appl
49	6	25.0	287	4	PCT-US95-07537-37	Sequence 37, Appl
50	6	25.0	295	2	US-09-248-796A-14734	Sequence 14734, A
51	6	25.0	314	2	US-09-248-796A-22297	Sequence 22297, A
52	6	25.0	327	2	US-09-270-767-44614	Sequence 44614, A
53	6	25.0	351	2	US-09-248-796A-16176	Sequence 16176, A
54	6	25.0	354	2	US-09-538-092-677	Sequence 677, App
55	6	25.0	354	2	US-09-487-558B-414	Sequence 414, App
56	6	25.0	357	2	US-09-248-796A-14735	Sequence 14735, A
57	6	25.0	364	2	US-09-248-796A-16905	Sequence 16905, A
58	6	25.0	374	2	US-09-270-767-42761	Sequence 42761, A
59	6	25.0	377	2	US-09-248-796A-20227	Sequence 20227, A
60	6	25.0	394	2	US-09-270-767-37939	Sequence 37939, A
61	6	25.0	394	2	US-09-270-767-53156	Sequence 53156, A
62	6	25.0	402	2	US-09-252-991A-26529	Sequence 26529, A
63	6	25.0	416	2	US-09-248-796A-16796	Sequence 16796, A
64	6	25.0	423	2	US-09-248-796A-14462	Sequence 14462, A
65	6	25.0	433	2	US-09-270-767-38291	Sequence 38291, A
66	6	25.0	433	2	US-09-270-767-53508	Sequence 53508, A
67	6	25.0	447	2	US-09-538-092-220	Sequence 220, App
68	6	25.0	462	2	US-09-270-767-44315	Sequence 44315, A
69	6	25.0	463	2	US-09-248-796A-18855	Sequence 18855, A
70	6	25.0	473	2	US-09-248-796A-27126	Sequence 27126, A
71	6	25.0	478	2	US-09-700-397-8	Sequence 8, Appli
72	6	25.0	501	2	US-09-248-796A-18735	Sequence 18735, A
73	6	25.0	517	2	US-09-248-796A-14652	Sequence 14652, A
74	6	25.0	521	2	US-09-248-796A-23363	Sequence 23363, A
75	6	25.0	555	2	US-09-270-767-43300	Sequence 43300, A
76	6	25.0	605	2	US-09-487-558B-428	Sequence 428, App
77	6	25.0	628	1	US-08-261-822A-6	Sequence 6, Appli
78	6	25.0	628	4	PCT-US95-07744A-6	Sequence 6, Appli
79	6	25.0	631	2	US-09-270-767-61990	Sequence 61990, A
80	6	25.0	675	1	US-08-386-495-10	Sequence 10, Appl
81	6	25.0	675	4	PCT-US96-02331-10	Sequence 10, Appl
82	6	25.0	676	2	US-09-487-558B-302	Sequence 302, App
83	6	25.0	704	2	US-08-792-832A-2	Sequence 2, Appli
84	6	25.0	710	2	US-09-270-767-46412	Sequence 46412, A
85	6	25.0	719	2	US-09-248-796A-17559	Sequence 17559, A
86	6	25.0	730	2	US-09-487-558B-126	Sequence 126, App
87	6	25.0	732	2	US-08-914-999-8	Sequence 8, Appli
88	6	25.0	842	4	PCT-US96-02331-15	Sequence 15, Appl
89	6	25.0	925	2	US-09-248-796A-14284	Sequence 14284, A
90	6	25.0	945	2	US-09-248-796A-15743	Sequence 15743, A
91	6	25.0	1058	2	US-10-464-939-4	Sequence 4, Appli
92	6	25.0	1111	2	US-09-914-259-28	Sequence 28, Appl
93	6	25.0	1244	2	US-09-538-092-12	Sequence 12, Appl
94	6	25.0	1420	2	US-09-903-540-11946	Sequence 11946, A
95	6	25.0	1531	2	US-09-976-594-203	Sequence 203, App
96	6	25.0	1584	2	US-09-457-040B-27	Sequence 27, Appl
97	6	25.0	1621	2	US-09-949-016-8450	Sequence 8450, Ap
98	6	25.0	1664	1	US-08-642-846-2	Sequence 2, Appli
99	6	25.0	1664	2	US-09-264-604-2	Sequence 2, Appli
100	6	25.0	1664	2	US-09-978-343-2	Sequence 2, Appli

101	6	25.0	1664	5	US-09-599-652-2	Sequence 2, Appli	174	5	20.8	89	2	US-09-746-311B-171	Sequence 171, App
102	6	25.0	2071	2	US-09-415-522-6	Sequence 6, Appli	175	5	20.8	89	2	US-09-746-311B-174	Sequence 174, App
103	6	25.0	2167	2	US-09-487-558B-56	Sequence 56, Appli	176	5	20.8	89	2	US-09-746-311B-213	Sequence 213, App
104	5	20.8	17	1	US-08-728-152-32	Sequence 32, Appl	177	5	20.8	89	2	US-09-746-311B-340	Sequence 340, App
105	5	20.8	21	2	US-09-963-756-501	Sequence 501, App	178	5	20.8	89	2	US-09-841-091B-19	Sequence 19, Appl
106	5	20.8	23	1	US-08-486-953A-48	Sequence 48, Appl	179	5	20.8	90	2	US-09-270-767-40580	Sequence 40580, A
107	5	20.8	23	2	US-08-204-052-48	Sequence 48, Appl	180	5	20.8	90	2	US-09-270-767-55796	Sequence 55796, A
108	5	20.8	23	2	US-09-967-869A-1	Sequence 1, Appli	181	5	20.8	91	2	US-09-248-796A-21654	Sequence 21654, A
109	5	20.8	30	2	US-09-270-767-58530	Sequence 58530, A	182	5	20.8	92	2	US-08-905-223-408	Sequence 408, App
110	5	20.8	31	2	US-09-902-540-14542	Sequence 14542, A	183	5	20.8	93	2	US-09-149-476A-111	Sequence 411, App
111	5	20.8	36	2	US-09-106-568E-128	Sequence 128, App	184	5	20.8	93	2	US-09-248-796A-22627	Sequence 22627, A
112	5	20.8	48	2	US-09-270-767-40710	Sequence 40710, A	185	5	20.8	94	2	US-09-147-550-62	Sequence 62, Appl
113	5	20.8	48	2	US-09-270-767-55926	Sequence 55926, A	186	5	20.8	94	2	US-09-557-917-62	Sequence 62, Appl
114	5	20.8	54	2	US-09-513-999C-6274	Sequence 6274, Ap	187	5	20.8	94	2	US-10-012-819-50	Sequence 50, Appl
115	5	20.8	55	2	US-09-270-767-40672	Sequence 40672, A	188	5	20.8	95	2	US-09-248-796A-21181	Sequence 21181, A
116	5	20.8	55	2	US-09-270-767-55888	Sequence 55888, A	189	5	20.8	99	2	US-09-248-796A-22361	Sequence 22361, A
117	5	20.8	57	1	US-08-107-676-32	Sequence 32, Appl	190	5	20.8	100	2	US-09-248-796A-27458	Sequence 27458, A
118	5	20.8	57	2	US-09-295-820-32	Sequence 32, Appl	191	5	20.8	102	2	US-09-333-809-85	Sequence 85, Appl
119	5	20.8	57	2	US-09-270-767-34963	Sequence 34963, A	192	5	20.8	102	2	US-09-333-809-102	Sequence 102, App
120	5	20.8	57	2	US-09-270-767-50180	Sequence 50180, A	193	5	20.8	102	2	US-09-270-767-56662	Sequence 56662, A
121	5	20.8	59	2	US-09-270-767-42689	Sequence 42689, A	194	5	20.8	102	2	US-09-248-796A-23248	Sequence 23248, A
122	5	20.8	63	1	US-08-194-338-14	Sequence 14, Appl	195	5	20.8	104	2	US-09-583-110-3078	Sequence 3078, Ap
123	5	20.8	63	2	US-09-107-532A-6109	Sequence 6109, Ap	196	5	20.8	106	2	US-09-248-796A-23730	Sequence 23730, A
124	5	20.8	63	2	US-09-540-236-3706	Sequence 3706, Ap	197	5	20.8	108	2	US-09-893-737-238	Sequence 238, App
125	5	20.8	63	2	US-09-248-796A-27293	Sequence 27293, A	198	5	20.8	108	2	US-10-104-047-3446	Sequence 3446, Ap
126	5	20.8	64	2	US-09-513-998C-6899	Sequence 6899, Ap	199	5	20.8	109	2	US-09-583-110-3970	Sequence 3970, Ap
127	5	20.8	64	2	US-09-248-796A-24160	Sequence 24160, A	200	5	20.8	109	2	US-09-248-796A-27108	Sequence 27108, A
128	5	20.8	65	2	US-09-543-681A-6786	Sequence 6786, Ap	201	5	20.8	110	1	US-08-569-166-34	Sequence 34, Appl
129	5	20.8	65	2	US-09-248-796A-24533	Sequence 24533, A	202	5	20.8	110	2	US-09-605-703B-2056	Sequence 2056, Ap
130	5	20.8	66	2	US-09-248-796A-21335	Sequence 21335, A	203	5	20.8	111	2	US-09-248-796A-26077	Sequence 26077, A
131	5	20.8	66	2	US-09-248-796A-28075	Sequence 28075, A	204	5	20.8	111	2	US-09-746-311B-338	Sequence 338, App
132	5	20.8	67	2	US-09-270-767-34000	Sequence 34000, A	205	5	20.8	111	2	US-09-640-211A-966	Sequence 966, App
133	5	20.8	67	2	US-09-270-767-49217	Sequence 49217, A	206	5	20.8	112	2	US-09-746-311B-136	Sequence 136, App
134	5	20.8	68	2	US-09-489-039A-10460	Sequence 10460, A	207	5	20.8	113	2	US-09-489-039A-8131	Sequence 8131, Ap
135	5	20.8	68	2	US-09-270-767-34348	Sequence 34348, A	208	5	20.8	113	2	US-09-640-211A-2273	Sequence 2273, Ap
136	5	20.8	69	2	US-09-270-767-49565	Sequence 49565, A	209	5	20.8	114	2	US-09-270-767-34308	Sequence 34308, A
137	5	20.8	70	2	US-09-248-796A-25437	Sequence 25437, A	210	5	20.8	114	2	US-09-270-767-49525	Sequence 49525, A
138	5	20.8	71	2	US-09-248-796A-19288	Sequence 19288, A	211	5	20.8	114	2	US-09-107-433-2930	Sequence 2930, Ap
139	5	20.8	71	2	US-09-248-796A-21321	Sequence 21321, A	212	5	20.8	116	2	US-09-248-796A-21516	Sequence 21516, A
140	5	20.8	71	2	US-09-248-796A-23760	Sequence 23760, A	213	5	20.8	116	2	US-09-248-796A-25995	Sequence 25995, A
141	5	20.8	73	2	US-09-248-796A-21776	Sequence 21776, A	214	5	20.8	116	2	US-09-248-796A-27754	Sequence 27754, A
142	5	20.8	75	2	US-08-803-346-59	Sequence 59, Appl	215	5	20.8	117	2	US-09-270-767-41222	Sequence 41222, A
143	5	20.8	77	2	US-09-270-767-34403	Sequence 34403, A	216	5	20.8	117	2	US-09-270-767-56438	Sequence 56438, A
144	5	20.8	77	2	US-09-270-767-49620	Sequence 49620, A	217	5	20.8	117	2	US-09-270-767-61650	Sequence 61650, A
145	5	20.8	77	2	US-09-248-796A-22348	Sequence 22348, A	218	5	20.8	118	2	US-09-489-039A-12655	Sequence 12655, A
146	5	20.8	77	2	US-09-248-796A-26998	Sequence 26998, A	219	5	20.8	120	2	US-09-513-999C-4290	Sequence 4290, Ap
147	5	20.8	78	2	US-09-663-600A-131	Sequence 131, App	220	5	20.8	121	2	US-09-248-796A-15678	Sequence 15678, A
148	5	20.8	78	2	US-09-663-600A-225	Sequence 225, App	221	5	20.8	121	2	US-09-248-796A-26597	Sequence 26597, A
149	5	20.8	78	2	US-09-333-809-106	Sequence 106, App	222	5	20.8	121	2	US-09-248-796A-26595	Sequence 26595, A
150	5	20.8	78	2	US-09-248-796A-24254	Sequence 24254, A	223	5	20.8	122	2	US-09-248-796A-23665	Sequence 23665, A
151	5	20.8	78	2	US-09-746-311B-170	Sequence 170, App	224	5	20.8	122	2	US-09-248-796A-23944	Sequence 23944, A
152	5	20.8	79	2	US-09-248-796A-22673	Sequence 22673, A	225	5	20.8	123	2	US-09-830-230A-756	Sequence 756, App
153	5	20.8	80	2	US-09-270-767-60158	Sequence 60158, A	226	5	20.8	124	2	US-09-248-796A-27855	Sequence 27855, A
154	5	20.8	81	2	US-09-333-809-103	Sequence 103, App	227	5	20.8	125	2	US-09-489-039A-7420	Sequence 7420, Ap
155	5	20.8	81	2	US-09-333-809-104	Sequence 104, App	228	5	20.8	125	2	US-09-830-230A-668	Sequence 668, App
156	5	20.8	81	2	US-09-746-311B-167	Sequence 167, App	229	5	20.8	126	2	US-09-270-767-37937	Sequence 37937, A
157	5	20.8	81	2	US-09-746-311B-168	Sequence 168, App	230	5	20.8	126	2	US-09-270-767-38219	Sequence 38219, A
158	5	20.8	81	2	US-09-746-311B-298	Sequence 298, App	231	5	20.8	126	2	US-09-270-767-53154	Sequence 53154, A
159	5	20.8	81	2	US-09-746-311B-341	Sequence 341, App	232	5	20.8	126	2	US-09-270-767-53436	Sequence 53436, A
160	5	20.8	81	2	US-09-746-311B-343	Sequence 343, App	233	5	20.8	127	2	US-09-134-000C-6434	Sequence 6434, Ap
161	5	20.8	82	2	US-09-253-991A-32127	Sequence 32127, A	234	5	20.8	127	2	US-09-248-796A-27585	Sequence 27585, A
162	5	20.8	83	2	US-09-134-000C-4975	Sequence 4975, Ap	235	5	20.8	130	2	US-09-270-767-41135	Sequence 41135, A
163	5	20.8	83	2	US-09-270-767-58075	Sequence 58075, A	236	5	20.8	130	2	US-09-270-767-56351	Sequence 56351, A
164	5	20.8	83	2	US-09-746-311B-300	Sequence 300, App	237	5	20.8	135	2	US-09-270-767-38992	Sequence 38992, A
165	5	20.8	85	2	US-09-746-311B-301	Sequence 301, App	238	5	20.8	135	2	US-09-270-767-54209	Sequence 54209, A
166	5	20.8	85	2	US-09-746-311B-335	Sequence 335, App	239	5	20.8	135	2	US-09-248-796A-21635	Sequence 21635, A
167	5	20.8	86	2	US-09-178-093B-34	Sequence 34, Appl	240	5	20.8	138	2	US-09-270-767-42296	Sequence 42296, A
168	5	20.8	88	2	US-09-333-809-105	Sequence 105, App	241	5	20.8	139	2	US-09-635-192A-297	Sequence 297, App
169	5	20.8	88	2	US-09-746-311B-169	Sequence 169, App	242	5	20.8	139	2	US-09-270-767-37514	Sequence 37514, A
170	5	20.8	88	2	US-09-746-311B-299	Sequence 299, App	243	5	20.8	139	2	US-09-270-767-52731	Sequence 52731, A
171	5	20.8	88	2	US-09-746-311B-297	Sequence 297, App	244	5	20.8	140	2	US-09-270-767-31947	Sequence 31947, A
172	5	20.8	88	2	US-09-746-311B-302	Sequence 302, App	245	5	20.8	140	2	US-09-270-767-47164	Sequence 47164, A
173	5	20.8	89	2	US-09-333-809-107	Sequence 107, App	246	5	20.8	140	2	US-09-248-796A-23981	Sequence 23981, A

247	5	20.8	140	2	US-10-104-047-3489	Sequence 3489, Ap	320	5	20.8	188	2	US-09-134-000C-4373	Sequence 4373, Ap
248	5	20.8	141	2	US-09-248-796A-20650	Sequence 20650, A	321	5	20.8	188	2	US-09-746-311B-294	Sequence 294, App
249	5	20.8	142	2	US-09-270-767-34825	Sequence 34825, A	322	5	20.8	188	2	US-09-893-737-16	Sequence 16, Appl
250	5	20.8	143	2	US-09-270-767-50042	Sequence 50042, A	323	5	20.8	189	2	US-09-248-796A-19441	Sequence 19441, A
251	5	20.8	144	2	US-09-198-452A-657	Sequence 657, App	324	5	20.8	190	2	US-09-615-192A-301	Sequence 301, App
252	5	20.8	144	2	US-09-270-767-48661	Sequence 48661, A	325	5	20.8	190	2	US-09-270-767-58731	Sequence 58731, A
253	5	20.8	144	2	US-09-248-796A-21043	Sequence 21043, A	326	5	20.8	190	2	US-09-248-796A-20502	Sequence 20502, A
254	5	20.8	146	2	US-09-270-767-34388	Sequence 34388, A	327	5	20.8	190	2	US-09-248-796A-27916	Sequence 27916, A
255	5	20.8	146	2	US-09-270-767-49605	Sequence 49605, A	328	5	20.8	191	2	US-09-270-767-36747	Sequence 36747, A
256	5	20.8	146	2	US-09-248-796A-28095	Sequence 28095, A	329	5	20.8	191	2	US-09-270-767-51964	Sequence 51964, A
257	5	20.8	146	2	US-09-640-211A-680	Sequence 680, App	330	5	20.8	191	2	US-09-107-433-3302	Sequence 3302, Ap
258	5	20.8	147	2	US-09-270-767-38918	Sequence 38918, A	331	5	20.8	192	2	US-09-248-796A-24168	Sequence 24168, A
259	5	20.8	147	2	US-09-270-767-54135	Sequence 54135, A	332	5	20.8	192	2	US-09-248-796A-27575	Sequence 27575, A
260	5	20.8	147	2	US-09-270-767-60042	Sequence 60042, A	333	5	20.8	192	2	US-09-949-016-8859	Sequence 8859, Ap
261	5	20.8	149	2	US-09-830-230A-755	Sequence 755, App	334	5	20.8	195	2	US-09-248-796A-20410	Sequence 20410, A
262	5	20.8	150	2	US-09-540-236-3497	Sequence 3497, Ap	335	5	20.8	196	2	US-09-270-767-61292	Sequence 61292, A
263	5	20.8	150	2	US-09-438-185A-621	Sequence 621, App	336	5	20.8	196	2	US-09-248-796A-17562	Sequence 17562, A
264	5	20.8	151	2	US-09-328-352-6429	Sequence 6429, Ap	337	5	20.8	198	2	US-09-252-991A-25186	Sequence 25186, A
265	5	20.8	151	2	US-09-830-230A-667	Sequence 667, App	338	5	20.8	199	2	US-09-543-681A-4701	Sequence 4701, Ap
266	5	20.8	155	2	US-09-053-197A-25	Sequence 25, Appl	339	5	20.8	199	2	US-09-583-110-2932	Sequence 2932, Ap
267	5	20.8	155	2	US-09-085-761A-25	Sequence 25, Appl	340	5	20.8	199	2	US-09-248-796A-14467	Sequence 14467, A
268	5	20.8	155	2	US-09-270-767-41181	Sequence 41181, A	341	5	20.8	201	2	US-09-270-767-39000	Sequence 39000, A
269	5	20.8	155	2	US-09-270-767-56397	Sequence 56397, A	342	5	20.8	201	2	US-09-270-767-54217	Sequence 54217, A
270	5	20.8	155	2	US-09-710-278-716	Sequence 716, App	343	5	20.8	201	2	US-09-248-796A-27116	Sequence 27116, A
271	5	20.8	155	2	US-09-248-796A-18789	Sequence 18789, A	344	5	20.8	201	6	5171840-11	Patent No. 5171840
272	5	20.8	157	2	US-09-270-767-39944	Sequence 39944, A	345	5	20.8	202	2	US-09-540-236-2012	Sequence 2012, Ap
273	5	20.8	157	2	US-09-270-767-40195	Sequence 40195, A	346	5	20.8	202	2	US-09-270-767-34966	Sequence 34966, A
274	5	20.8	157	2	US-09-270-767-55161	Sequence 55161, A	347	5	20.8	202	2	US-09-270-767-50183	Sequence 50183, A
275	5	20.8	157	2	US-09-270-767-55411	Sequence 55411, A	348	5	20.8	205	1	US-08-729-152-8	Sequence 8, Appl
276	5	20.8	157	2	US-09-248-796A-27888	Sequence 27888, A	349	5	20.8	206	2	US-09-134-000C-3622	Sequence 3622, Ap
277	5	20.8	159	2	US-09-248-796A-16325	Sequence 16325, A	350	5	20.8	207	2	US-09-949-016-10814	Sequence 10814, A
278	5	20.8	159	2	US-09-248-796A-27510	Sequence 27510, A	351	5	20.8	208	2	US-08-956-171E-5202	Sequence 5202, Ap
279	5	20.8	160	2	US-09-902-540-13876	Sequence 13876, A	352	5	20.8	208	2	US-09-134-000C-3698	Sequence 3698, Ap
280	5	20.8	161	2	US-09-270-767-34267	Sequence 34267, A	353	5	20.8	208	2	US-08-781-986A-5202	Sequence 5202, Ap
281	5	20.8	161	2	US-09-270-767-43484	Sequence 43484, A	354	5	20.8	208	2	US-09-248-796A-26815	Sequence 26815, A
282	5	20.8	161	2	US-09-248-796A-16597	Sequence 16597, A	355	5	20.8	209	2	US-09-248-796A-24512	Sequence 24512, A
283	5	20.8	162	2	US-09-270-767-39335	Sequence 39335, A	356	5	20.8	209	2	US-09-248-796A-15963	Sequence 15963, A
284	5	20.8	162	2	US-09-270-767-54552	Sequence 54552, A	357	5	20.8	209	2	US-09-248-796A-28163	Sequence 28163, A
285	5	20.8	162	2	US-09-248-796A-28017	Sequence 28017, A	358	5	20.8	209	2	US-09-746-311B-172	Sequence 172, App
286	5	20.8	164	2	US-09-543-681A-8262	Sequence 8262, Ap	359	5	20.8	209	2	US-09-949-016-10830	Sequence 10830, A
287	5	20.8	165	2	US-09-270-767-34694	Sequence 34694, A	360	5	20.8	210	2	US-09-043-785-1	Sequence 1, Appl
288	5	20.8	165	2	US-09-270-767-49911	Sequence 49911, A	361	5	20.8	210	2	US-09-134-001C-3671	Sequence 3671, Ap
289	5	20.8	165	2	US-09-248-796A-16738	Sequence 16738, A	362	5	20.8	212	2	US-09-328-352-7678	Sequence 7678, Ap
290	5	20.8	166	2	US-09-270-767-33721	Sequence 33721, A	363	5	20.8	212	2	US-09-107-433-4196	Sequence 4196, Ap
291	5	20.8	166	2	US-09-270-767-41330	Sequence 41330, A	364	5	20.8	213	2	US-09-248-796A-14823	Sequence 14823, A
292	5	20.8	166	2	US-09-270-767-54938	Sequence 54938, A	365	5	20.8	213	2	US-09-248-796A-22484	Sequence 22484, A
293	5	20.8	166	2	US-09-270-767-55546	Sequence 55546, A	366	5	20.8	214	2	US-09-435-054A-12	Sequence 12, Appl
294	5	20.8	166	2	US-09-248-796A-23059	Sequence 23059, A	367	5	20.8	214	2	US-09-903-540-13849	Sequence 13849, A
295	5	20.8	167	2	US-09-710-279-808	Sequence 808, App	368	5	20.8	215	2	US-09-248-796A-21597	Sequence 21597, A
296	5	20.8	167	2	US-09-710-279-986	Sequence 986, App	369	5	20.8	216	2	US-09-270-767-57457	Sequence 57457, A
297	5	20.8	167	2	US-09-710-279-2128	Sequence 2128, Ap	370	5	20.8	217	2	US-09-270-767-31877	Sequence 31877, A
298	5	20.8	167	2	US-09-902-540-13709	Sequence 13709, A	371	5	20.8	217	2	US-09-270-767-47094	Sequence 47094, A
299	5	20.8	168	2	US-09-149-476-563	Sequence 563, App	372	5	20.8	217	2	US-09-248-796A-14395	Sequence 14395, A
300	5	20.8	170	2	US-09-248-796A-19281	Sequence 19281, A	373	5	20.8	217	2	US-09-248-796A-25844	Sequence 25844, A
301	5	20.8	170	2	US-09-248-796A-27791	Sequence 27791, A	374	5	20.8	218	2	US-09-543-681A-7848	Sequence 7848, Ap
302	5	20.8	171	2	US-09-270-767-33740	Sequence 33740, A	375	5	20.8	218	2	US-09-248-796A-19981	Sequence 19981, A
303	5	20.8	171	2	US-09-270-767-54957	Sequence 54957, A	376	5	20.8	225	1	US-09-248-796A-14183	Sequence 14183, A
304	5	20.8	174	2	US-09-153-586-23	Sequence 23, Appl	377	5	20.8	225	1	US-08-477-451-43	Sequence 43, Appl
305	5	20.8	174	2	US-09-248-796A-15154	Sequence 15154, A	378	5	20.8	226	2	US-09-270-767-44368	Sequence 44368, A
306	5	20.8	174	2	US-09-746-311B-173	Sequence 173, App	379	5	20.8	226	2	US-09-248-796A-20804	Sequence 20804, A
307	5	20.8	174	2	US-09-858-580-23	Sequence 23, Appl	380	5	20.8	226	2	US-09-248-796A-26342	Sequence 26342, A
308	5	20.8	176	2	US-09-248-796A-23424	Sequence 23424, A	381	5	20.8	226	2	US-09-967-869A-15	Sequence 15, Appl
309	5	20.8	179	2	US-09-198-452A-1064	Sequence 1064, Ap	382	5	20.8	228	2	US-09-270-767-46270	Sequence 46270, A
310	5	20.8	179	2	US-09-270-767-45711	Sequence 45711, A	383	5	20.8	228	2	US-09-270-767-47053	Sequence 47053, A
311	5	20.8	179	2	US-09-248-796A-28205	Sequence 28205, A	384	5	20.8	229	2	US-09-248-796A-20026	Sequence 20026, A
312	5	20.8	179	2	US-09-438-185A-990	Sequence 990, App	385	5	20.8	230	2	US-09-333-809-221	Sequence 221, App
313	5	20.8	180	2	US-09-583-110-4398	Sequence 4398, Ap	386	5	20.8	230	2	US-09-333-809-222	Sequence 222, App
314	5	20.8	181	2	US-09-198-452A-16846	Sequence 16846, A	387	5	20.8	230	2	US-09-248-796A-26509	Sequence 26509, A
315	5	20.8	181	2	US-09-270-767-61846	Sequence 61846, A	388	5	20.8	230	2	US-09-746-311B-370	Sequence 370, App
316	5	20.8	185	2	US-09-248-796A-21596	Sequence 21596, A	389	5	20.8	230	2	US-09-746-311B-371	Sequence 371, App
317	5	20.8	185	2	US-09-134-001C-3596	Sequence 3596, Ap	390	5	20.8	230	2	US-09-746-311B-377	Sequence 377, App
318	5	20.8	186	2	US-09-602-787A-2	Sequence 2, Appl	391	5	20.8	230	2	US-09-640-211A-1926	Sequence 1926, Ap
319	5	20.8	188	2	US-09-248-796A-18477	Sequence 18477, A	392	5	20.8	230	2		

393	5	20.8	232	2	US-09-543-681A-5424	Sequence 5424, Ap	466	5	20.8	275	2	US-09-85A-133-584	Sequence 584, App
394	5	20.8	232	2	US-09-248-796A-16788	Sequence 16788, A	467	5	20.8	277	2	US-09-107-532A-7213	Sequence 7213, Ap
395	5	20.8	235	2	US-09-270-767-43381	Sequence 43381, A	468	5	20.8	277	2	US-09-759-143-906	Sequence 906, App
396	5	20.8	234	2	US-09-583-110-3490	Sequence 3490, Ap	469	5	20.8	277	2	US-10-012-896-906	Sequence 906, App
397	5	20.8	235	2	US-09-248-796A-24725	Sequence 24725, A	470	5	20.8	278	2	US-09-270-767-41910	Sequence 41910, A
398	5	20.8	236	2	US-09-248-796A-23590	Sequence 23590, A	471	5	20.8	278	2	US-09-270-767-42034	Sequence 42034, A
399	5	20.8	237	2	US-08-470-535-14	Sequence 14, Appl	472	5	20.8	278	2	US-09-710-279-2700	Sequence 2700, Ap
400	5	20.8	237	2	US-09-333-809-209	Sequence 209, App	473	5	20.8	278	2	US-09-902-540-13159	Sequence 13159, A
401	5	20.8	237	2	US-09-270-767-33181	Sequence 33181, A	474	5	20.8	283	2	US-09-248-796A-15180	Sequence 15180, A
402	5	20.8	237	2	US-09-270-767-53398	Sequence 53398, A	475	5	20.8	284	2	US-09-270-767-36574	Sequence 36574, A
403	5	20.8	237	2	US-09-746-311B-359	Sequence 359, App	476	5	20.8	284	2	US-09-270-767-51791	Sequence 51791, A
404	5	20.8	238	2	US-09-489-039A-12131	Sequence 12131, A	477	5	20.8	288	2	US-09-248-796A-16676	Sequence 16676, A
405	5	20.8	240	2	US-09-270-767-36250	Sequence 36250, A	478	5	20.8	288	2	US-09-248-796A-27671	Sequence 27671, A
406	5	20.8	240	2	US-09-270-767-51467	Sequence 51467, A	479	5	20.8	288	2	US-09-902-540-11785	Sequence 11785, A
407	5	20.8	240	2	US-09-248-796A-23599	Sequence 23599, A	480	5	20.8	289	2	US-09-270-767-44503	Sequence 44503, A
408	5	20.8	241	2	US-09-543-681A-6205	Sequence 6205, Ap	481	5	20.8	290	2	US-09-248-796A-16233	Sequence 16233, A
409	5	20.8	241	2	US-09-489-039A-8983	Sequence 8983, Ap	482	5	20.8	291	2	US-09-248-796A-20963	Sequence 20963, A
410	5	20.8	243	2	US-09-479-645A-56	Sequence 56, Appl	483	5	20.8	292	2	US-09-248-796A-25055	Sequence 25055, A
411	5	20.8	243	2	US-09-479-645A-58	Sequence 58, Appl	484	5	20.8	294	2	US-09-489-039A-8762	Sequence 8762, Ap
412	5	20.8	243	2	US-09-248-796A-15919	Sequence 15919, A	485	5	20.8	295	2	US-09-248-796A-14635	Sequence 14635, A
413	5	20.8	243	2	US-09-900-345A-22	Sequence 22, Appl	486	5	20.8	296	1	US-08-261-662-2	Sequence 2, Appl
414	5	20.8	243	2	US-09-900-345A-24	Sequence 24, Appl	487	5	20.8	296	4	PCT-US95-07752-2	Sequence 2, Appl
415	5	20.8	244	2	US-09-328-352-7894	Sequence 7894, Ap	488	5	20.8	298	2	US-09-248-796A-27737	Sequence 27737, A
416	5	20.8	244	2	US-09-248-796A-18903	Sequence 18903, A	489	5	20.8	299	2	US-09-710-279-1192	Sequence 1192, Ap
417	5	20.8	245	2	US-09-270-767-36519	Sequence 36519, A	490	5	20.8	299	2	US-09-710-279-1768	Sequence 1768, Ap
418	5	20.8	245	2	US-09-270-767-51736	Sequence 51736, A	491	5	20.8	300	2	US-09-248-796A-23225	Sequence 23225, A
419	5	20.8	245	2	US-09-270-767-60752	Sequence 60752, A	492	5	20.8	303	2	US-09-543-681A-6212	Sequence 6212, Ap
420	5	20.8	246	2	US-09-451-117-2	Sequence 2, Appl	493	5	20.8	303	2	US-09-270-767-46272	Sequence 46272, A
421	5	20.8	246	2	US-09-888-655-2	Sequence 2, Appl	494	5	20.8	303	2	US-09-248-796A-19122	Sequence 19122, A
422	5	20.8	246	2	US-09-710-279-900	Sequence 900, App	495	5	20.8	305	2	US-09-248-796A-14506	Sequence 14506, A
423	5	20.8	246	2	US-09-710-279-1956	Sequence 1956, Ap	496	5	20.8	305	2	US-09-248-796A-15533	Sequence 15533, A
424	5	20.8	246	2	US-09-888-501-2	Sequence 2, Appl	497	5	20.8	306	2	US-09-538-092-519	Sequence 519, App
425	5	20.8	248	2	US-09-270-767-42758	Sequence 42758, A	498	5	20.8	307	2	US-09-134-001C-3792	Sequence 3792, Ap
426	5	20.8	248	2	US-09-270-767-44243	Sequence 44243, A	499	5	20.8	307	2	US-09-583-110-3427	Sequence 3427, Ap
427	5	20.8	249	2	US-09-248-796A-15815	Sequence 15815, A	500	5	20.8	308	2	US-08-508-761B-35	Sequence 35, Appl
428	5	20.8	251	2	US-09-248-796A-17563	Sequence 17563, A	501	5	20.8	308	2	US-09-252-991A-31991	Sequence 31991, A
429	5	20.8	252	2	US-09-270-767-33633	Sequence 33633, A	502	5	20.8	308	2	US-09-248-796A-21293	Sequence 21293, A
430	5	20.8	252	2	US-09-270-767-48850	Sequence 48850, A	503	5	20.8	309	2	US-09-248-796A-20432	Sequence 20432, A
431	5	20.8	252	2	US-09-248-796A-18139	Sequence 18139, A	504	5	20.8	309	2	US-09-248-796A-25339	Sequence 25339, A
432	5	20.8	252	2	US-09-248-796A-26644	Sequence 26644, A	505	5	20.8	310	2	US-09-538-092-309	Sequence 309, App
433	5	20.8	253	2	US-09-270-767-47163	Sequence 47163, A	506	5	20.8	311	2	US-09-248-796A-25849	Sequence 25849, A
434	5	20.8	254	1	US-08-207-481-20	Sequence 20, Appl	507	5	20.8	312	2	US-09-248-796A-19593	Sequence 19593, A
435	5	20.8	254	4	PCT-US95-02689-20	Sequence 20, Appl	508	5	20.8	313	2	US-09-107-433-5045	Sequence 5045, Ap
436	5	20.8	255	2	US-09-248-796A-18387	Sequence 18387, A	509	5	20.8	315	2	US-09-313-942-16	Sequence 16, Appl
437	5	20.8	255	2	US-09-640-211A-2261	Sequence 2261, Ap	510	5	20.8	315	2	US-09-248-796A-17439	Sequence 17439, A
438	5	20.8	258	2	US-09-270-767-34189	Sequence 34189, A	511	5	20.8	315	2	US-10-282-162-16	Sequence 16, Appl
439	5	20.8	258	2	US-09-270-767-49406	Sequence 49406, A	512	5	20.8	316	2	US-09-248-796A-18293	Sequence 18293, A
440	5	20.8	258	2	US-09-248-796A-20326	Sequence 20326, A	513	5	20.8	316	2	US-09-248-796A-20499	Sequence 20499, A
441	5	20.8	260	2	US-09-489-039A-7490	Sequence 7490, Ap	514	5	20.8	320	2	US-09-248-796A-22140	Sequence 22140, A
442	5	20.8	260	2	US-09-248-796A-24025	Sequence 24025, A	515	5	20.8	321	2	US-09-582-660-5	Sequence 5, Appl
443	5	20.8	261	2	US-09-248-796A-19121	Sequence 19121, A	516	5	20.8	323	6	5171840-6	Patent No. 5171840
444	5	20.8	262	2	US-09-248-796A-25774	Sequence 25774, A	517	5	20.8	323	6	5480796-6	Patent No. 5480796
445	5	20.8	263	2	US-09-543-681A-7789	Sequence 7789, Ap	518	5	20.8	324	2	US-09-248-796A-21777	Sequence 21777, A
446	5	20.8	263	2	US-09-248-796A-14154	Sequence 14154, A	519	5	20.8	325	2	US-09-711-164-358	Sequence 358, App
447	5	20.8	263	2	US-09-248-796A-15305	Sequence 15305, A	520	5	20.8	325	2	US-09-270-767-41440	Sequence 41440, A
448	5	20.8	263	2	US-09-248-796A-19569	Sequence 19569, A	521	5	20.8	325	2	US-09-248-796A-19440	Sequence 19440, A
449	5	20.8	264	1	US-08-484-905-120	Sequence 120, App	522	5	20.8	326	1	US-08-997-080-43	Sequence 43, Appl
450	5	20.8	264	2	US-08-481-985B-120	Sequence 120, App	523	5	20.8	326	1	US-08-997-362-43	Sequence 43, Appl
451	5	20.8	264	2	US-08-370-476-120	Sequence 120, App	524	5	20.8	326	2	US-08-873-970-43	Sequence 43, Appl
452	5	20.8	266	2	US-09-144-776B-14	Sequence 14, Appl	525	5	20.8	326	2	US-09-095-855-43	Sequence 43, Appl
453	5	20.8	266	2	US-08-882-431B-14	Sequence 14, Appl	526	5	20.8	326	2	US-08-705-347A-43	Sequence 43, Appl
454	5	20.8	266	2	US-09-746-311B-165	Sequence 165, App	527	5	20.8	326	2	US-09-324-542-43	Sequence 43, Appl
455	5	20.8	266	2	US-09-746-311B-166	Sequence 166, App	528	5	20.8	326	2	US-09-205-426-43	Sequence 43, Appl
456	5	20.8	266	2	US-09-746-311B-295	Sequence 295, App	529	5	20.8	326	2	US-09-200-643-43	Sequence 43, Appl
457	5	20.8	266	2	US-09-746-311B-296	Sequence 296, App	530	5	20.8	326	2	US-10-194-125-4	Sequence 4, Appl
458	5	20.8	266	2	US-09-746-311B-334	Sequence 334, App	531	5	20.8	328	2	US-09-300-672-2	Sequence 2, Appl
459	5	20.8	269	2	US-09-270-767-44704	Sequence 44704, A	532	5	20.8	329	2	US-09-489-039A-14082	Sequence 14082, A
460	5	20.8	269	2	US-09-248-796A-22276	Sequence 22276, A	533	5	20.8	331	2	US-09-248-796A-18701	Sequence 18701, A
461	5	20.8	271	2	US-09-543-681A-6644	Sequence 6644, Ap	534	5	20.8	332	1	US-08-118-270-53	Sequence 53, Appl
462	5	20.8	273	2	US-09-270-767-42116	Sequence 42116, A	535	5	20.8	332	2	US-09-248-796A-15783	Sequence 15783, A
463	5	20.8	274	2	US-09-270-767-62098	Sequence 62098, A	536	5	20.8	332	2	US-09-248-796A-20189	Sequence 20189, A
464	5	20.8	274	2	US-09-248-796A-17624	Sequence 17624, A	537	5	20.8	332	4	PCT-US93-08528-53	Sequence 53, Appl
465	5	20.8	275	2	US-09-248-796A-27507	Sequence 27507, A	538	5	20.8	335	2	US-09-252-991A-31961	Sequence 31961, A

539	5	20.8	335	2	US-09-248-796A-14317	Sequence 14317, A	612	5	20.8	384	2	US-09-045-583-2	Sequence 2, Appli
540	5	20.8	336	2	US-09-248-796A-17941	Sequence 17941, A	613	5	20.8	384	2	US-09-534-185-2	Sequence 2, Appli
541	5	20.8	337	2	US-09-841-786-7	Sequence 7, Appli	614	5	20.8	384	2	US-09-270-767-47918	Sequence 47918, A
542	5	20.8	338	2	US-09-543-681A-6965	Sequence 6965, Ap	615	5	20.8	384	2	US-09-248-796A-20580	Sequence 20580, A
543	5	20.8	339	2	US-09-270-767-60870	Sequence 60870, A	616	5	20.8	386	6	517840-5	Patent No. 5480796
544	5	20.8	339	2	US-09-248-796A-15032	Sequence 15032, A	617	5	20.8	386	6	5480796-5	Patent No. 5480796
545	5	20.8	339	2	US-09-248-796A-16100	Sequence 16100, A	618	5	20.8	389	2	US-09-270-767-44335	Sequence 44335, A
546	5	20.8	339	2	US-09-248-796A-20595	Sequence 20595, A	619	5	20.8	389	2	US-09-248-796A-15248	Sequence 15248, A
547	5	20.8	339	2	US-09-967-869A-14	Sequence 14, Appli	620	5	20.8	389	2	US-09-198-452A-505	Sequence 505, App
548	5	20.8	340	1	US-08-107-676-3	Sequence 3, Appli	621	5	20.8	392	2	US-09-248-796A-21883	Sequence 21883, A
549	5	20.8	340	1	US-08-107-676-31	Sequence 31, Appli	622	5	20.8	392	2	US-09-438-185A-472	Sequence 472, App
550	5	20.8	340	1	US-08-997-080-37	Sequence 37, Appli	623	5	20.8	393	2	US-09-248-796A-18493	Sequence 18493, A
551	5	20.8	340	1	US-08-997-362-37	Sequence 37, Appli	624	5	20.8	393	2	US-09-248-796A-26699	Sequence 26699, A
552	5	20.8	340	2	US-08-873-970-37	Sequence 37, Appli	625	5	20.8	394	2	US-09-248-796A-19661	Sequence 19661, A
553	5	20.8	340	2	US-09-095-855-37	Sequence 37, Appli	626	5	20.8	395	2	US-09-270-767-46098	Sequence 46098, A
554	5	20.8	340	2	US-08-705-347A-37	Sequence 37, Appli	627	5	20.8	395	2	US-09-538-092-857	Sequence 857, App
555	5	20.8	340	2	US-09-324-542-37	Sequence 37, Appli	628	5	20.8	396	1	US-07-841-646-5	Sequence 5, Appli
556	5	20.8	340	2	US-09-205-426-37	Sequence 37, Appli	629	5	20.8	396	1	US-07-901-703-15	Sequence 15, Appli
557	5	20.8	340	2	US-09-200-643-37	Sequence 37, Appli	630	5	20.8	396	1	US-08-147-023-5	Sequence 5, Appli
558	5	20.8	340	2	US-09-107-532A-3720	Sequence 3720, Ap	631	5	20.8	396	1	US-08-447-570-5	Sequence 5, Appli
559	5	20.8	340	2	US-09-295-820-3	Sequence 3, Appli	632	5	20.8	396	1	US-08-459-346-10	Sequence 10, Appli
560	5	20.8	340	2	US-09-295-820-31	Sequence 31, Appli	633	5	20.8	396	1	US-08-449-700-5	Sequence 5, Appli
561	5	20.8	341	2	US-09-248-796A-26889	Sequence 26889, A	634	5	20.8	396	1	US-07-989-847-2	Sequence 5, Appli
562	5	20.8	344	6	517840-7	Patent No. 517840	635	5	20.8	396	1	US-08-449-699A-5	Sequence 5, Appli
563	5	20.8	344	6	5480796-7	Patent No. 5480796	636	5	20.8	396	1	US-08-889-419-10	Sequence 10, Appli
564	5	20.8	349	2	US-09-248-796A-14572	Sequence 14572, A	637	5	20.8	396	2	US-07-721-847A-4	Sequence 4, Appli
565	5	20.8	349	2	US-09-248-796A-17015	Sequence 17015, A	638	5	20.8	396	2	US-08-469-411-2	Sequence 2, Appli
566	5	20.8	351	2	US-09-248-796A-25420	Sequence 25420, A	639	5	20.8	396	2	US-08-925-779-4	Sequence 4, Appli
567	5	20.8	354	2	US-09-574-942-2	Sequence 2, Appli	640	5	20.8	396	2	US-08-402-542-10	Sequence 10, Appli
568	5	20.8	354	2	US-09-807-784B-1	Sequence 1, Appli	641	5	20.8	396	2	US-09-148-925C-5	Sequence 5, Appli
569	5	20.8	354	2	US-09-248-796A-16881	Sequence 16881, A	642	5	20.8	396	2	US-08-957-425-5	Sequence 5, Appli
570	5	20.8	354	2	US-09-949-434-2	Sequence 2, Appli	643	5	20.8	396	2	US-09-780-601A-2	Sequence 2, Appli
571	5	20.8	354	2	US-10-194-125-2	Sequence 2, Appli	644	5	20.8	396	2	US-09-661-887-2	Sequence 2, Appli
572	5	20.8	355	2	US-09-270-767-45275	Sequence 45275, A	645	5	20.8	396	2	US-09-248-796A-18742	Sequence 18742, A
573	5	20.8	355	2	US-09-248-796A-18861	Sequence 18861, A	646	5	20.8	396	2	US-10-321-799-5	Sequence 5, Appli
574	5	20.8	355	2	US-09-248-796A-20938	Sequence 20938, A	647	5	20.8	396	4	PCT-US91-03540A-8	Sequence 8, Appli
575	5	20.8	359	2	US-09-248-796A-15017	Sequence 15017, A	648	5	20.8	396	4	PCT-US93-05446-15	Sequence 15, Appli
576	5	20.8	360	2	US-09-313-942-15	Sequence 15, Appli	649	5	20.8	396	4	PCT-US93-07189-10	Sequence 10, Appli
577	5	20.8	360	2	US-09-248-796A-27270	Sequence 27270, A	650	5	20.8	396	6	5166058-4	Patent No. 5166058
578	5	20.8	360	2	US-10-282-162-15	Sequence 15, Appli	651	5	20.8	399	2	US-09-949-016-10539	Sequence 10539, A
579	5	20.8	361	1	US-08-415-751-3	Sequence 3, Appli	652	5	20.8	400	4	PCT-US91-03540A-10	Sequence 10, Appli
580	5	20.8	361	2	US-09-362-842-14	Sequence 14, Appli	653	5	20.8	400	6	5168050-5	Patent No. 5168050
581	5	20.8	361	2	US-09-404-296B-30	Sequence 30, Appli	654	5	20.8	401	2	US-09-631-863A-2	Sequence 2, Appli
582	5	20.8	361	2	US-09-248-796A-20099	Sequence 20099, A	655	5	20.8	402	2	US-09-248-796A-18910	Sequence 18910, A
583	5	20.8	362	2	US-09-270-767-58295	Sequence 58295, A	656	5	20.8	403	2	US-09-248-796A-14239	Sequence 14239, A
584	5	20.8	362	2	US-09-248-796A-14994	Sequence 14994, A	657	5	20.8	403	2	US-09-248-796A-20479	Sequence 20479, A
585	5	20.8	362	2	US-09-949-016-8242	Sequence 8242, Ap	658	5	20.8	405	1	US-08-283-197C-61	Sequence 61, Appli
586	5	20.8	362	2	US-09-270-767-45770	Sequence 45770, A	659	5	20.8	406	1	US-07-973-431B-1	Sequence 1, Appli
587	5	20.8	364	2	US-09-051-755-14	Sequence 14, Appli	660	5	20.8	409	2	US-09-270-767-44594	Sequence 44594, A
588	5	20.8	364	2	US-09-270-767-59756	Sequence 59756, A	661	5	20.8	409	2	US-09-248-796A-16363	Sequence 16363, A
589	5	20.8	369	2	US-09-487-558B-468	Sequence 268, App	662	5	20.8	409	2	US-09-248-796A-23321	Sequence 23321, A
590	5	20.8	370	2	US-09-108-020-39	Sequence 39, Appli	663	5	20.8	411	1	US-08-362-670B-28	Sequence 28, Appli
591	5	20.8	370	2	US-09-248-796A-21722	Sequence 21722, A	664	5	20.8	411	1	US-08-333-576C-28	Sequence 28, Appli
592	5	20.8	370	2	US-09-685-296-39	Sequence 39, Appli	665	5	20.8	411	2	US-08-808-324-28	Sequence 28, Appli
593	5	20.8	371	2	US-09-574-141A-56	Sequence 56, Appli	666	5	20.8	411	2	US-09-948-182-28	Sequence 28, Appli
594	5	20.8	371	2	US-09-568-189A-56	Sequence 56, Appli	667	5	20.8	411	2	US-09-248-796A-18500	Sequence 18500, A
595	5	20.8	371	6	5168050-3	Patent No. 5168050	668	5	20.8	411	2	PCT-US94-14030A-28	Sequence 28, Appli
596	5	20.8	372	2	US-09-270-767-46033	Sequence 46033, A	669	5	20.8	412	4	US-09-248-796A-16539	Sequence 16539, A
597	5	20.8	372	2	US-09-538-092-1035	Sequence 1035, Ap	670	5	20.8	413	2	US-08-942-572-2	Sequence 2, Appli
598	5	20.8	372	2	US-09-543-681A-5137	Sequence 5137, Ap	671	5	20.8	413	2	US-09-614-069-13	Sequence 13, Appli
599	5	20.8	373	2	US-09-248-796A-14832	Sequence 14832, A	672	5	20.8	413	2	US-09-821-803A-7	Sequence 7, Appli
600	5	20.8	373	2	US-09-538-092-683	Sequence 683, App	673	5	20.8	413	2	US-09-821-803A-8	Sequence 8, Appli
601	5	20.8	374	2	US-09-270-767-43192	Sequence 43192, A	674	5	20.8	413	2	US-09-248-796A-15624	Sequence 15624, A
602	5	20.8	374	2	US-09-248-796A-16020	Sequence 16020, A	675	5	20.8	413	2	US-09-248-796A-24537	Sequence 24537, A
603	5	20.8	374	2	US-09-248-796A-21934	Sequence 21934, A	676	5	20.8	413	2	US-09-248-796A-20956	Sequence 20956, A
604	5	20.8	375	2	US-09-273-164-34	Sequence 34, Appli	677	5	20.8	414	2	US-09-248-796A-16399	Sequence 16399, A
605	5	20.8	376	2	US-09-248-796A-14749	Sequence 14749, A	678	5	20.8	415	2	US-09-248-796A-16399	Sequence 16399, A
606	5	20.8	376	2	US-09-248-796A-21995	Sequence 21995, A	679	5	20.8	418	2	US-09-248-796A-20578	Sequence 20578, A
607	5	20.8	378	2	US-09-902-540-15795	Sequence 15795, A	680	5	20.8	419	2	US-09-248-796A-21670	Sequence 21670, A
608	5	20.8	378	2	US-09-543-681A-7089	Sequence 7089, Ap	681	5	20.8	419	2	US-09-248-796A-23289	Sequence 23289, A
609	5	20.8	379	2	US-09-270-767-46415	Sequence 46415, A	682	5	20.8	421	2	US-09-198-452A-535	Sequence 535, App
610	5	20.8	380	2			683	5	20.8	422	2	US-09-248-796A-14141	Sequence 14141, A
611	5	20.8					684	5	20.8				

685	5	20.8	422	2	US-09-248-796A-23455	Sequence 23455, A	758	5	20.8	497	2	US-09-248-796A-16678	Sequence 16678, A
686	5	20.8	427	2	US-09-543-681A-8095	Sequence 8095, Ap	759	5	20.8	498	2	US-09-252-991A-29345	Sequence 29345, A
687	5	20.8	428	1	US-08-190-802A-29	Sequence 29, Appl	760	5	20.8	499	2	US-09-993-777-8	Sequence 8, Appl
688	5	20.8	428	2	US-08-477-346-29	Sequence 29, Appl	761	5	20.8	499	2	US-09-993-777-69	Sequence 69, Appl
689	5	20.8	428	2	US-08-473-089-29	Sequence 29, Appl	762	5	20.8	499	4	PCT-US96-03916-8	Sequence 8, Appl
690	5	20.8	428	2	US-08-487-072A-29	Sequence 29, Appl	763	5	20.8	499	4	PCT-US96-03916-69	Sequence 69, Appl
691	5	20.8	429	2	US-09-438-185A-497	Sequence 497, App	764	5	20.8	508	1	US-07-891-942G-10	Sequence 10, Appl
692	5	20.8	431	2	US-09-107-532A-7056	Sequence 7056, Ap	765	5	20.8	508	2	US-09-248-796A-20809	Sequence 20809, A
693	5	20.8	431	2	US-09-489-039A-12670	Sequence 12670, A	766	5	20.8	508	2	US-09-639-207-1	Sequence 1, Appl
694	5	20.8	432	2	US-09-118-319-2	Sequence 2, Appl	767	5	20.8	509	2	US-09-252-991A-22513	Sequence 22513, A
695	5	20.8	433	2	US-09-710-279-1332	Sequence 1332, Ap	768	5	20.8	510	2	US-09-270-767-43633	Sequence 43633, A
696	5	20.8	434	2	US-09-248-796A-16502	Sequence 16502, A	769	5	20.8	510	2	US-09-270-767-44374	Sequence 44374, A
697	5	20.8	435	2	US-09-248-796A-15070	Sequence 15070, A	770	5	20.8	510	2	US-09-248-796A-18513	Sequence 18513, A
698	5	20.8	437	2	US-08-713-556F-40	Sequence 40, Appl	771	5	20.8	512	2	US-09-142-108C-6	Sequence 6, Appl
699	5	20.8	437	2	US-09-134-001C-3418	Sequence 3418, Ap	772	5	20.8	513	1	US-08-464-266-2	Sequence 2, Appl
700	5	20.8	440	2	US-10-104-047-3856	Sequence 3856, Ap	773	5	20.8	513	1	US-08-464-272-2	Sequence 2, Appl
701	5	20.8	442	2	US-09-248-796A-17027	Sequence 17027, A	774	5	20.8	513	2	US-08-464-514-2	Sequence 2, Appl
702	5	20.8	444	1	US-07-881-075-3	Sequence 3, Appl	775	5	20.8	513	2	US-08-486-403-2	Sequence 2, Appl
703	5	20.8	444	1	US-08-120-827-3	Sequence 3, Appl	776	5	20.8	513	2	US-09-248-796A-25078	Sequence 25078, A
704	5	20.8	444	1	US-08-478-675-3	Sequence 3, Appl	777	5	20.8	514	2	US-09-679-686B-22	Sequence 22, Appl
705	5	20.8	445	2	US-09-270-767-46024	Sequence 46024, A	778	5	20.8	515	2	US-09-270-767-45839	Sequence 45839, A
706	5	20.8	445	2	US-09-248-796A-15251	Sequence 15251, A	779	5	20.8	517	2	US-09-248-796A-20437	Sequence 20437, A
707	5	20.8	448	1	US-08-231-342-23	Sequence 23, Appl	780	5	20.8	518	2	US-09-881-578A-4	Sequence 4, Appl
708	5	20.8	448	2	US-09-270-767-32701	Sequence 32701, A	781	5	20.8	518	2	US-09-424-978B-24	Sequence 24, Appl
709	5	20.8	448	2	US-09-639-576-8	Sequence 8, Appl	782	5	20.8	518	2	US-09-976-594-287	Sequence 287, App
710	5	20.8	450	2	US-09-248-796A-15183	Sequence 15183, A	783	5	20.8	518	2	US-09-919-039-143	Sequence 143, App
711	5	20.8	451	2	US-09-248-796A-15356	Sequence 15356, A	784	5	20.8	518	2	US-09-248-796A-19845	Sequence 19845, A
712	5	20.8	454	2	US-09-717-364A-23	Sequence 23, Appl	785	5	20.8	519	2	US-09-248-796A-14534	Sequence 14534, A
713	5	20.8	454	2	US-09-270-767-45646	Sequence 45646, A	786	5	20.8	523	2	US-09-910-174B-11	Sequence 11, Appl
714	5	20.8	460	2	US-09-270-767-60881	Sequence 60881, A	787	5	20.8	523	2	US-09-620-461-11	Sequence 11, Appl
715	5	20.8	461	2	US-09-248-796A-23597	Sequence 23597, A	788	5	20.8	524	2	US-09-248-796A-20256	Sequence 20256, A
716	5	20.8	463	2	US-09-082-310-1	Sequence 1, Appl	789	5	20.8	525	2	US-09-976-594-64	Sequence 64, Appl
717	5	20.8	463	2	US-09-575-205-1	Sequence 1, Appl	790	5	20.8	525	2	US-09-919-039-62	Sequence 62, Appl
718	5	20.8	463	2	US-09-976-594-721	Sequence 721, App	791	5	20.8	525	2	US-09-248-796A-15927	Sequence 15927, A
719	5	20.8	464	2	US-09-426-072-2	Sequence 2, Appl	792	5	20.8	527	2	US-09-910-174B-10	Sequence 10, Appl
720	5	20.8	468	2	US-08-795-473B-5	Sequence 5, Appl	793	5	20.8	527	2	US-09-620-461-10	Sequence 10, Appl
721	5	20.8	468	2	US-09-439-856-5	Sequence 5, Appl	794	5	20.8	529	1	US-07-891-942G-8	Sequence 8, Appl
722	5	20.8	468	2	US-09-949-016-5959	Sequence 5959, Ap	795	5	20.8	529	1	US-08-370-909-19	Sequence 19, Appl
723	5	20.8	468	6	5171840-2	Sequence 5171840	796	5	20.8	529	1	US-08-504-048-8	Sequence 8, Appl
724	5	20.8	468	6	5480796-2	Patent No. 5480796	797	5	20.8	529	1	US-09-341-982-1	Sequence 1, Appl
725	5	20.8	470	2	US-09-583-110-4689	Sequence 4689, Ap	798	5	20.8	529	2	US-09-910-174B-13	Sequence 13, Appl
726	5	20.8	472	2	US-09-004-838-40	Sequence 40, Appl	799	5	20.8	529	2	US-09-620-461-13	Sequence 13, Appl
727	5	20.8	472	2	US-09-004-838-48	Sequence 48, Appl	800	5	20.8	529	2	US-09-620-461-39	Sequence 39, Appl
728	5	20.8	472	2	US-09-004-838-103	Sequence 103, App	801	5	20.8	529	2	US-09-169-717E-39	Sequence 39, Appl
729	5	20.8	472	2	US-09-538-092-312	Sequence 312, App	802	5	20.8	529	2	US-10-011-436-4	Sequence 4, Appl
730	5	20.8	473	2	US-09-107-433-4669	Sequence 4669, Ap	803	5	20.8	532	2	US-08-533-895A-39	Sequence 39, Appl
731	5	20.8	475	2	US-09-248-796A-17531	Sequence 17531, A	804	5	20.8	533	2	US-09-826-509-521	Sequence 521, App
732	5	20.8	478	2	US-09-004-838-105	Sequence 105, App	805	5	20.8	535	2	US-09-487-558B-162	Sequence 162, App
733	5	20.8	479	2	US-09-004-838-50	Sequence 50, Appl	806	5	20.8	535	2	US-09-269-731-4	Sequence 4, Appl
734	5	20.8	479	2	US-09-248-796A-15907	Sequence 15907, A	807	5	20.8	537	2	US-09-988-200-4	Sequence 4, Appl
735	5	20.8	479	2	US-09-248-796A-17560	Sequence 17560, A	808	5	20.8	537	2	US-09-110-959A-4	Sequence 4, Appl
736	5	20.8	479	2	US-09-248-796A-20464	Sequence 20464, A	809	5	20.8	537	2	US-08-540-922D-12	Sequence 12, Appl
737	5	20.8	480	2	US-09-004-838-49	Sequence 49, Appl	810	5	20.8	539	2	US-09-198-452A-246	Sequence 246, App
738	5	20.8	480	2	US-09-328-352-7877	Sequence 7877, Ap	811	5	20.8	540	2	US-09-248-796A-16542	Sequence 16542, A
739	5	20.8	480	2	US-09-489-039A-13045	Sequence 13045, A	812	5	20.8	541	2	US-09-248-796A-16674	Sequence 16674, A
740	5	20.8	480	2	US-09-270-767-60465	Sequence 60465, A	813	5	20.8	541	2	US-09-248-796A-18318	Sequence 18318, A
741	5	20.8	480	2	US-09-248-796A-20136	Sequence 20136, A	814	5	20.8	542	2	US-09-248-796A-25057	Sequence 25057, A
742	5	20.8	480	2	US-09-248-796A-23564	Sequence 23564, A	815	5	20.8	543	2	US-09-583-110-4474	Sequence 4474, Ap
743	5	20.8	483	2	US-09-693-746-20	Sequence 20, Appl	816	5	20.8	543	2	US-09-248-796A-22504	Sequence 22504, A
744	5	20.8	484	2	US-09-328-352-7797	Sequence 7797, Ap	817	5	20.8	546	2	US-09-438-185A-238	Sequence 238, App
745	5	20.8	485	2	US-09-004-838-131	Sequence 131, App	818	5	20.8	546	2	US-09-809-665A-26	Sequence 26, Appl
746	5	20.8	486	2	US-09-270-767-45178	Sequence 45178, A	819	5	20.8	546	2	US-09-107-433-3368	Sequence 3368, Ap
747	5	20.8	486	2	US-09-248-796A-20515	Sequence 20515, A	820	5	20.8	548	2	US-09-601-091-2	Sequence 2, Appl
748	5	20.8	487	2	US-09-004-838-101	Sequence 101, App	821	5	20.8	548	2	US-09-398-395A-52	Sequence 52, Appl
749	5	20.8	487	2	US-09-248-796A-20378	Sequence 20378, A	822	5	20.8	548	2	US-09-887-586A-52	Sequence 52, Appl
750	5	20.8	488	2	US-09-004-838-47	Sequence 47, Appl	823	5	20.8	548	2	US-09-895-752-52	Sequence 52, Appl
751	5	20.8	488	2	US-09-248-796A-15985	Sequence 15985, A	824	5	20.8	548	2	US-09-903-012B-52	Sequence 52, Appl
752	5	20.8	489	2	US-09-631-594-74	Sequence 74, Appl	825	5	20.8	548	2	US-09-900-797-52	Sequence 52, Appl
753	5	20.8	489	2	US-09-248-796A-25826	Sequence 25826, A	826	5	20.8	548	2	US-09-248-796A-18235	Sequence 18235, A
754	5	20.8	491	2	US-09-248-796A-15789	Sequence 15789, A	827	5	20.8	548	2	US-09-893-820-52	Sequence 52, Appl
755	5	20.8	493	2	US-09-538-092-1147	Sequence 1147, Ap	828	5	20.8	550	2	US-09-248-796A-14439	Sequence 14439, A
756	5	20.8	493	2	US-09-949-016-5979	Sequence 5979, Ap	829	5	20.8	553	2	US-09-949-016-7505	Sequence 7505, Ap
757	5	20.8	495	2	US-09-248-796A-21845	Sequence 21845, A	830	5	20.8	555	2	US-09-252-991A-20604	Sequence 20604, A

831	5	20.8	555	2	US-09-248-796A-19331	Sequence 19331, A	904	5	20.8	667	2	US-09-248-796A-22880	Sequence 22880, A
832	5	20.8	560	1	US-07-891-9420-5	Sequence 56, Appl	905	5	20.8	668	1	US-08-468-036-5	Sequence 5, Appl
833	5	20.8	560	2	US-09-734-237B-66	Sequence 66, Appl	906	5	20.8	668	1	US-08-376-843-5	Sequence 5, Appl
834	5	20.8	561	2	US-09-734-237B-68	Sequence 68, Appl	907	5	20.8	668	2	US-09-538-092-19	Sequence 19, Appl
835	5	20.8	562	2	US-09-393-627B-2	Sequence 2, Appl	908	5	20.8	670	2	US-09-328-352-6725	Sequence 6725, Ap
836	5	20.8	568	2	US-09-248-796A-19556	Sequence 19556, A	909	5	20.8	672	2	US-09-487-558B-200	Sequence 200, App
837	5	20.8	570	2	US-09-248-796A-19123	Sequence 19123, A	910	5	20.8	674	2	US-07-757-342D-10	Sequence 10, Appl
838	5	20.8	570	2	US-09-538-092-133	Sequence 133, App	911	5	20.8	674	2	US-08-653-648A-14	Sequence 14, Appl
839	5	20.8	572	2	US-09-248-796A-15736	Sequence 15736, A	912	5	20.8	674	2	US-09-461-657B-10	Sequence 10, Appl
840	5	20.8	574	2	US-09-248-796A-16849	Sequence 16849, A	913	5	20.8	675	2	US-09-564-418-12	Sequence 12, Appl
841	5	20.8	575	2	US-09-248-796A-17643	Sequence 17643, A	914	5	20.8	677	2	US-09-540-236-3700	Sequence 3700, Ap
842	5	20.8	581	1	US-08-724-394A-2	Sequence 2, Appl	915	5	20.8	679	2	US-09-248-796A-25953	Sequence 25953, A
843	5	20.8	581	1	US-08-724-394A-3	Sequence 3, Appl	916	5	20.8	680	2	US-09-489-039A-8422	Sequence 8422, Ap
844	5	20.8	581	2	US-09-248-796A-22499	Sequence 22499, A	917	5	20.8	685	2	US-09-720-317A-31	Sequence 31, Appl
845	5	20.8	583	2	US-08-481-190-19	Sequence 19, Appl	918	5	20.8	685	2	US-10-262-083-22	Sequence 22, Appl
846	5	20.8	583	4	PCT-US93-00869-19	Sequence 19, Appl	919	5	20.8	688	2	US-10-262-083-25	Sequence 25, Appl
847	5	20.8	587	2	US-09-248-796A-16260	Sequence 16260, A	920	5	20.8	688	2	US-09-248-796A-15264	Sequence 15264, A
848	5	20.8	588	2	US-08-481-190-16	Sequence 16, Appl	921	5	20.8	689	2	US-08-235-836C-68	Sequence 68, Appl
849	5	20.8	588	2	US-09-248-796A-20839	Sequence 20839, A	922	5	20.8	696	2	US-09-248-796A-14133	Sequence 14133, A
850	5	20.8	588	4	PCT-US93-00869-16	Sequence 16, Appl	923	5	20.8	697	2	US-09-248-796A-15295	Sequence 15295, A
851	5	20.8	589	2	US-09-270-767-45378	Sequence 45378, A	924	5	20.8	698	2	US-09-248-796A-19233	Sequence 19233, A
852	5	20.8	589	2	US-09-809-665A-18	Sequence 18, Appl	925	5	20.8	699	2	US-07-757-342D-2	Sequence 2, Appl
853	5	20.8	590	2	US-09-248-796A-18826	Sequence 18826, A	926	5	20.8	699	2	US-09-461-657B-2	Sequence 2, Appl
854	5	20.8	590	2	US-09-248-796A-20379	Sequence 20379, A	927	5	20.8	700	2	US-07-757-342D-3	Sequence 3, Appl
855	5	20.8	591	2	US-08-565-903B-2	Sequence 2, Appl	928	5	20.8	700	2	US-07-461-657B-3	Sequence 3, Appl
856	5	20.8	592	2	US-09-313-942-8	Sequence 8, Appl	929	5	20.8	701	2	US-09-248-796A-16628	Sequence 16628, A
857	5	20.8	592	2	US-10-282-162-8	Sequence 8, Appl	930	5	20.8	702	2	US-10-197-220-170	Sequence 170, App
858	5	20.8	593	2	US-09-248-796A-19340	Sequence 8, Appl	931	5	20.8	703	2	US-09-543-681A-7429	Sequence 7429, Ap
859	5	20.8	598	2	US-09-248-796A-16395	Sequence 16395, A	932	5	20.8	704	2	US-09-252-991A-30631	Sequence 30631, A
860	5	20.8	600	2	US-09-248-796A-23971	Sequence 23971, A	933	5	20.8	705	2	US-09-248-796A-20201	Sequence 20201, A
861	5	20.8	602	2	US-09-248-796A-19204	Sequence 19204, A	934	5	20.8	710	2	US-09-487-558B-276	Sequence 276, App
862	5	20.8	604	2	US-09-270-767-42188	Sequence 42188, A	935	5	20.8	713	2	US-09-489-039A-9317	Sequence 9317, Ap
863	5	20.8	605	2	US-09-252-991A-32874	Sequence 32874, A	936	5	20.8	715	2	US-09-620-412C-321	Sequence 321, App
864	5	20.8	605	2	US-09-640-419C-22	Sequence 22, Appl	937	5	20.8	715	2	US-09-598-419-321	Sequence 321, App
865	5	20.8	606	1	US-08-392-808A-6	Sequence 6, Appl	938	5	20.8	716	2	US-09-107-532A-5208	Sequence 5208, Ap
866	5	20.8	606	2	US-09-257-490-6	Sequence 6, Appl	939	5	20.8	718	1	US-08-560-398-12	Sequence 12, Appl
867	5	20.8	607	2	US-09-204-208A-11	Sequence 11, Appl	940	5	20.8	729	2	US-09-270-767-57903	Sequence 57903, A
868	5	20.8	607	2	US-10-072-436-11	Sequence 11, Appl	941	5	20.8	733	2	US-09-270-767-41626	Sequence 41626, A
869	5	20.8	609	2	US-09-311-021-196	Sequence 196, App	942	5	20.8	734	2	US-09-248-796A-18305	Sequence 18305, A
870	5	20.8	610	2	US-09-248-796A-18471	Sequence 18471, A	943	5	20.8	739	2	US-09-328-352-6048	Sequence 6048, Ap
871	5	20.8	611	2	US-07-757-342D-8	Sequence 8, Appl	944	5	20.8	742	1	US-07-921-807B-2	Sequence 2, Appl
872	5	20.8	611	2	US-09-461-657B-8	Sequence 8, Appl	945	5	20.8	742	1	US-08-441-944A-2	Sequence 2, Appl
873	5	20.8	613	2	US-09-270-767-62323	Sequence 62323, A	946	5	20.8	746	2	US-09-248-796A-19979	Sequence 19979, A
874	5	20.8	613	2	US-09-248-796A-14110	Sequence 14110, A	947	5	20.8	747	2	US-08-089-397A-16	Sequence 16, Appl
875	5	20.8	617	2	US-09-248-796A-26692	Sequence 26692, A	948	5	20.8	752	2	US-08-943-667-29	Sequence 29, Appl
876	5	20.8	622	2	US-09-270-767-42577	Sequence 42577, A	949	5	20.8	753	2	US-09-543-681A-5022	Sequence 5022, Ap
877	5	20.8	629	2	US-09-853-180B-2	Sequence 2, Appl	950	5	20.8	758	2	US-09-487-558B-224	Sequence 224, App
878	5	20.8	630	2	US-09-270-767-46708	Sequence 46708, A	951	5	20.8	766	2	US-09-710-279-2578	Sequence 2578, Ap
879	5	20.8	631	2	US-09-270-767-44123	Sequence 44123, A	952	5	20.8	772	2	US-09-107-532A-5724	Sequence 5724, Ap
880	5	20.8	632	2	US-09-248-796A-15266	Sequence 15266, A	953	5	20.8	772	2	US-09-999-833A-264	Sequence 264, App
881	5	20.8	632	2	US-09-438-185A-71	Sequence 71, Appl	954	5	20.8	772	2	US-10-020-445A-264	Sequence 264, App
882	5	20.8	635	2	US-09-248-796A-23137	Sequence 23137, A	955	5	20.8	776	1	US-07-603-133B-17	Sequence 17, Appl
883	5	20.8	636	2	US-07-757-342D-7	Sequence 7, Appl	956	5	20.8	776	1	US-07-603-133B-20	Sequence 20, Appl
884	5	20.8	636	2	US-09-461-657B-7	Sequence 7, Appl	957	5	20.8	776	2	US-08-089-397A-15	Sequence 15, Appl
885	5	20.8	638	2	US-09-248-796A-18750	Sequence 18750, A	958	5	20.8	783	2	US-09-949-016-7187	Sequence 7187, Ap
886	5	20.8	639	2	US-09-823-240A-5	Sequence 5, Appl	959	5	20.8	795	2	US-07-741-453A-55	Sequence 55, Appl
887	5	20.8	640	2	US-09-248-796A-18883	Sequence 18883, A	960	5	20.8	797	2	US-09-540-236-2813	Sequence 2813, Ap
888	5	20.8	641	2	US-09-248-796A-17974	Sequence 17974, A	961	5	20.8	798	1	US-08-222-617A-8	Sequence 8, Appl
889	5	20.8	642	2	US-09-248-796A-16106	Sequence 16106, A	962	5	20.8	802	2	US-09-433-043B-120	Sequence 120, App
890	5	20.8	650	2	US-09-487-558B-430	Sequence 430, App	963	5	20.8	803	2	US-09-543-681A-4886	Sequence 4886, Ap
891	5	20.8	651	2	US-09-270-767-41463	Sequence 41463, A	964	5	20.8	805	2	US-09-134-001C-4821	Sequence 4821, Ap
892	5	20.8	655	2	US-09-245-808-1	Sequence 1, Appl	965	5	20.8	809	2	US-09-270-767-42295	Sequence 42295, A
893	5	20.8	655	2	US-09-767-594-1	Sequence 1, Appl	966	5	20.8	815	2	US-09-248-796A-19069	Sequence 19069, A
894	5	20.8	655	2	US-09-584-586-10	Sequence 10, Appl	967	5	20.8	817	2	US-09-248-796A-15038	Sequence 15038, A
895	5	20.8	655	2	US-10-104-047-2502	Sequence 2502, Ap	968	5	20.8	820	2	US-09-248-796A-17231	Sequence 17231, A
896	5	20.8	657	2	US-09-543-681A-7109	Sequence 7109, Ap	969	5	20.8	824	2	US-09-487-558B-312	Sequence 312, App
897	5	20.8	657	2	US-09-248-796A-27210	Sequence 27210, A	970	5	20.8	827	2	US-09-134-000C-4612	Sequence 4612, Ap
898	5	20.8	660	2	US-09-181-706-8	Sequence 8, Appl	971	5	20.8	827	2	US-09-270-767-46276	Sequence 46276, A
899	5	20.8	660	2	US-09-458-791-8	Sequence 8, Appl	972	5	20.8	831	2	US-09-269-861A-8	Sequence 8, Appl
900	5	20.8	660	2	US-09-459-066-8	Sequence 8, Appl	973	5	20.8	836	2	US-09-538-092-173	Sequence 173, App
901	5	20.8	660	2	US-09-459-066-8	Sequence 8, Appl	974	5	20.8	852	2	US-09-897-427A-6	Sequence 6, Appl
902	5	20.8	666	2	US-09-248-796A-20656	Sequence 20656, A	975	5	20.8	858	2	US-09-248-796A-19055	Sequence 19055, A
903	5	20.8	666	2	US-09-487-558B-36	Sequence 36, Appl	976	5	20.8	864	2	US-09-248-796A-20612	Sequence 20612, A


```
977 5 20.8 866 2 US-09-134-001C-4930 Sequence 4930, Ap
978 5 20.8 875 2 US-09-585-858-18 Sequence 18, Appl
979 5 20.8 875 2 US-10-270-878-18 Sequence 18, Appl
980 5 20.8 881 2 US-09-248-796A-18627 Sequence 18627, A
981 5 20.8 888 1 US-08-861-464-6 Sequence 6, Appli
982 5 20.8 888 1 US-08-396-001-6 Sequence 6, Appli
983 5 20.8 888 2 US-09-323-433A-6 Sequence 6, Appli
984 5 20.8 888 2 US-09-826-752-6 Sequence 6, Appli
985 5 20.8 890 1 US-08-483-101-14 Sequence 14, Appl
986 5 20.8 895 2 US-08-827-962-19 Sequence 19, Appl
987 5 20.8 895 2 US-08-827-962-21 Sequence 21, Appl
988 5 20.8 899 2 US-09-758-007-2 Sequence 2, Appli
989 5 20.8 901 2 US-09-538-092-826 Sequence 826, App
990 5 20.8 905 2 US-09-340-620A-52 Sequence 52, Appl
991 5 20.8 905 2 US-09-728-721-52 Sequence 52, Appl
992 5 20.8 908 2 US-09-248-796A-14741 Sequence 14741, A
993 5 20.8 912 1 US-07-789-915A-8 Sequence 8, Appli
994 5 20.8 912 1 US-08-005-002C-8 Sequence 8, Appli
995 5 20.8 912 1 US-08-487-203A-8 Sequence 8, Appli
996 5 20.8 915 2 US-09-538-092-63 Sequence 63, Appl
997 5 20.8 925 2 US-09-924-097A-14 Sequence 14, Appl
998 5 20.8 926 2 US-09-489-039A-13928 Sequence 13928, A
999 5 20.8 928 2 US-09-487-558B-282 Sequence 282, App
1000 5 20.8 929 2 US-09-949-016-11143 Sequence 11143, A
```

ALIGNMENTS

```
RESULT 1
US-09-513-999C-5651
; Sequence 5651, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5651
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5651
```

```
Query Match 100.0%; Score 24; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LRFDSTKSIPEQETNNNSFYT 24
Db 35 LRFDSTKSIPEQETNNNSFYT 58
|||||
```

```
RESULT 2
US-08-254-493-1
; Sequence 1, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-1
```

```
Query Match 100.0%; Score 24; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LRFDSTKSIPEQETNNNSFYT 24
Db 34 LRFDSTKSIPEQETNNNSFYT 57
|||||
```

```
RESULT 3
US-08-253-751-6
; Sequence 6, Application US/08253751
; Patent No. 5858358
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
```


;
; FILING DATE: March 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-253A-6

Query Match 100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSTKSIPEQETNNNSFYT 24
Db 34 LRFDSTKSIPEQETNNNSFYT 57

RESULT 6
US-08-435-816A-6
; Sequence 6, Application US/08435816A
; Patent No. 6534055
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,816A

;
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-816A-6

Query Match 100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSTKSIPEQETNNNSFYT 24
Db 34 LRFDSTKSIPEQETNNNSFYT 57

RESULT 7
US-09-350-202-6
; Sequence 6, Application US/09350202
; Patent No. 6887466
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,202
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-350-202-6

Query Match 100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQETNNNSPYT 24
Db 34 LRFDSQTKSIFQETNNNSPYT 57

RESULT 8
US-08-592-711-6
Sequence 6, Application US/08592711
Patent No. 6905680
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Remert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-711-6

Query Match 100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQETNNNSPYT 24
Db 34 LRFDSQTKSIFQETNNNSPYT 57

RESULT 9
US-09-349-915B-6
Sequence 6, Application US/09349915B
Patent No. 6905681
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Remert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25


```
;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-7

Query Match 95.8%; Score 23; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.8e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDSTKSIFFEQETNNNSFFYT 24
Db 1 RFDSTKSIFFEQETNNNSFFYT 23

RESULT 12
US-08-408-222B-7
; Sequence 7, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masaharu
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-408-222B-7

Query Match 95.8%; Score 23; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.8e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDSTKSIFFEQETNNNSFFYT 24
Db 1 RFDSTKSIFFEQETNNNSFFYT 23

RESULT 13
US-09-270-767-41112
; Sequence 41112, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41112

Query Match 29.2%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNSS 21
Db 141 TNNNSS 147

RESULT 14
US-09-270-767-56328
; Sequence 56328, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56328
; LENGTH: 153
```

```

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56328

Query Match          29.2%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      15 TNNNSS 21
Db      141 TNNNSS 147

```

```

RESULT 15
US-08-642-846-4
; Sequence 4, Application US/08642846
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; APPLICANT: GALE, CHERYL A.
; APPLICANT: BENDEL, CATHERINE M.
; APPLICANT: TAO, NIAN-JUN
; APPLICANT: KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GERHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,846
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110,00280101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-642-846-4

```

```

Query Match          25.0%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TNNNSS 20
Db      5 TNNNSS 10

```

Search completed: January 20, 2006, 17:45:19
Job time : 15.7692 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:38:51 ; Search time 25.6154 Seconds
(without alignments)
391.480 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24
Sequence: 1 LRFDSQTSIFQETNNNSFYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications_AA_Main:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pcp:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pcp:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pcp:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pcp:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	209	4	US-10-106-698-6825
2	24	100.0	227	2	US-08-592-711-6
3	24	100.0	227	3	US-09-183-055-6
4	24	100.0	227	3	US-09-350-202-6
5	24	100.0	227	4	US-10-390-330-6
6	24	100.0	227	5	US-10-473-127-1723
7	24	100.0	227	5	US-10-473-127-1726
8	24	100.0	228	4	US-10-156-136-39
9	24	100.0	228	4	US-10-331-496A-41
10	24	100.0	228	4	US-10-619-323-1
11	24	100.0	228	4	US-10-794-899-97
12	24	100.0	228	5	US-10-473-127-1714
13	24	100.0	228	5	US-10-473-127-1715
14	24	100.0	228	5	US-10-473-127-1716
15	24	100.0	228	5	US-10-473-127-1718
16	24	100.0	228	5	US-10-473-127-1719
17	24	100.0	228	5	US-10-473-127-1725
18	24	100.0	228	5	US-10-789-378-18
19	24	100.0	228	5	US-10-482-029-144
20	24	100.0	228	5	US-10-852-335A-187
21	24	100.0	228	6	US-11-041-419-39
22	24	100.0	275	3	US-09-925-301-1381
23	24	100.0	275	4	US-10-106-698-5930
24	24	100.0	275	5	US-10-473-127-1720
25	24	100.0	275	5	US-10-473-127-1721
26	24	100.0	454	5	US-10-450-763-44426
27	21	87.5	228	5	US-10-473-127-1722

28	16	66.7	71	4	US-10-425-115-229906	Sequence 229906,
29	16	66.7	226	4	US-10-205-194-162	Sequence 162, App
30	11	45.8	63	5	US-10-450-763-44427	Sequence 44427, A
31	10	41.7	41	4	US-10-425-115-325581	Sequence 325581,
32	9	37.5	288	4	US-10-002-631C-2	Sequence 2, Appli
33	8	33.3	680	4	US-10-225-066A-336	Sequence 336, App
34	8	33.3	680	4	US-10-374-780A-2672	Sequence 2672, Ap
35	8	33.3	680	5	US-10-495-918-154	Sequence 154, App
36	8	33.3	680	5	US-10-225-066A-336	Sequence 336, App
37	7	29.2	204	4	US-10-424-599-248655	Sequence 248655,
38	7	29.2	350	4	US-10-425-114-39736	Sequence 39736, A
39	7	29.2	1304	6	US-11-097-143-14034	Sequence 14034, A
40	7	29.2	3502	6	US-11-097-143-1938	Sequence 1938, Ap
41	6	25.0	23	3	US-09-978-343-4	Sequence 4, Appli
42	6	25.0	50	4	US-10-029-386-30554	Sequence 30554, A
43	6	25.0	58	4	US-10-424-599-153462	Sequence 153462,
44	6	25.0	60	4	US-10-425-115-294870	Sequence 294870,
45	6	25.0	64	5	US-10-450-763-33603	Sequence 33603, A
46	6	25.0	66	3	US-09-764-877-1057	Sequence 1057, Ap
47	6	25.0	66	4	US-10-242-515-1057	Sequence 1057, Ap
48	6	25.0	67	4	US-10-424-599-238725	Sequence 238725,
49	6	25.0	69	4	US-10-416-800-50	Sequence 50, Appli
50	6	25.0	72	4	US-10-424-599-153952	Sequence 153952,
51	6	25.0	73	4	US-10-424-599-264934	Sequence 264934,
52	6	25.0	89	4	US-10-437-963-165597	Sequence 165597,
53	6	25.0	96	4	US-10-424-599-248797	Sequence 248797,
54	6	25.0	104	4	US-10-425-115-286923	Sequence 286923,
55	6	25.0	110	4	US-10-437-963-142155	Sequence 142155,
56	6	25.0	111	4	US-10-424-599-274504	Sequence 274504,
57	6	25.0	117	4	US-10-425-115-190934	Sequence 190934,
58	6	25.0	117	5	US-10-425-115-367225	Sequence 367225,
59	6	25.0	119	4	US-10-732-923-5954	Sequence 5954, Ap
60	6	25.0	120	4	US-10-424-599-210464	Sequence 210464,
61	6	25.0	125	4	US-10-424-599-174940	Sequence 174940,
62	6	25.0	125	4	US-10-425-115-351076	Sequence 351076,
63	6	25.0	125	5	US-10-805-177-53	Sequence 53, Appli
64	6	25.0	127	4	US-10-424-599-210574	Sequence 210574,
65	6	25.0	127	4	US-10-424-599-237265	Sequence 237265,
66	6	25.0	127	5	US-10-732-923-5493	Sequence 5493, Ap
67	6	25.0	133	4	US-10-437-963-151806	Sequence 151806,
68	6	25.0	135	4	US-10-424-599-193142	Sequence 193142,
69	6	25.0	137	4	US-10-183-687-310	Sequence 310, App
70	6	25.0	139	4	US-10-425-115-323340	Sequence 323340,
71	6	25.0	146	4	US-10-424-599-148797	Sequence 148797,
72	6	25.0	147	4	US-10-424-599-225143	Sequence 225143,
73	6	25.0	147	4	US-10-437-963-195387	Sequence 195387,
74	6	25.0	150	5	US-10-472-928-2268	Sequence 2268, Ap
75	6	25.0	154	6	US-11-097-143-32862	Sequence 32862, A
76	6	25.0	157	6	US-11-097-143-30828	Sequence 30828, A
77	6	25.0	158	4	US-10-424-599-181189	Sequence 181189,
78	6	25.0	169	4	US-10-282-122A-70869	Sequence 70869, A
79	6	25.0	169	4	US-10-724-972A-6896	Sequence 6896, Ap
80	6	25.0	170	4	US-10-282-122A-71583	Sequence 71583, A
81	6	25.0	170	4	US-10-767-701-48622	Sequence 48622, A
82	6	25.0	175	4	US-10-424-599-207660	Sequence 207660,
83	6	25.0	176	5	US-10-471-756-7	Sequence 7, Appli
84	6	25.0	177	4	US-10-424-599-199221	Sequence 199221,
85	6	25.0	188	4	US-10-425-115-366203	Sequence 366203,
86	6	25.0	192	4	US-10-425-114-39726	Sequence 39726, A
87	6	25.0	200	4	US-10-424-599-214836	Sequence 214836,
88	6	25.0	203	5	US-10-739-930-8673	Sequence 8673, Ap
89	6	25.0	210	4	US-10-424-599-265691	Sequence 265691,
90	6	25.0	214	6	US-11-097-143-38108	Sequence 38108, A
91	6	25.0	217	4	US-10-425-115-281526	Sequence 281526,
92	6	25.0	221	6	US-11-097-143-19665	Sequence 19665, A
93	6	25.0	225	4	US-10-424-599-280515	Sequence 280515,
94	6	25.0	228	6	US-11-097-143-14283	Sequence 14283, A
95	6	25.0	234	4	US-10-424-599-274514	Sequence 274514,
96	6	25.0	236	3	US-09-978-343--1	Sequence 0, Appli
97	6	25.0	242	4	US-10-225-066A-676	Sequence 676, App
98	6	25.0	242	4	US-10-374-780A-2148	Sequence 2148, Ap
99	6	25.0	242	4	US-10-425-114-37418	Sequence 37418, A
100	6	25.0	242	4	US-10-412-699B-1890	Sequence 1890, Ap

101	6	25.0	242	5	US-10-225-066A-676	Sequence 676, App	174	440	3	US-09-932-367A-19	Sequence 19, Appl
102	6	25.0	244	6	US-11-097-143-23409	Sequence 23409, A	175	440	6	US-11-097-143-42834	Sequence 42834, A
103	6	25.0	248	4	US-10-424-599-256129	Sequence 256129, A	176	443	6	US-11-097-143-24102	Sequence 24102, A
104	6	25.0	249	6	US-11-097-143-9453	Sequence 9453, Ap	177	445	5	US-10-942-711-2	Sequence 2, Appl
105	6	25.0	252	4	US-10-278-173-92	Sequence 92, Appl	178	449	4	US-10-437-963-197343	Sequence 197343, A
106	6	25.0	252	4	US-10-286-264-54	Sequence 54, Appl	179	463	4	US-10-424-599-198122	Sequence 198122, A
107	6	25.0	252	4	US-10-295-403-134	Sequence 134, App	180	477	6	US-11-097-143-27585	Sequence 27585, A
108	6	25.0	252	4	US-10-412-699B-510	Sequence 510, App	181	478	4	US-10-657-103-8	Sequence 8, Appl
109	6	25.0	253	4	US-10-424-599-282062	Sequence 282062, A	182	478	4	US-10-408-765A-698	Sequence 698, App
110	6	25.0	259	4	US-10-424-599-158958	Sequence 158958, A	183	480	6	US-11-097-143-34194	Sequence 34194, A
111	6	25.0	261	4	US-10-424-599-255067	Sequence 255067, A	184	482	4	US-10-389-566-1014	Sequence 1014, Ap
112	6	25.0	265	5	US-10-732-923-5491	Sequence 5491, Ap	185	482	5	US-10-732-923-2771	Sequence 2771, Ap
113	6	25.0	269	4	US-10-424-599-268211	Sequence 268211, A	186	483	4	US-10-389-566-1013	Sequence 1013, Ap
114	6	25.0	270	6	US-11-097-143-28769	Sequence 28769, A	187	483	4	US-10-389-566-2401	Sequence 2401, Ap
115	6	25.0	278	6	US-11-097-143-36609	Sequence 36609, A	188	483	4	US-10-424-599-245827	Sequence 245827, A
116	6	25.0	280	6	US-11-097-143-24141	Sequence 24141, A	189	483	5	US-10-732-923-2772	Sequence 2772, Ap
117	6	25.0	284	6	US-11-097-143-36096	Sequence 36096, A	190	483	5	US-10-732-923-2773	Sequence 2773, Ap
118	6	25.0	287	2	US-08-964-716-37	Sequence 37, Appl	191	485	4	US-10-425-114-54017	Sequence 54017, A
119	6	25.0	287	4	US-10-425-114-37007	Sequence 37007, A	192	490	4	US-10-389-566-2213	Sequence 2213, Ap
120	6	25.0	289	4	US-10-424-599-236110	Sequence 236110, A	193	490	5	US-10-732-923-2770	Sequence 2770, Ap
121	6	25.0	289	4	US-10-424-599-261270	Sequence 261270, A	194	493	6	US-11-097-143-42432	Sequence 42432, A
122	6	25.0	293	4	US-10-425-115-335141	Sequence 335141, A	195	496	4	US-10-421-654-54	Sequence 54, Appl
123	6	25.0	293	5	US-10-739-930-8758	Sequence 8758, Ap	196	496	5	US-10-796-907-54	Sequence 54, Appl
124	6	25.0	298	4	US-10-286-264-36	Sequence 36, Appl	197	508	6	US-11-097-143-40827	Sequence 40827, A
125	6	25.0	298	4	US-10-278-536-188	Sequence 188, App	198	512	3	US-09-769-736-4	Sequence 4, Appl
126	6	25.0	298	4	US-10-302-267-158	Sequence 158, App	199	520	4	US-10-425-114-38941	Sequence 38941, A
127	6	25.0	298	4	US-10-412-699B-864	Sequence 864, App	200	526	6	US-11-097-143-28218	Sequence 28218, A
128	6	25.0	304	5	US-10-739-930-7984	Sequence 7984, Ap	201	526	6	US-11-097-143-32694	Sequence 32694, A
129	6	25.0	309	4	US-10-424-599-159904	Sequence 159904, A	202	535	5	US-11-097-143-3537	Sequence 3537, Ap
130	6	25.0	311	4	US-10-424-599-250638	Sequence 250638, A	203	552	5	US-10-467-555-47	Sequence 47, Appl
131	6	25.0	313	4	US-10-425-114-52321	Sequence 52321, A	204	561	6	US-11-097-143-30426	Sequence 30426, A
132	6	25.0	323	4	US-10-424-599-192101	Sequence 192101, A	205	570	6	US-11-097-143-20868	Sequence 20868, A
133	6	25.0	323	6	US-11-097-143-6867	Sequence 6867, Ap	206	574	4	US-10-424-599-272474	Sequence 272474, A
134	6	25.0	332	4	US-10-424-599-153984	Sequence 153984, A	207	578	4	US-10-282-1270A-58779	Sequence 58779, A
135	6	25.0	336	4	US-10-424-599-162163	Sequence 162163, A	208	581	4	US-10-198-070-20	Sequence 20, Appl
136	6	25.0	337	4	US-10-424-599-233789	Sequence 233789, A	209	582	4	US-10-335-977-7288	Sequence 7288, Ap
137	6	25.0	337	4	US-10-425-114-39945	Sequence 39945, A	210	583	4	US-10-424-599-226024	Sequence 226024, A
138	6	25.0	341	4	US-10-425-114-37118	Sequence 37118, A	211	586	4	US-10-335-977-7289	Sequence 7289, Ap
139	6	25.0	354	3	US-09-801-368-414	Sequence 414, App	212	588	5	US-10-732-923-13794	Sequence 13794, A
140	6	25.0	354	6	US-11-004-418A-4	Sequence 4, Appl	213	592	4	US-10-041-018-209	Sequence 209, App
141	6	25.0	355	4	US-10-425-114-58441	Sequence 58441, A	214	592	4	US-10-041-018-219	Sequence 219, App
142	6	25.0	359	4	US-10-306-762-236	Sequence 236, App	215	592	4	US-10-041-018-247	Sequence 247, App
143	6	25.0	363	4	US-10-425-115-335145	Sequence 335145, A	216	592	4	US-10-041-018-357	Sequence 357, App
144	6	25.0	366	4	US-10-424-599-241793	Sequence 241793, A	217	601	6	US-11-097-143-11721	Sequence 11721, A
145	6	25.0	368	4	US-10-369-493-21627	Sequence 21627, A	218	602	4	US-10-225-066A-610	Sequence 610, App
146	6	25.0	368	4	US-10-424-599-245634	Sequence 245634, A	219	602	4	US-10-302-267-190	Sequence 190, App
147	6	25.0	368	4	US-10-451-467A-30	Sequence 30, Appl	220	602	4	US-10-374-780A-132	Sequence 132, App
148	6	25.0	368	6	US-11-097-143-882	Sequence 882, App	221	602	4	US-10-412-699B-418	Sequence 418, App
149	6	25.0	369	4	US-10-225-066A-396	Sequence 396, App	222	602	5	US-10-225-066A-610	Sequence 610, App
150	6	25.0	369	4	US-10-374-780A-2750	Sequence 2750, Ap	223	603	5	US-10-732-923-13033	Sequence 13033, A
151	6	25.0	369	5	US-10-225-066A-396	Sequence 396, App	224	605	3	US-09-801-368-428	Sequence 428, App
152	6	25.0	370	5	US-10-732-923-6512	Sequence 6512, Ap	225	605	4	US-10-369-493-22016	Sequence 22016, A
153	6	25.0	370	5	US-10-732-923-6513	Sequence 6513, Ap	226	608	4	US-10-424-599-174826	Sequence 174826, A
154	6	25.0	371	5	US-10-732-923-3020	Sequence 3020, Ap	227	610	6	US-11-097-143-40743	Sequence 40743, A
155	6	25.0	373	5	US-10-473-741-30	Sequence 30, Appl	228	613	6	US-11-097-143-23940	Sequence 23940, A
156	6	25.0	375	4	US-10-369-493-2344	Sequence 2344, Ap	229	628	3	US-09-934-455-410	Sequence 410, App
157	6	25.0	378	6	US-11-097-143-31425	Sequence 31425, A	230	628	3	US-10-500-361A-132	Sequence 132, App
158	6	25.0	381	4	US-10-374-780A-1391	Sequence 1391, Ap	231	638	5	US-10-732-923-9918	Sequence 9918, Ap
159	6	25.0	383	4	US-10-425-115-315650	Sequence 315650, A	232	645	5	US-11-097-143-11427	Sequence 11427, A
160	6	25.0	386	4	US-11-097-143-38682	Sequence 38682, A	233	648	5	US-10-732-923-10742	Sequence 10742, A
161	6	25.0	390	4	US-10-425-114-41685	Sequence 41685, A	234	649	5	US-10-509-558-4	Sequence 4, Appl
162	6	25.0	398	5	US-10-732-923-23342	Sequence 23342, A	235	653	4	US-10-081-872-194	Sequence 194, App
163	6	25.0	398	6	US-11-097-143-37767	Sequence 37767, A	236	653	4	US-10-385-305-194	Sequence 194, App
164	6	25.0	400	5	US-10-732-923-23343	Sequence 23343, A	237	656	4	US-10-437-963-179954	Sequence 179954, A
165	6	25.0	400	5	US-10-732-923-23344	Sequence 23344, A	238	659	6	US-11-097-143-21381	Sequence 21381, A
166	6	25.0	401	4	US-10-425-115-274075	Sequence 274075, A	239	660	6	US-11-097-143-31293	Sequence 31293, A
167	6	25.0	402	6	US-11-097-143-38394	Sequence 38394, A	240	669	6	US-11-097-143-5658	Sequence 5658, Ap
168	6	25.0	405	4	US-10-369-493-13402	Sequence 13402, A	241	676	3	US-09-801-368-302	Sequence 302, App
169	6	25.0	409	4	US-10-183-687-477	Sequence 477, App	242	676	4	US-10-451-467A-386	Sequence 386, App
170	6	25.0	416	6	US-11-097-143-4545	Sequence 4545, Ap	243	676	5	US-10-732-923-16873	Sequence 16873, A
171	6	25.0	423	4	US-10-437-963-129901	Sequence 129901, A	244	688	4	US-10-032-585-7876	Sequence 7876, Ap
172	6	25.0	426	6	US-11-097-143-28551	Sequence 28551, A	245	706	5	US-10-840-060-172	Sequence 172, App
173	6	25.0	437	6	US-11-097-143-15138	Sequence 15138, A	246	706	6	US-11-097-143-5748	Sequence 5748, Ap

247	6	25.0	713	6	US-11-097-143-42672	Sequence 42672, A	320	6	25.0	1423	6	US-11-097-143-42390	Sequence 42390, A
248	6	25.0	720	4	US-10-369-493-12449	Sequence 12449, A	321	6	25.0	1447	5	US-10-745-237-76	Sequence 76, Appl
249	6	25.0	722	4	US-10-282-122A-51562	Sequence 51562, A	322	6	25.0	1464	6	US-11-097-143-10389	Sequence 10389, A
250	6	25.0	730	3	US-09-801-368-126	Sequence 126, Appl	323	6	25.0	1472	5	US-10-732-923-8767	Sequence 8767, Appl
251	6	25.0	732	3	US-09-994-485-8	Sequence 8, Appl	324	6	25.0	1476	6	US-11-097-143-2910	Sequence 2910, Appl
252	6	25.0	732	3	US-09-832-292-12	Sequence 12, Appl	325	6	25.0	1487	4	US-10-437-963-161300	Sequence 161300, Appl
253	6	25.0	732	6	US-11-097-143-23142	Sequence 23142, A	326	6	25.0	1501	3	US-09-924-154-17	Sequence 17, Appl
254	6	25.0	742	5	US-10-741-849-7274	Sequence 7274, Appl	327	6	25.0	1504	4	US-10-369-493-2471	Sequence 2471, Appl
255	6	25.0	752	6	US-10-732-923-6886	Sequence 6886, Appl	328	6	25.0	1520	4	US-10-369-493-5596	Sequence 5596, Appl
256	6	25.0	761	5	US-11-097-143-41475	Sequence 41475, Appl	329	6	25.0	1520	4	US-10-369-493-5597	Sequence 5597, Appl
257	6	25.0	764	4	US-10-032-585-7597	Sequence 7597, Appl	330	6	25.0	1526	5	US-10-471-758-2	Sequence 2, Appl
258	6	25.0	765	6	US-11-097-143-37089	Sequence 37089, A	331	6	25.0	1531	3	US-09-876-883-347	Sequence 347, Appl
259	6	25.0	790	6	US-11-097-143-9105	Sequence 9105, Appl	332	6	25.0	1531	3	US-09-998-598-2593	Sequence 2593, Appl
260	6	25.0	814	6	US-11-097-143-31314	Sequence 31314, A	333	6	25.0	1531	4	US-10-171-311-222	Sequence 222, Appl
261	6	25.0	844	6	US-11-097-143-23046	Sequence 23046, A	334	6	25.0	1531	4	US-10-301-822-211	Sequence 211, Appl
262	6	25.0	848	4	US-10-369-493-18353	Sequence 18353, A	335	6	25.0	1531	4	US-10-435-695-46	Sequence 46, Appl
263	6	25.0	849	5	US-10-780-507-101	Sequence 101, Appl	336	6	25.0	1531	5	US-10-723-860-2100	Sequence 2100, Appl
264	6	25.0	856	3	US-09-949-029-66	Sequence 66, Appl	337	6	25.0	1531	5	US-10-645-756-42	Sequence 42, Appl
265	6	25.0	856	6	US-11-097-143-9741	Sequence 9741, Appl	338	6	25.0	1531	5	US-10-756-149-5261	Sequence 5261, Appl
266	6	25.0	856	6	US-11-097-143-33216	Sequence 33216, A	339	6	25.0	1531	5	US-10-745-237-268	Sequence 268, Appl
267	6	25.0	865	5	US-10-477-173-1036	Sequence 1036, Appl	340	6	25.0	1568	5	US-10-712-533A-12	Sequence 12, Appl
268	6	25.0	916	4	US-10-263-929-146	Sequence 146, Appl	341	6	25.0	1572	4	US-10-225-567A-344	Sequence 344, Appl
269	6	25.0	916	6	US-11-097-143-17637	Sequence 17637, A	342	6	25.0	1572	5	US-10-781-581-183	Sequence 183, Appl
270	6	25.0	920	6	US-11-097-143-12861	Sequence 12861, A	343	6	25.0	1574	4	US-10-292-798-870	Sequence 870, Appl
271	6	25.0	921	4	US-10-389-566-1850	Sequence 1850, Appl	344	6	25.0	1583	5	US-10-732-923-13548	Sequence 13548, A
272	6	25.0	921	5	US-10-477-173-1035	Sequence 1035, Appl	345	6	25.0	1613	4	US-10-464-368-84	Sequence 84, Appl
273	6	25.0	922	4	US-10-389-566-1848	Sequence 1848, Appl	346	6	25.0	1613	4	US-10-464-368-84	Sequence 84, Appl
274	6	25.0	924	4	US-10-389-566-1849	Sequence 1849, Appl	347	6	25.0	1613	5	US-10-477-238A-811	Sequence 811, Appl
275	6	25.0	924	4	US-10-389-566-1851	Sequence 1851, Appl	348	6	25.0	1613	5	US-10-680-287A-811	Sequence 811, Appl
276	6	25.0	938	6	US-11-097-143-8478	Sequence 8478, Appl	349	6	25.0	1613	5	US-10-477-173-764	Sequence 764, Appl
277	6	25.0	941	4	US-10-032-585-7930	Sequence 7930, A	350	6	25.0	1626	4	US-10-296-115-1161	Sequence 1161, Appl
278	6	25.0	941	5	US-10-450-763-56160	Sequence 56160, A	351	6	25.0	1626	4	US-10-408-765A-3017	Sequence 3017, Appl
279	6	25.0	943	6	US-11-097-143-13047	Sequence 13047, A	352	6	25.0	1626	5	US-10-745-237-270	Sequence 270, Appl
280	6	25.0	950	4	US-10-369-493-21918	Sequence 21918, A	353	6	25.0	1664	3	US-09-978-343-2	Sequence 2, Appl
281	6	25.0	950	6	US-11-097-143-40605	Sequence 40605, A	354	6	25.0	1664	3	US-09-964-858-1	Sequence 1, Appl
282	6	25.0	960	5	US-10-840-060-259	Sequence 259, Appl	355	6	25.0	1665	6	US-11-097-143-18822	Sequence 18822, A
283	6	25.0	960	5	US-10-840-060-261	Sequence 261, Appl	356	6	25.0	1703	6	US-11-097-143-25461	Sequence 25461, A
284	6	25.0	968	4	US-11-097-143-2094	Sequence 2094, Appl	357	6	25.0	1778	6	US-11-097-143-7035	Sequence 7035, Appl
285	6	25.0	968	4	US-10-263-929-158	Sequence 158, Appl	358	6	25.0	1805	6	US-11-097-143-22578	Sequence 22578, A
286	6	25.0	998	4	US-11-097-143-8061	Sequence 8061, A	359	6	25.0	1810	5	US-10-505-486-128	Sequence 128, Appl
287	6	25.0	1001	6	US-10-282-122A-58746	Sequence 58746, A	360	6	25.0	1874	4	US-10-424-599-248103	Sequence 248103, Appl
288	6	25.0	1046	6	US-11-097-143-47113	Sequence 47113, A	361	6	25.0	1893	6	US-11-097-143-6279	Sequence 6279, Appl
289	6	25.0	1058	4	US-10-464-939-4	Sequence 4, Appl	362	6	25.0	1954	6	US-11-097-143-4383	Sequence 4383, Appl
290	6	25.0	1070	5	US-10-732-923-6885	Sequence 6885, Appl	363	6	25.0	1980	6	US-11-097-143-29559	Sequence 29559, A
291	6	25.0	1083	4	US-10-087-192-480	Sequence 480, Appl	364	6	25.0	1987	6	US-11-097-143-10041	Sequence 10041, A
292	6	25.0	1100	5	US-10-741-849-7239	Sequence 7239, Appl	365	6	25.0	2006	6	US-11-097-143-4623	Sequence 4623, A
293	6	25.0	1111	4	US-10-080-608A-28	Sequence 28, Appl	366	6	25.0	2023	6	US-11-097-143-17253	Sequence 17253, A
294	6	25.0	1111	4	US-10-370-685-117	Sequence 117, Appl	367	6	25.0	2133	5	US-10-732-923-15030	Sequence 15030, A
295	6	25.0	1111	4	US-10-369-493-1413	Sequence 1413, A	368	6	25.0	2150	4	US-10-135-322-17	Sequence 17, Appl
296	6	25.0	1138	4	US-10-782-020-11	Sequence 11, Appl	369	6	25.0	2167	3	US-09-801-368-56	Sequence 56, Appl
297	6	25.0	1138	4	US-10-782-141-15	Sequence 15, Appl	370	6	25.0	2167	4	US-10-369-493-1773	Sequence 1773, Appl
298	6	25.0	1138	4	US-10-782-096-16	Sequence 16, Appl	371	6	25.0	2175	6	US-11-097-143-23886	Sequence 23886, A
299	6	25.0	1138	4	US-10-782-570-12	Sequence 12, Appl	372	6	25.0	2280	6	US-11-097-143-11742	Sequence 11742, A
300	6	25.0	1138	5	US-10-783-417-10	Sequence 10, Appl	373	6	25.0	2344	5	US-10-732-923-13978	Sequence 13978, A
301	6	25.0	1138	5	US-10-781-979-17	Sequence 17, Appl	374	6	25.0	2370	6	US-11-097-143-7542	Sequence 7542, Appl
302	6	25.0	1138	5	US-10-926-819-14	Sequence 14, Appl	375	6	25.0	2406	6	US-11-097-143-19386	Sequence 19386, A
303	6	25.0	1164	6	US-11-097-143-11277	Sequence 11277, A	376	6	25.0	2548	5	US-10-732-923-15009	Sequence 15009, A
304	6	25.0	1169	6	US-11-097-143-41781	Sequence 41781, A	377	6	25.0	2564	5	US-10-732-923-13552	Sequence 13552, A
305	6	25.0	1173	6	US-11-097-143-13527	Sequence 13527, A	378	6	25.0	3190	5	US-10-732-923-18448	Sequence 18448, A
306	6	25.0	1194	6	US-11-097-143-5730	Sequence 5730, Appl	379	6	25.0	3275	5	US-10-840-060-90	Sequence 90, Appl
307	6	25.0	1195	5	US-10-732-923-4353	Sequence 4353, Appl	380	6	25.0	3275	5	US-11-097-143-38103	Sequence 38103, A
308	6	25.0	1195	6	US-11-097-143-17874	Sequence 17874, A	381	6	25.0	3276	5	US-10-732-923-18447	Sequence 18447, A
309	6	25.0	1228	5	US-10-732-923-22375	Sequence 22375, A	382	6	25.0	3328	5	US-10-732-923-8311	Sequence 8311, Appl
310	6	25.0	1228	5	US-10-732-923-22378	Sequence 22378, A	383	6	25.0	3336	6	US-11-097-143-23232	Sequence 23232, A
311	6	25.0	1228	5	US-10-732-923-22466	Sequence 22466, A	384	6	25.0	3614	6	US-11-097-143-14784	Sequence 14784, A
312	6	25.0	1234	4	US-10-369-493-3432	Sequence 3432, Appl	385	6	25.0	6761	5	US-10-732-923-15035	Sequence 15035, A
313	6	25.0	1235	5	US-10-732-923-8669	Sequence 8669, Appl	386	5	20.8	9	3	US-09-935-384-41	Sequence 41, Appl
314	6	25.0	1244	4	US-10-369-493-1425	Sequence 1425, Appl	387	5	20.8	9	3	US-09-935-384-131	Sequence 131, Appl
315	6	25.0	1262	6	US-11-097-143-39309	Sequence 39309, A	388	5	20.8	9	3	US-09-935-384-229	Sequence 229, Appl
316	6	25.0	1266	4	US-10-320-797-3352	Sequence 3352, Appl	389	5	20.8	9	3	US-09-935-384-310	Sequence 310, Appl
317	6	25.0	1288	4	US-10-006-780-2	Sequence 2, Appl	390	5	20.8	9	3	US-09-935-384-419	Sequence 419, Appl
318	6	25.0	1402	4	US-10-369-493-5502	Sequence 5502, Appl	391	5	20.8	9	3	US-09-935-384-529	Sequence 529, Appl
319	6	25.0	1403	4	US-10-108-605-93	Sequence 93, Appl	392	5	20.8	9	3	US-09-935-384-616	Sequence 616, Appl

393	5	20.8	9	5	US-10-808-187-1154	Sequence 1154, Ap	466	5	20.8	58	4	US-10-424-598-224443	Sequence 224443,
394	5	20.8	9	5	US-10-705-459-307	Sequence 307, App	467	5	20.8	58	4	US-10-425-115-243522	Sequence 243522,
395	5	20.8	9	5	US-10-807-807-1154	Sequence 1154, Ap	468	5	20.8	59	4	US-10-424-599-174968	Sequence 174968,
396	5	20.8	10	3	US-09-935-384-368	Sequence 368, App	469	5	20.8	59	4	US-10-424-599-193462	Sequence 193462,
397	5	20.8	10	3	US-09-935-384-661	Sequence 661, App	470	5	20.8	59	4	US-10-437-963-138122	Sequence 138122,
398	5	20.8	12	3	US-09-982-172-186	Sequence 186, App	471	5	20.8	60	4	US-10-424-598-239679	Sequence 239679,
399	5	20.8	12	3	US-09-982-172-245	Sequence 245, App	472	5	20.8	60	4	US-10-424-599-245557	Sequence 245557,
400	5	20.8	12	4	US-10-378-173-67	Sequence 67, Appl	473	5	20.8	60	4	US-10-424-599-267325	Sequence 267325,
401	5	20.8	16	4	US-10-239-313A-590	Sequence 590, App	474	5	20.8	61	4	US-10-425-115-280841	Sequence 280841,
402	5	20.8	16	4	US-10-312-732A-18	Sequence 18, Appl	475	5	20.8	62	4	US-10-424-599-254465	Sequence 254465,
403	5	20.8	18	4	US-10-225-567A-1150	Sequence 1150, Ap	476	5	20.8	62	4	US-10-424-599-232715	Sequence 232715,
404	5	20.8	18	4	US-10-225-567A-1588	Sequence 1588, Ap	477	5	20.8	63	4	US-10-425-115-340966	Sequence 340966,
405	5	20.8	21	3	US-09-962-756-501	Sequence 501, App	478	5	20.8	64	4	US-10-424-599-249185	Sequence 249185,
406	5	20.8	21	4	US-10-253-471-501	Sequence 501, App	479	5	20.8	64	4	US-10-425-115-366085	Sequence 366085,
407	5	20.8	21	4	US-10-253-493-501	Sequence 501, App	480	5	20.8	65	4	US-10-424-599-216258	Sequence 216258,
408	5	20.8	23	3	US-09-967-869A-1	Sequence 1, Appli	481	5	20.8	65	4	US-10-424-599-216258	Sequence 216258,
409	5	20.8	23	6	US-11-045-828-1	Sequence 1, Appli	482	5	20.8	65	4	US-10-425-115-209526	Sequence 209526,
410	5	20.8	25	4	US-10-416-249-377	Sequence 377, App	483	5	20.8	65	4	US-10-425-115-246319	Sequence 246319,
411	5	20.8	28	5	US-10-485-758-60	Sequence 60, Appl	484	5	20.8	65	5	US-10-425-115-267115	Sequence 267115,
412	5	20.8	30	3	US-09-864-761-42566	Sequence 42566, A	485	5	20.8	65	5	US-10-450-763-35937	Sequence 35937, A
413	5	20.8	30	4	US-10-424-599-199129	Sequence 199129, A	486	5	20.8	66	4	US-10-424-599-180651	Sequence 180651,
414	5	20.8	30	4	US-10-296-734-1022	Sequence 1022, Ap	487	5	20.8	66	4	US-10-424-599-250835	Sequence 250835,
415	5	20.8	30	4	US-10-296-734-1024	Sequence 1024, Ap	488	5	20.8	66	4	US-10-437-963-203810	Sequence 203810,
416	5	20.8	31	5	US-10-742-469-121	Sequence 121, App	489	5	20.8	66	4	US-10-425-115-188731	Sequence 188731,
417	5	20.8	32	4	US-10-425-115-263987	Sequence 263987, A	490	5	20.8	66	4	US-10-425-115-230429	Sequence 230429,
418	5	20.8	32	5	US-10-742-469-198	Sequence 198, App	491	5	20.8	66	5	US-10-734-049A-227	Sequence 227, App
419	5	20.8	35	4	US-10-425-114-54234	Sequence 54234, A	492	5	20.8	67	4	US-10-424-599-153314	Sequence 153314,
420	5	20.8	36	3	US-09-994-595-128	Sequence 128, App	493	5	20.8	67	4	US-10-424-599-166051	Sequence 166051,
421	5	20.8	37	4	US-10-289-228-34	Sequence 34, Appl	494	5	20.8	67	4	US-10-424-599-262490	Sequence 262490,
422	5	20.8	37	4	US-10-373-592-34	Sequence 34, Appl	495	5	20.8	67	4	US-10-424-599-282430	Sequence 282430,
423	5	20.8	37	4	US-10-373-592-93	Sequence 93, Appl	496	5	20.8	67	4	US-10-416-800-43	Sequence 43, Appl
424	5	20.8	37	4	US-10-431-596-34	Sequence 34, Appl	497	5	20.8	67	4	US-10-416-800-51	Sequence 51, Appl
425	5	20.8	40	4	US-10-029-386-31049	Sequence 31049, A	498	5	20.8	67	4	US-10-437-963-156391	Sequence 156391,
426	5	20.8	41	3	US-09-864-761-44443	Sequence 44443, A	499	5	20.8	67	4	US-10-437-963-197536	Sequence 197536,
427	5	20.8	41	5	US-10-450-763-49964	Sequence 49964, A	500	5	20.8	67	4	US-10-425-115-274211	Sequence 274211,
428	5	20.8	42	3	US-09-764-860-351	Sequence 351, App	501	5	20.8	68	4	US-10-424-599-171534	Sequence 171534,
429	5	20.8	42	4	US-10-074-095-351	Sequence 351, App	502	5	20.8	68	4	US-10-424-599-198750	Sequence 198750,
430	5	20.8	42	4	US-10-212-872-351	Sequence 351, App	503	5	20.8	68	4	US-10-416-800-37	Sequence 37, Appl
431	5	20.8	44	4	US-10-424-599-187438	Sequence 187438, A	504	5	20.8	69	4	US-10-424-599-221673	Sequence 221673,
432	5	20.8	44	4	US-10-724-972A-5486	Sequence 5486, Ap	505	5	20.8	69	4	US-10-424-599-232914	Sequence 232914,
433	5	20.8	46	3	US-09-864-761-37857	Sequence 37857, A	506	5	20.8	69	4	US-10-416-800-1	Sequence 1, Appli
434	5	20.8	46	4	US-10-424-599-236912	Sequence 236912, A	507	5	20.8	69	4	US-10-425-115-320695	Sequence 32, Appl
435	5	20.8	47	4	US-10-424-599-276698	Sequence 276698, A	508	5	20.8	69	6	US-11-097-143-14817	Sequence 14817, A
436	5	20.8	48	4	US-10-424-599-193892	Sequence 193892, A	509	5	20.8	70	4	US-10-424-599-213751	Sequence 213751,
437	5	20.8	48	4	US-10-424-599-261363	Sequence 261363, A	510	5	20.8	70	4	US-10-424-599-214206	Sequence 214206,
438	5	20.8	49	4	US-10-239-423-22	Sequence 22, Appl	511	5	20.8	70	4	US-10-424-599-235907	Sequence 235907,
439	5	20.8	51	4	US-10-424-599-254039	Sequence 254039, A	512	5	20.8	70	4	US-10-424-599-279449	Sequence 279449,
440	5	20.8	51	4	US-10-425-115-267942	Sequence 267942, A	513	5	20.8	70	4	US-10-416-800-44	Sequence 44, Appl
441	5	20.8	51	6	US-11-097-143-34218	Sequence 34218, A	514	5	20.8	72	4	US-10-424-599-253301	Sequence 253301,
442	5	20.8	52	4	US-10-218-102-350	Sequence 350, App	515	5	20.8	72	4	US-10-424-599-254522	Sequence 254522,
443	5	20.8	52	4	US-10-424-599-186362	Sequence 186362, A	516	5	20.8	72	4	US-10-416-800-49	Sequence 49, Appl
444	5	20.8	52	4	US-10-424-599-282154	Sequence 282154, A	517	5	20.8	72	4	US-10-425-115-313944	Sequence 313944,
445	5	20.8	52	4	US-10-716-293-12	Sequence 12, Appl	518	5	20.8	73	3	US-09-925-302-543	Sequence 543, App
446	5	20.8	52	4	US-10-716-293-14	Sequence 14, Appl	519	5	20.8	73	3	US-09-864-761-47535	Sequence 47535, A
447	5	20.8	53	4	US-10-424-599-174380	Sequence 174380, A	520	5	20.8	73	3	US-09-925-302-543	Sequence 543, App
448	5	20.8	53	4	US-10-424-599-180369	Sequence 180369, A	521	5	20.8	73	4	US-10-424-599-162722	Sequence 162722,
449	5	20.8	54	4	US-10-424-599-233625	Sequence 233625, A	522	5	20.8	73	4	US-10-424-599-233066	Sequence 233066,
450	5	20.8	54	4	US-10-424-599-279281	Sequence 279281, A	523	5	20.8	74	4	US-10-424-599-279629	Sequence 279629,
451	5	20.8	54	4	US-10-724-972A-7061	Sequence 7061, Ap	524	5	20.8	74	4	US-10-425-115-244533	Sequence 244533,
452	5	20.8	54	4	US-10-425-115-189457	Sequence 189457, A	525	5	20.8	75	4	US-10-424-599-152143	Sequence 152143,
453	5	20.8	55	4	US-10-424-599-290899	Sequence 290899, A	526	5	20.8	75	4	US-10-424-599-262609	Sequence 262609,
454	5	20.8	55	4	US-10-724-972A-4732	Sequence 4732, Ap	527	5	20.8	75	4	US-10-335-977-9292	Sequence 9292, Ap
455	5	20.8	55	4	US-10-425-115-327085	Sequence 327085, A	528	5	20.8	75	4	US-10-437-963-198858	Sequence 198858,
456	5	20.8	56	3	US-09-864-408A-1642	Sequence 1642, Ap	529	5	20.8	75	4	US-10-716-293-26	Sequence 26, Appl
457	5	20.8	56	4	US-10-424-599-150535	Sequence 150535, A	530	5	20.8	75	4	US-10-425-115-196578	Sequence 196578,
458	5	20.8	56	4	US-10-425-115-258787	Sequence 258787, A	531	5	20.8	75	4	US-10-425-115-260625	Sequence 260625,
459	5	20.8	56	4	US-10-425-115-314698	Sequence 314698, A	532	5	20.8	75	6	US-11-097-143-38079	Sequence 38079, A
460	5	20.8	56	4	US-10-425-115-331697	Sequence 331697, A	533	5	20.8	76	4	US-10-437-963-178928	Sequence 178928,
461	5	20.8	57	4	US-10-424-599-158891	Sequence 158891, A	534	5	20.8	76	4	US-10-767-701-36181	Sequence 36181, A
462	5	20.8	57	4	US-10-424-599-210184	Sequence 210184, A	535	5	20.8	76	4	US-10-425-115-209955	Sequence 209955,
463	5	20.8	57	4	US-10-437-963-104783	Sequence 104783, A	536	5	20.8	76	4	US-10-425-115-245707	Sequence 245707,
464	5	20.8	57	4	US-10-425-115-200795	Sequence 200795, A	537	5	20.8	76	4	US-10-425-115-268561	Sequence 268561,
465	5	20.8	57	4	US-10-425-115-356100	Sequence 356100, A	538	5	20.8	76	4	US-10-425-115-328069	Sequence 328069,

685	5	20.8	112	4	US-10-264-049-2600	Sequence 2600, Ap	758	5	20.8	137	4	US-10-424-599-202899	Sequence 202899, A
686	5	20.8	112	4	US-10-282-122A-72534	Sequence 72534, A	759	5	20.8	137	4	US-10-767-701-43598	Sequence 43598, A
687	5	20.8	112	4	US-10-437-963-103151	Sequence 103151, A	760	5	20.8	137	4	US-10-425-115-293188	Sequence 293188, A
688	5	20.8	112	4	US-10-425-115-311717	Sequence 311717, A	761	5	20.8	138	4	US-10-425-115-230268	Sequence 230268, A
689	5	20.8	113	3	US-09-815-242-13424	Sequence 13424, A	762	5	20.8	139	4	US-10-174-693-297	Sequence 297, App
690	5	20.8	113	4	US-10-282-122A-73787	Sequence 73787, A	763	5	20.8	139	4	US-10-424-599-164342	Sequence 164342, A
691	5	20.8	113	4	US-10-424-599-144607	Sequence 144607, A	764	5	20.8	139	4	US-10-424-599-197470	Sequence 197470, A
692	5	20.8	113	4	US-10-424-599-173708	Sequence 173708, A	765	5	20.8	139	4	US-10-424-599-216622	Sequence 216622, A
693	5	20.8	113	4	US-10-474-776-627	Sequence 627, App	766	5	20.8	139	4	US-10-424-599-216622	Sequence 216622, A
694	5	20.8	113	4	US-10-425-115-185413	Sequence 185413, A	767	5	20.8	140	4	US-10-104-047-3489	Sequence 3489, Ap
695	5	20.8	113	5	US-10-856-499-2273	Sequence 2273, Ap	768	5	20.8	140	4	US-10-074-978A-94	Sequence 94, Appl
696	5	20.8	114	4	US-10-424-599-242696	Sequence 242696, A	769	5	20.8	140	4	US-10-424-599-175044	Sequence 175044, A
697	5	20.8	114	4	US-10-437-963-150565	Sequence 150565, A	770	5	20.8	141	4	US-10-424-599-183591	Sequence 183591, A
698	5	20.8	114	5	US-10-617-320-2930	Sequence 2930, Ap	771	5	20.8	141	4	US-10-424-599-256478	Sequence 256478, A
699	5	20.8	115	4	US-10-424-599-207815	Sequence 207815, A	772	5	20.8	141	4	US-10-425-115-290160	Sequence 290160, A
700	5	20.8	115	4	US-10-424-599-241442	Sequence 241442, A	773	5	20.8	141	6	US-11-097-143-38211	Sequence 38211, A
701	5	20.8	115	4	US-10-424-599-285615	Sequence 285615, A	774	5	20.8	142	4	US-10-424-599-271512	Sequence 271512, A
702	5	20.8	115	4	US-10-767-701-57062	Sequence 57062, A	775	5	20.8	142	4	US-10-767-701-56959	Sequence 56959, A
703	5	20.8	115	4	US-10-425-115-282532	Sequence 282532, A	776	5	20.8	142	4	US-10-425-115-193871	Sequence 193871, A
704	5	20.8	115	4	US-10-425-115-330358	Sequence 330358, A	777	5	20.8	142	4	US-10-425-115-307098	Sequence 307098, A
705	5	20.8	116	4	US-10-425-114-72663	Sequence 72663, A	778	5	20.8	143	4	US-10-424-599-227954	Sequence 227954, A
706	5	20.8	117	4	US-10-424-599-192469	Sequence 192469, A	779	5	20.8	143	4	US-10-424-599-247154	Sequence 247154, A
707	5	20.8	117	4	US-10-424-599-229241	Sequence 229241, A	780	5	20.8	143	6	US-11-097-143-39795	Sequence 39795, A
708	5	20.8	117	4	US-10-425-115-227689	Sequence 227689, A	781	5	20.8	144	4	US-10-289-762-657	Sequence 657, App
709	5	20.8	118	3	US-09-764-869-626	Sequence 626, App	782	5	20.8	144	4	US-10-767-701-40824	Sequence 40824, A
710	5	20.8	118	4	US-10-091-504-626	Sequence 626, App	783	5	20.8	144	4	US-10-732-923-13142	Sequence 13142, A
711	5	20.8	118	4	US-10-227-577-626	Sequence 626, App	784	5	20.8	144	5	US-10-996-306-262	Sequence 262, App
712	5	20.8	118	4	US-10-424-599-154820	Sequence 154820, A	785	5	20.8	145	5	US-10-450-763-44918	Sequence 44918, A
713	5	20.8	118	5	US-10-501-283-3998	Sequence 3998, Ap	786	5	20.8	146	4	US-10-425-115-318498	Sequence 318498, A
714	5	20.8	119	3	US-09-738-626-5535	Sequence 5535, Ap	787	5	20.8	146	5	US-10-856-499-680	Sequence 680, App
715	5	20.8	119	4	US-10-437-963-131295	Sequence 131295, A	788	5	20.8	147	4	US-10-424-599-182863	Sequence 182863, A
716	5	20.8	119	4	US-10-767-701-56701	Sequence 56701, A	789	5	20.8	147	4	US-10-424-599-210185	Sequence 210185, A
717	5	20.8	121	4	US-10-425-115-233474	Sequence 233474, A	790	5	20.8	147	4	US-10-739-930-6022	Sequence 6022, Ap
718	5	20.8	122	4	US-10-424-599-210994	Sequence 210994, A	791	5	20.8	148	3	US-09-864-761-37790	Sequence 37790, A
719	5	20.8	122	4	US-10-425-115-53289	Sequence 53289, A	792	5	20.8	149	4	US-10-424-599-178582	Sequence 178582, A
720	5	20.8	122	4	US-10-425-115-240321	Sequence 240321, A	793	5	20.8	149	5	US-10-994-726-755	Sequence 755, App
721	5	20.8	123	4	US-10-437-963-183237	Sequence 183237, A	794	5	20.8	150	4	US-10-450-763-35938	Sequence 35938, A
722	5	20.8	123	4	US-10-767-701-59341	Sequence 59341, A	795	5	20.8	150	4	US-10-029-386-33316	Sequence 33316, A
723	5	20.8	123	5	US-10-425-115-351375	Sequence 351375, A	796	5	20.8	150	5	US-10-450-763-32010	Sequence 32010, A
724	5	20.8	123	5	US-10-994-726-756	Sequence 756, App	797	5	20.8	151	5	US-10-472-928-1078	Sequence 1078, Ap
725	5	20.8	124	4	US-10-424-599-198195	Sequence 198195, A	798	5	20.8	151	5	US-10-994-726-667	Sequence 667, App
726	5	20.8	124	4	US-10-424-599-230127	Sequence 230127, A	799	5	20.8	152	4	US-10-424-599-165694	Sequence 165694, A
727	5	20.8	124	4	US-10-425-114-54553	Sequence 54553, A	800	5	20.8	152	4	US-10-424-599-242685	Sequence 242685, A
728	5	20.8	124	4	US-10-437-963-144871	Sequence 144871, A	801	5	20.8	152	4	US-10-424-599-245733	Sequence 245733, A
729	5	20.8	125	3	US-09-864-761-39087	Sequence 39087, A	802	5	20.8	152	6	US-11-097-143-21246	Sequence 21246, A
730	5	20.8	125	3	US-09-894-159-90	Sequence 90, Appl	803	5	20.8	153	3	US-09-864-761-47313	Sequence 47313, A
731	5	20.8	125	5	US-10-994-726-668	Sequence 668, App	804	5	20.8	153	4	US-10-425-115-202969	Sequence 202969, A
732	5	20.8	126	3	US-09-935-384-759	Sequence 759, App	805	5	20.8	153	6	US-11-097-143-17457	Sequence 17457, A
733	5	20.8	126	3	US-09-935-384-760	Sequence 760, App	806	5	20.8	154	4	US-10-424-599-235411	Sequence 235411, A
734	5	20.8	126	4	US-10-767-701-55526	Sequence 55526, A	807	5	20.8	154	4	US-10-424-599-245889	Sequence 245889, A
735	5	20.8	126	4	US-10-425-115-234977	Sequence 234977, A	808	5	20.8	154	4	US-10-425-114-41634	Sequence 41634, A
736	5	20.8	127	4	US-10-424-599-251391	Sequence 251391, A	809	5	20.8	154	4	US-10-437-963-146130	Sequence 146130, A
737	5	20.8	127	4	US-10-437-963-162918	Sequence 162918, A	810	5	20.8	154	4	US-10-425-115-228983	Sequence 228983, A
738	5	20.8	128	4	US-10-424-599-202944	Sequence 202944, A	811	5	20.8	155	4	US-10-023-171-25	Sequence 25, Appl
739	5	20.8	129	4	US-10-074-978A-393	Sequence 393, App	812	5	20.8	155	6	US-11-097-143-39561	Sequence 39561, A
740	5	20.8	129	4	US-10-424-599-185774	Sequence 185774, A	813	5	20.8	156	4	US-10-335-977-5542	Sequence 5542, Ap
741	5	20.8	129	4	US-10-424-599-216619	Sequence 216619, A	814	5	20.8	156	4	US-10-425-115-209540	Sequence 209540, A
742	5	20.8	129	6	US-11-097-143-33276	Sequence 33276, A	815	5	20.8	157	4	US-10-424-599-258954	Sequence 258954, A
743	5	20.8	130	4	US-10-424-599-239230	Sequence 239230, A	816	5	20.8	157	4	US-10-424-599-278655	Sequence 278655, A
744	5	20.8	130	4	US-10-424-599-271682	Sequence 271682, A	817	5	20.8	158	4	US-10-424-599-196565	Sequence 196565, A
745	5	20.8	130	4	US-10-767-701-51174	Sequence 51174, A	818	5	20.8	158	4	US-10-767-701-36360	Sequence 36360, A
746	5	20.8	131	4	US-10-424-599-151360	Sequence 151360, A	819	5	20.8	158	6	US-11-097-143-8469	Sequence 8469, Ap
747	5	20.8	131	4	US-10-424-599-213801	Sequence 213801, A	820	5	20.8	159	4	US-10-156-761-13330	Sequence 13330, A
748	5	20.8	132	4	US-10-078-929-36	Sequence 36, Appl	821	5	20.8	159	4	US-10-424-599-169769	Sequence 169769, A
749	5	20.8	132	4	US-10-074-978A-388	Sequence 388, App	822	5	20.8	160	3	US-09-727-892-84	Sequence 84, Appl
750	5	20.8	133	4	US-10-425-115-196233	Sequence 196233, A	823	5	20.8	160	4	US-10-424-599-158823	Sequence 158823, A
751	5	20.8	133	5	US-10-450-763-36345	Sequence 36345, A	824	5	20.8	160	4	US-10-424-599-170227	Sequence 170227, A
752	5	20.8	134	4	US-10-424-599-164466	Sequence 164466, A	825	5	20.8	160	4	US-10-425-115-241494	Sequence 241494, A
753	5	20.8	134	4	US-10-424-599-284174	Sequence 284174, A	826	5	20.8	161	4	US-10-424-599-195936	Sequence 195936, A
754	5	20.8	134	4	US-10-424-599-285553	Sequence 285553, A	827	5	20.8	161	5	US-10-485-758-10	Sequence 10, Appl
755	5	20.8	134	4	US-10-425-115-198302	Sequence 198302, A	828	5	20.8	162	6	US-11-097-143-32418	Sequence 32418, A
756	5	20.8	136	4	US-10-437-963-111327	Sequence 111327, A	829	5	20.8	163	4	US-10-282-122A-54926	Sequence 54926, A
757	5	20.8	137	4	US-10-424-599-184409	Sequence 184409, A	830	5	20.8	163	4		

831	5	20.8	165	4	US-10-424-599-209270	Sequence 209270,	904	5	20.8	189	4	US-10-424-599-164170	Sequence 164170,
832	5	20.8	166	3	US-09-934-455-314	Sequence 314, App	905	5	20.8	189	4	US-10-424-599-271572	Sequence 271572,
833	5	20.8	166	4	US-10-225-066A-622	Sequence 622, App	906	5	20.8	190	4	US-10-174-693-301	Sequence 301, App
834	5	20.8	166	4	US-10-302-267-40	Sequence 40, Appl	907	5	20.8	190	4	US-10-437-963-121764	Sequence 121764, A
835	5	20.8	166	4	US-10-374-780A-2522	Sequence 2522, Ap	908	5	20.8	190	4	US-10-767-701-38672	Sequence 38672, A
836	5	20.8	166	4	US-10-424-599-161684	Sequence 161684,	909	5	20.8	191	4	US-10-424-599-210718	Sequence 210718,
837	5	20.8	166	4	US-10-412-698B-702	Sequence 702, App	909	5	20.8	191	4	US-10-617-320-3302	Sequence 3302, Ap
838	5	20.8	166	5	US-10-225-066A-622	Sequence 622, App	910	5	20.8	191	5	US-10-424-599-191640	Sequence 191640,
839	5	20.8	167	4	US-10-424-599-229211	Sequence 229211,	911	5	20.8	193	4	US-10-424-599-235091	Sequence 235091,
840	5	20.8	168	3	US-09-809-391-563	Sequence 563, App	912	5	20.8	193	4	US-10-424-599-246077	Sequence 246077,
841	5	20.8	168	3	US-09-882-171-563	Sequence 563, App	913	5	20.8	193	4	US-10-424-599-278612	Sequence 278612,
842	5	20.8	168	4	US-10-164-861-563	Sequence 563, App	914	5	20.8	193	4	US-10-732-923-15925	Sequence 15925, A
843	5	20.8	168	4	US-10-424-599-173625	Sequence 173625,	915	5	20.8	194	5	US-10-295-027-160	Sequence 160, App
844	5	20.8	168	4	US-10-424-599-266129	Sequence 266129,	916	5	20.8	194	4	US-10-424-599-155684	Sequence 155684,
845	5	20.8	168	5	US-10-732-923-4970	Sequence 4970, Ap	917	5	20.8	195	4	US-10-156-761-12656	Sequence 12656, A
846	5	20.8	169	4	US-10-424-599-251207	Sequence 251207,	918	5	20.8	196	4	US-10-091-007-244	Sequence 244, App
847	5	20.8	170	4	US-10-032-585-7106	Sequence 7106, Ap	919	5	20.8	196	4	US-10-029-386-34085	Sequence 34085, A
848	5	20.8	170	4	US-10-424-599-203608	Sequence 203608,	920	5	20.8	196	4	US-10-424-599-229632	Sequence 229632,
849	5	20.8	171	4	US-10-424-599-190412	Sequence 190412,	921	5	20.8	196	4	US-10-425-115-343935	Sequence 343935,
850	5	20.8	171	4	US-10-437-963-187800	Sequence 187800,	922	5	20.8	197	4	US-10-425-115-362023	Sequence 362023,
851	5	20.8	171	4	US-10-425-115-271245	Sequence 271245,	923	5	20.8	197	4	US-10-424-599-229545	Sequence 229545,
852	5	20.8	172	4	US-10-424-599-156080	Sequence 156080,	924	5	20.8	198	4	US-10-815-837-101	Sequence 101, App
853	5	20.8	172	4	US-10-425-114-50373	Sequence 50373, A	925	5	20.8	199	3	US-10-282-122A-52399	Sequence 52399, A
854	5	20.8	172	4	US-10-767-701-54725	Sequence 54725, A	926	5	20.8	199	4	US-09-815-837-87	Sequence 87, Appl
855	5	20.8	172	4	US-10-767-701-59428	Sequence 59428, A	927	5	20.8	200	3	US-10-424-599-224901	Sequence 224901,
856	5	20.8	172	4	US-10-425-115-189238	Sequence 189238,	928	5	20.8	201	4	US-10-424-599-244851	Sequence 244851,
857	5	20.8	172	4	US-10-425-115-264843	Sequence 264843,	929	5	20.8	201	4	US-10-282-122A-52797	Sequence 52797, A
858	5	20.8	173	4	US-10-425-115-369318	Sequence 369318,	930	5	20.8	202	4	US-10-424-599-273434	Sequence 273434,
859	5	20.8	174	3	US-09-858-580-23	Sequence 23, Appl	931	5	20.8	202	4	US-10-425-114-39956	Sequence 39956, A
860	5	20.8	174	3	US-09-847-172-23	Sequence 23, Appl	932	5	20.8	203	4	US-10-087-192-1305	Sequence 1305, Ap
861	5	20.8	174	4	US-10-424-599-179990	Sequence 179990,	933	5	20.8	203	4	US-10-369-493-11309	Sequence 11309, A
862	5	20.8	174	5	US-10-941-152-23	Sequence 23, Appl	934	5	20.8	204	4	US-10-424-599-188696	Sequence 188696,
863	5	20.8	175	4	US-10-425-115-261783	Sequence 261783,	935	5	20.8	204	4	US-10-486-924-113	Sequence 113, App
864	5	20.8	176	4	US-10-767-701-52367	Sequence 52367, A	936	5	20.8	205	5	US-10-450-763-32029	Sequence 32029, A
865	5	20.8	176	4	US-10-425-115-361415	Sequence 361415,	937	5	20.8	206	3	US-09-815-837-86	Sequence 86, Appl
866	5	20.8	177	4	US-10-282-122A-63483	Sequence 63483, A	938	5	20.8	206	3	US-10-486-924-128	Sequence 128, App
867	5	20.8	177	4	US-10-424-599-256892	Sequence 256892,	939	5	20.8	206	5	US-10-486-924-136	Sequence 136, App
868	5	20.8	177	4	US-10-424-599-281307	Sequence 281307,	940	5	20.8	206	5	US-10-486-924-132	Sequence 132, App
869	5	20.8	177	4	US-10-424-599-283365	Sequence 283365,	941	5	20.8	206	5	US-10-486-924-140	Sequence 140, App
870	5	20.8	177	4	US-10-437-963-169626	Sequence 169626,	942	5	20.8	206	5	US-10-486-924-142	Sequence 142, App
871	5	20.8	178	4	US-10-282-122A-74330	Sequence 74330, A	943	5	20.8	206	5	US-10-486-924-144	Sequence 144, App
872	5	20.8	178	4	US-10-424-599-233102	Sequence 233102,	944	5	20.8	206	5	US-10-486-924-146	Sequence 146, App
873	5	20.8	179	4	US-10-289-762-1064	Sequence 1064, Ap	945	5	20.8	206	5	US-10-486-924-183	Sequence 183, App
874	5	20.8	179	4	US-10-282-122A-56301	Sequence 56301, A	946	5	20.8	207	4	US-10-424-599-161020	Sequence 161020,
875	5	20.8	179	4	US-10-424-599-147362	Sequence 147362,	947	5	20.8	207	4	US-10-424-599-253944	Sequence 253944,
876	5	20.8	179	6	US-11-097-143-25389	Sequence 25389, A	948	5	20.8	207	4	US-10-486-924-135	Sequence 135, App
877	5	20.8	180	4	US-10-282-122A-74246	Sequence 74246, A	949	5	20.8	208	2	US-08-781-986A-5202	Sequence 5202, Ap
878	5	20.8	180	4	US-10-437-963-130487	Sequence 130487,	950	5	20.8	208	4	US-10-329-624-5202	Sequence 5202, Ap
879	5	20.8	180	5	US-10-472-928-4688	Sequence 4688, Ap	951	5	20.8	208	5	US-10-424-599-262320	Sequence 262320,
880	5	20.8	181	4	US-10-767-701-44758	Sequence 44758, A	952	5	20.8	209	4	US-10-486-924-121	Sequence 121, App
881	5	20.8	182	4	US-10-183-687-154	Sequence 154, App	953	5	20.8	210	3	US-09-815-837-98	Sequence 98, Appl
882	5	20.8	184	4	US-10-369-493-19615	Sequence 19615, A	954	5	20.8	210	3	US-09-815-837-100	Sequence 100, App
883	5	20.8	184	4	US-10-282-122A-63484	Sequence 63484, A	955	5	20.8	211	6	US-11-097-143-38931	Sequence 38931, A
884	5	20.8	184	4	US-10-424-599-264891	Sequence 264891,	956	5	20.8	211	3	US-09-815-837-89	Sequence 89, Appl
885	5	20.8	185	4	US-10-627-476-2	Sequence 2, Appl	957	5	20.8	211	4	US-10-437-963-115384	Sequence 115384,
886	5	20.8	185	4	US-10-739-096-19	Sequence 19, Appl	958	5	20.8	211	4	US-10-180-375-146	Sequence 146, App
887	5	20.8	185	4	US-10-424-599-19	Sequence 4079, Ap	959	5	20.8	211	4	US-10-183-687-276	Sequence 276, App
888	5	20.8	185	5	US-10-494-364-19	Sequence 19, Appl	960	5	20.8	214	4	US-10-282-122A-68205	Sequence 68205, A
889	5	20.8	185	6	US-11-097-143-18153	Sequence 18153, A	961	5	20.8	214	4	US-10-424-599-230307	Sequence 230307,
890	5	20.8	186	4	US-10-295-403-154	Sequence 154, App	962	5	20.8	214	4	US-10-744-149-12	Sequence 12, Appl
891	5	20.8	186	4	US-10-369-493-18972	Sequence 18972, A	963	5	20.8	214	4	US-10-767-701-45086	Sequence 45086, A
892	5	20.8	186	6	US-11-097-143-31449	Sequence 31449, A	964	5	20.8	214	4		
893	5	20.8	186	6	US-10-412-699B-410	Sequence 410, App	965	5	20.8	214	4		
894	5	20.8	187	4	US-10-425-114-38142	Sequence 38142, A	966	5	20.8	214	4		
895	5	20.8	187	4	US-10-425-114-62223	Sequence 62223, A	967	5	20.8	214	4		
896	5	20.8	187	4	US-10-425-115-275054	Sequence 275054,	968	5	20.8	214	4		
897	5	20.8	188	3	US-09-815-242-4981	Sequence 4981, Ap	969	5	20.8	214	4		
898	5	20.8	188	3	US-09-815-242-10949	Sequence 10949, A	970	5	20.8	214	4		
899	5	20.8	188	3	US-09-893-737-16	Sequence 16, Appl	971	5	20.8	214	4		
900	5	20.8	188	4	US-10-282-122A-42430	Sequence 42430, A	972	5	20.8	214	4		
901	5	20.8	188	4	US-10-424-599-160446	Sequence 160446,	973	5	20.8	214	4		
902	5	20.8	188	4	US-10-424-599-187715	Sequence 187715,	974	5	20.8	214	4		
903	5	20.8	188	5	US-10-970-713-16	Sequence 1677, Appl	975	5	20.8	214	4		
						Sequence 1677, Appl	976	5	20.8	214	4		

US-08-592-711-6

Query Match 100.0%; Score 24; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFFYT 24
|||||
Db 34 LRFDSQTSIFEQETNNNSFFYT 57

RESULT 3

US-09-183-055-6
; Sequence 6, Application US/09183055
; Publication No. US20020076407A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

; TITLE OF INVENTION: Methods For Selectively Stimulating
; Proliferation Of T-Cells

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HALE AND DORR LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/183,055

; FILING DATE: 30-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/403,253

; FILING DATE: March 10, 1995

; APPLICATION NUMBER: US 08/253,964

; FILING DATE: 3 JUNE 1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Suparko, Colleen

; REGISTRATION NUMBER: 39,850

; REFERENCE/DOCKET NUMBER: 36119-12US8

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 526-6564

; TELEFAX: (617) 526-5000

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-183-055-6

Query Match 100.0%; Score 24; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFFYT 24
|||||
Db 34 LRFDSQTSIFEQETNNNSFFYT 57

RESULT 4

US-09-350-202-6
; Sequence 6, Application US/09350202
; Publication No. US20030099643A1
; GENERAL INFORMATION:

; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

; APPLICANT: Gray, Gary S., Rennert, Paul D.

; TITLE OF INVENTION: Methods For Selectively Stimulating

; Proliferation Of T-Cells

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/350,202

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/403,253

; FILING DATE: March 10, 1995

; APPLICATION NUMBER: US 08/253,964

; FILING DATE: 3 JUNE 1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-002CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-350-202-6

Query Match 100.0%; Score 24; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTSKIFQETNNNSFYT 24
|||||
Db 34 LRPDSQTSKIFQETNNNSFYT 57

RESULT 5

US-10-390-330-6
; Sequence 6, Application US/10390330
; Publication No. US20040001829A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Renner, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation
; TITLE OF INVENTION: Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/390,330
; FILING DATE: March 17, 2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,816A
; FILING DATE: May 4, 1995
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-390-330-6

Query Match 100.0%; Score 24; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTSKIFQETNNNSFYT 24
|||||
Db 34 LRPDSQTSKIFQETNNNSFYT 57

RESULT 6

US-10-473-127-1723
; Sequence 1723, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1723

Query Match 100.0%; Score 24; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTSKIFQETNNNSFYT 24
|||||
Db 34 LRPDSQTSKIFQETNNNSFYT 57

RESULT 7

US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370

;; PRIOR FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: 60/336,780
;; PRIOR FILING DATE: 2001-12-04
;; PRIOR APPLICATION NUMBER: 60/358,985
;; PRIOR FILING DATE: 2002-02-20
;; NUMBER OF SEQ ID NOS: 2041
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1726
;; LENGTH: 227
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match 100.0%; Score 24; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFYT 24
Db 34 LRFDSQTSIFEQETNNNSFYT 57

RESULT 8
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/156,136
FILING DATE: 29-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,146
FILING DATE: <Unknown>
APPLICATION NUMBER: WO US98/00959
FILING DATE: 21-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF354PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-156-136-39

Query Match 100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58

RESULT 9
US-10-331-496A-41
; Sequence 41, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

Query Match 100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRFDSQTSIFEQETNNNSFYT 24
Db 35 LRFDSQTSIFEQETNNNSFYT 58

RESULT 10
US-10-619-323-1
; Sequence 1, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241

```
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homosapien
US-10-619-323-1
```

```
Query Match          100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LRPDSQTKSIFQEQTNNNSFFYT 24
Db 35 LRPDSQTKSIFQEQTNNNSFFYT 58
```

```
RESULT 11
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97
```

```
Query Match          100.0%; Score 24; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LRPDSQTKSIFQEQTNNNSFFYT 24
Db 35 LRPDSQTKSIFQEQTNNNSFFYT 58
```

```
RESULT 12
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR FILING DATE: 2001-05-21
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-10-01
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
```

```
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match          100.0%; Score 24; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LRPDSQTKSIFQEQTNNNSFFYT 24
Db 35 LRPDSQTKSIFQEQTNNNSFFYT 58
```

```
RESULT 13
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715
```

```
Query Match          100.0%; Score 24; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LRPDSQTKSIFQEQTNNNSFFYT 24
Db 35 LRPDSQTKSIFQEQTNNNSFFYT 58
```

```
RESULT 14
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
```

; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1716
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1716

Query Match 100.0%; Score 24; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRPDSQTKSIFEQETNNNSSFYT 24
|||
Db 35 LRPDSQTKSIFEQETNNNSSFYT 58

RESULT 15

US-10-473-127-1718
; Sequence 1718, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1718
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1718

Query Match 100.0%; Score 24; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.7e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRPDSQTKSIFEQETNNNSSFYT 24
|||
Db 35 LRPDSQTKSIFEQETNNNSSFYT 58

Search completed: January 20, 2006, 17:47:28
Job time : 38.6154 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:42:32 ; Search time 2.53846 Seconds
(without alignments)
95.811 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58
Perfect score: 24
Sequence: 1 LRFDSTKSIPEQETNNNSFYT 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 1013881 residues

Word size : 0
Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	228	6	US-10-821-234-1266
2	6	25.0	131	7	US-11-052-554A-58
3	6	25.0	354	7	US-11-089-551A-4
4	6	25.0	592	6	US-10-467-962B-95
5	6	25.0	592	6	US-10-524-647-112
6	6	25.0	1531	7	US-11-087-227-24
7	6	25.0	1531	7	US-11-186-284-211
8	6	25.0	1613	7	US-11-108-528-86
9	6	25.0	1613	7	US-11-108-528-86
10	6	25.0	2053	7	US-11-013-759-9
11	5	20.8	9	7	US-11-045-024-616
12	5	20.8	10	7	US-11-045-024-770
13	5	20.8	23	6	US-10-467-657-8871
14	5	20.8	56	6	US-10-467-657-6884
15	5	20.8	78	5	US-09-978-360A-737
16	5	20.8	78	6	US-10-884-730-167
17	5	20.8	81	6	US-10-884-730-167
18	5	20.8	81	6	US-10-884-730-168
19	5	20.8	81	6	US-10-884-730-298
20	5	20.8	81	6	US-10-884-730-341
21	5	20.8	81	6	US-10-884-730-343
22	5	20.8	81	6	US-10-884-730-300
23	5	20.8	85	6	US-10-884-730-301
24	5	20.8	85	6	US-10-884-730-335
25	5	20.8	88	6	US-10-884-730-169
					Sequence 1266, Ap
					Sequence 58, Appl
					Sequence 4, Appli
					Sequence 95, Appl
					Sequence 112, App
					Sequence 211, App
					Sequence 84, Appl
					Sequence 86, Appl
					Sequence 9, Appli
					Sequence 616, App
					Sequence 770, App
					Sequence 8871, Ap
					Sequence 6884, Ap
					Sequence 737, App
					Sequence 170, App
					Sequence 167, App
					Sequence 168, App
					Sequence 168, App
					Sequence 298, App
					Sequence 341, App
					Sequence 343, App
					Sequence 300, App
					Sequence 301, App
					Sequence 335, App
					Sequence 169, App

26	5	20.8	88	6	US-10-884-730-297	Sequence 297, App
27	5	20.8	88	6	US-10-884-730-299	Sequence 299, App
28	5	20.8	88	6	US-10-884-730-302	Sequence 302, App
29	5	20.8	89	6	US-10-884-730-171	Sequence 171, App
30	5	20.8	89	6	US-10-884-730-174	Sequence 174, App
31	5	20.8	89	6	US-10-884-730-213	Sequence 213, App
32	5	20.8	89	6	US-10-884-730-340	Sequence 340, App
33	5	20.8	103	7	US-11-090-916-6	Sequence 6, Appli
34	5	20.8	111	6	US-10-884-730-338	Sequence 338, App
35	5	20.8	112	6	US-10-884-730-136	Sequence 136, App
36	5	20.8	114	6	US-10-467-657-5012	Sequence 5012, Ap
37	5	20.8	148	7	US-11-052-554A-359	Sequence 359, App
38	5	20.8	155	6	US-10-793-626-716	Sequence 716, App
39	5	20.8	167	6	US-10-793-626-808	Sequence 808, App
40	5	20.8	167	6	US-10-793-626-986	Sequence 986, App
41	5	20.8	167	6	US-10-793-626-2128	Sequence 2128, Ap
42	5	20.8	174	6	US-10-884-730-173	Sequence 173, App
43	5	20.8	188	6	US-10-884-730-294	Sequence 294, App
44	5	20.8	209	6	US-10-884-730-172	Sequence 172, App
45	5	20.8	230	6	US-10-884-730-370	Sequence 370, App
46	5	20.8	230	6	US-10-884-730-371	Sequence 371, App
47	5	20.8	230	6	US-10-884-730-377	Sequence 377, App
48	5	20.8	237	6	US-10-884-730-359	Sequence 359, App
49	5	20.8	246	6	US-10-793-626-900	Sequence 900, App
50	5	20.8	246	6	US-10-793-626-1956	Sequence 1956, Ap
51	5	20.8	259	6	US-10-512-184-34	Sequence 34, Appl
52	5	20.8	266	6	US-10-884-730-165	Sequence 165, App
53	5	20.8	266	6	US-10-884-730-166	Sequence 166, App
54	5	20.8	266	6	US-10-884-730-296	Sequence 296, App
55	5	20.8	266	6	US-10-884-730-295	Sequence 295, App
56	5	20.8	266	6	US-10-884-730-334	Sequence 334, App
57	5	20.8	275	7	US-11-000-463-868	Sequence 868, App
58	5	20.8	278	6	US-10-793-626-2700	Sequence 2700, Ap
59	5	20.8	287	6	US-10-467-657-5866	Sequence 5866, Ap
60	5	20.8	291	7	US-11-000-463-396	Sequence 396, App
61	5	20.8	299	6	US-10-793-626-1192	Sequence 1192, Ap
62	5	20.8	299	6	US-10-793-626-1768	Sequence 1768, Ap
63	5	20.8	300	6	US-10-667-295-117	Sequence 117, App
64	5	20.8	302	6	US-10-667-295-116	Sequence 116, App
65	5	20.8	314	6	US-10-467-657-5094	Sequence 5094, Ap
66	5	20.8	316	6	US-10-667-295-115	Sequence 115, App
67	5	20.8	371	6	US-10-512-184-71	Sequence 71, Appl
68	5	20.8	382	7	US-11-069-185-8	Sequence 8, Appli
69	5	20.8	390	6	US-10-821-234-1273	Sequence 1273, Ap
70	5	20.8	396	7	US-11-051-568-5	Sequence 5, Appli
71	5	20.8	399	6	US-10-821-234-1163	Sequence 1163, Ap
72	5	20.8	406	6	US-10-821-234-1521	Sequence 1521, Ap
73	5	20.8	410	6	US-10-821-234-952	Sequence 952, App
74	5	20.8	415	6	US-10-467-657-10	Sequence 10, Appl
75	5	20.8	428	6	US-10-467-657-5468	Sequence 5468, Ap
76	5	20.8	428	6	US-10-485-517-371	Sequence 371, App
77	5	20.8	433	6	US-10-793-626-1332	Sequence 1332, Ap
78	5	20.8	434	6	US-10-667-295-141	Sequence 141, App
79	5	20.8	476	7	US-11-024-959-385	Sequence 385, App
80	5	20.8	477	7	US-11-089-551A-34	Sequence 34, Appl
81	5	20.8	486	7	US-11-067-425A-82	Sequence 82, Appl
82	5	20.8	506	6	US-10-667-295-140	Sequence 140, App
83	5	20.8	510	6	US-10-467-657-3260	Sequence 3260, Ap
84	5	20.8	526	6	US-10-667-295-139	Sequence 139, App
85	5	20.8	527	7	US-11-113-424-81	Sequence 81, Appl
86	5	20.8	529	7	US-11-113-424-82	Sequence 82, Appl
87	5	20.8	529	7	US-11-033-039-487	Sequence 487, App
88	5	20.8	529	7	US-11-155-288-1	Sequence 1, Appli
89	5	20.8	532	7	US-11-127-877-42	Sequence 42, Appl
90	5	20.8	587	7	US-11-024-959-412	Sequence 412, Appl
91	5	20.8	626	6	US-10-512-184-49	Sequence 49, Appl
92	5	20.8	655	7	US-11-184-860-1	Sequence 1, Appli
93	5	20.8	655	7	US-11-124-368A-296	Sequence 296, App
94	5	20.8	655	7	US-11-124-368A-297	Sequence 297, App
95	5	20.8	685	6	US-10-490-824-5	Sequence 5, Appli
96	5	20.8	693	7	US-11-196-475-68	Sequence 68, Appl
97	5	20.8	710	7	US-11-089-551A-33	Sequence 33, Appl
98	5	20.8	718	7	US-11-147-109-6	Sequence 6, Appli

99	5	20.8	750	7	US-11-089-551A-32	Sequence 32, Appl	172	4	16.7	78	6	US-10-884-730-242	Sequence 242, App
100	5	20.8	758	7	US-11-089-551A-31	Sequence 31, Appl	173	4	16.7	78	6	US-10-884-730-254	Sequence 254, App
101	5	20.8	766	6	US-10-793-626-2578	Sequence 2578, Ap	174	4	16.7	78	6	US-10-884-730-290	Sequence 290, App
102	5	20.8	852	6	US-10-645-441-15	Sequence 15, Appl	175	4	16.7	79	6	US-10-884-730-55	Sequence 55, Appl
103	5	20.8	852	7	US-11-050-804-6	Sequence 6, Appli	176	4	16.7	79	6	US-10-884-730-127	Sequence 127, App
104	5	20.8	964	7	US-11-089-551A-30	Sequence 30, Appl	177	4	16.7	79	6	US-10-884-730-128	Sequence 128, App
105	5	20.8	1034	7	US-11-103-957-11	Sequence 11, Appl	178	4	16.7	79	6	US-10-884-730-131	Sequence 131, App
106	5	20.8	1038	7	US-11-107-028-1	Sequence 1, Appli	179	4	16.7	79	6	US-10-884-730-219	Sequence 219, App
107	5	20.8	1075	7	US-11-089-551A-23	Sequence 23, Appl	180	4	16.7	80	6	US-10-884-730-24	Sequence 24, Appl
108	5	20.8	1268	7	US-11-052-554A-1	Sequence 1, Appli	181	4	16.7	80	6	US-10-884-730-61	Sequence 61, Appl
109	5	20.8	1448	6	US-10-485-517-212	Sequence 212, App	182	4	16.7	80	6	US-10-884-730-68	Sequence 68, Appl
110	5	20.8	1476	6	US-10-647-956A-4	Sequence 4, Appli	183	4	16.7	80	6	US-10-884-730-70	Sequence 70, Appl
111	5	20.8	1614	7	US-11-108-528-82	Sequence 82, Appl	184	4	16.7	80	6	US-10-884-730-96	Sequence 96, Appl
112	5	20.8	1615	7	US-11-108-528-80	Sequence 80, Appl	185	4	16.7	80	6	US-10-884-730-101	Sequence 101, App
113	5	20.8	2101	6	US-11-108-528-23	Sequence 23, Appl	186	4	16.7	80	6	US-10-884-730-142	Sequence 142, App
114	5	20.8	2399	7	US-11-052-554A-92	Sequence 92, Appl	187	4	16.7	80	6	US-10-884-730-147	Sequence 147, App
115	5	20.8	5335	6	US-10-995-561-776	Sequence 776, App	188	4	16.7	80	6	US-10-884-730-224	Sequence 224, App
116	5	20.8	6893	7	US-11-205-109-14	Sequence 14, Appl	189	4	16.7	80	6	US-10-884-730-245	Sequence 245, App
117	4	16.7	6	US-10-615-668-23	Sequence 23, Appl	190	4	16.7	80	6	US-10-884-730-249	Sequence 249, App	
118	4	16.7	7	US-11-096-706-96	Sequence 96, Appl	191	4	16.7	80	6	US-10-884-730-250	Sequence 250, App	
119	4	16.7	10	US-11-041-893-31	Sequence 31, Appl	192	4	16.7	80	6	US-10-884-730-288	Sequence 288, App	
120	4	16.7	11	US-10-914-842A-12	Sequence 12, Appl	193	4	16.7	80	6	US-10-884-730-291	Sequence 291, App	
121	4	16.7	12	US-11-069-834-14	Sequence 14, Appl	194	4	16.7	80	6	US-10-884-730-314	Sequence 314, App	
122	4	16.7	12	US-11-069-834-16	Sequence 16, Appl	195	4	16.7	80	6	US-10-467-657-618	Sequence 618, App	
123	4	16.7	12	US-11-069-834-18	Sequence 18, Appl	196	4	16.7	81	6	US-10-884-730-3	Sequence 3, Appli	
124	4	16.7	12	US-11-069-834-34	Sequence 34, Appl	197	4	16.7	81	6	US-10-884-730-28	Sequence 28, Appl	
125	4	16.7	15	US-10-467-657-8838	Sequence 8838, Ap	198	4	16.7	81	6	US-10-884-730-62	Sequence 62, Appl	
126	4	16.7	15	US-11-045-024-13116	Sequence 13116, A	199	4	16.7	81	6	US-10-884-730-80	Sequence 80, Appl	
127	4	16.7	18	US-11-033-039-1242	Sequence 1242, Ap	200	4	16.7	81	6	US-10-884-730-81	Sequence 81, Appl	
128	4	16.7	18	US-11-033-039-1308	Sequence 1308, Ap	201	4	16.7	81	6	US-10-884-730-93	Sequence 93, Appl	
129	4	16.7	19	US-10-503-575-312	Sequence 312, App	202	4	16.7	81	6	US-10-884-730-105	Sequence 105, App	
130	4	16.7	20	US-10-509-917-4	Sequence 4, Appli	203	4	16.7	81	6	US-10-884-730-148	Sequence 148, App	
131	4	16.7	20	US-11-022-562-134	Sequence 134, App	204	4	16.7	81	6	US-10-884-730-162	Sequence 162, App	
132	4	16.7	20	US-11-022-562-135	Sequence 135, App	205	4	16.7	81	6	US-10-884-730-212	Sequence 212, App	
133	4	16.7	25	US-11-006-119-8	Sequence 8, Appli	206	4	16.7	81	6	US-10-884-730-217	Sequence 217, App	
134	4	16.7	27	US-11-097-749-1	Sequence 1, Appli	207	4	16.7	81	6	US-10-884-730-230	Sequence 230, App	
135	4	16.7	34	US-10-467-657-3966	Sequence 3966, Ap	208	4	16.7	81	6	US-10-884-730-257	Sequence 257, App	
136	4	16.7	34	US-10-467-657-8991	Sequence 8991, Ap	209	4	16.7	81	6	US-10-884-730-275	Sequence 275, App	
137	4	16.7	35	US-10-957-351-165	Sequence 165, App	210	4	16.7	81	6	US-10-884-730-303	Sequence 303, App	
138	4	16.7	39	US-10-467-657-2820	Sequence 2820, Ap	211	4	16.7	81	6	US-10-884-730-304	Sequence 304, App	
139	4	16.7	43	US-10-957-887B-155	Sequence 155, App	212	4	16.7	81	6	US-10-884-730-308	Sequence 308, App	
140	4	16.7	44	US-10-957-887B-157	Sequence 157, App	213	4	16.7	81	6	US-10-884-730-313	Sequence 313, App	
141	4	16.7	47	US-10-467-657-6650	Sequence 6650, Ap	214	4	16.7	81	6	US-10-884-730-315	Sequence 315, App	
142	4	16.7	48	US-11-019-711-40	Sequence 40, Appl	215	4	16.7	81	6	US-10-884-730-324	Sequence 324, App	
143	4	16.7	50	US-10-729-121-39	Sequence 39, Appl	216	4	16.7	81	6	US-10-884-730-344	Sequence 344, App	
144	4	16.7	51	US-11-146-523-5	Sequence 5, Appli	217	4	16.7	82	6	US-10-884-730-51	Sequence 51, Appl	
145	4	16.7	52	US-10-914-165-21	Sequence 21, Appl	218	4	16.7	82	6	US-10-884-730-58	Sequence 58, Appl	
146	4	16.7	53	US-10-467-657-2716	Sequence 2716, Ap	219	4	16.7	82	6	US-10-884-730-82	Sequence 82, Appl	
147	4	16.7	56	US-11-000-463-768	Sequence 768, App	220	4	16.7	82	6	US-10-884-730-143	Sequence 143, App	
148	4	16.7	59	US-11-134-241-14	Sequence 14, Appl	221	4	16.7	82	6	US-10-884-730-144	Sequence 144, App	
149	4	16.7	61	US-10-467-657-1506	Sequence 1506, Ap	222	4	16.7	82	6	US-10-884-730-195	Sequence 195, App	
150	4	16.7	61	US-10-467-657-2012	Sequence 2012, Ap	223	4	16.7	82	6	US-10-884-730-204	Sequence 204, App	
151	4	16.7	70	US-10-467-657-6924	Sequence 6924, Ap	224	4	16.7	82	6	US-10-884-730-207	Sequence 207, App	
152	4	16.7	71	US-10-821-234-1252	Sequence 1252, Ap	225	4	16.7	82	6	US-10-884-730-244	Sequence 244, App	
153	4	16.7	72	US-11-176-868-15	Sequence 15, Appl	226	4	16.7	82	6	US-10-884-730-280	Sequence 280, App	
154	4	16.7	73	US-10-884-730-52	Sequence 52, Appl	227	4	16.7	82	6	US-10-884-730-283	Sequence 283, App	
155	4	16.7	73	US-10-884-730-53	Sequence 53, Appl	228	4	16.7	82	6	US-10-467-657-1462	Sequence 1462, Ap	
156	4	16.7	73	US-10-884-730-56	Sequence 56, Appl	229	4	16.7	82	6	US-10-467-657-9177	Sequence 9177, Ap	
157	4	16.7	73	US-10-884-730-130	Sequence 130, App	230	4	16.7	83	6	US-10-884-730-57	Sequence 57, Appl	
158	4	16.7	73	US-10-884-730-132	Sequence 132, App	231	4	16.7	83	6	US-10-884-730-145	Sequence 145, App	
159	4	16.7	73	US-10-884-730-138	Sequence 274, App	232	4	16.7	83	6	US-10-884-730-337	Sequence 337, App	
160	4	16.7	74	US-10-884-730-45	Sequence 45, Appl	233	4	16.7	83	6	US-10-746-959C-2	Sequence 2, Appli	
161	4	16.7	74	US-10-884-730-50	Sequence 50, Appl	234	4	16.7	83	7	US-11-000-463-434	Sequence 434, App	
162	4	16.7	74	US-10-884-730-241	Sequence 241, App	235	4	16.7	84	6	US-11-000-463-906	Sequence 906, App	
163	4	16.7	74	US-10-467-657-6160	Sequence 6160, Ap	236	4	16.7	84	6	US-10-884-730-46	Sequence 46, Appl	
164	4	16.7	75	US-10-467-657-6160	Sequence 932, App	237	4	16.7	84	6	US-10-884-730-103	Sequence 103, App	
165	4	16.7	76	US-10-884-730-192	Sequence 90, Appl	238	4	16.7	84	6	US-10-884-730-194	Sequence 194, App	
166	4	16.7	76	US-10-884-730-90	Sequence 123, App	239	4	16.7	84	6	US-10-884-730-209	Sequence 209, App	
167	4	16.7	77	US-10-884-730-183	Sequence 183, App	240	4	16.7	84	6	US-10-884-730-259	Sequence 259, App	
168	4	16.7	78	US-10-884-730-129	Sequence 129, App	241	4	16.7	84	6	US-10-884-730-260	Sequence 260, App	
169	4	16.7	78	US-10-884-730-49	Sequence 49, Appl	242	4	16.7	84	6	US-10-884-730-316	Sequence 316, App	
170	4	16.7	78	US-10-884-730-54	Sequence 54, Appl	243	4	16.7	84	6	US-10-884-730-325	Sequence 325, App	
171	4	16.7	78	US-10-884-730-236	Sequence 236, App	244	4	16.7	84	7	US-11-123-896-386	Sequence 386, App	

245	4	16.7	85	6	US-10-884-730-14	Sequence 14, Appl	318	4	16.7	89	6	US-10-884-730-26	Sequence 26, Appl
246	4	16.7	85	6	US-10-884-730-83	Sequence 83, Appl	319	4	16.7	89	6	US-10-884-730-27	Sequence 27, Appl
247	4	16.7	85	6	US-10-884-730-107	Sequence 107, Appl	320	4	16.7	89	6	US-10-884-730-29	Sequence 29, Appl
248	4	16.7	85	6	US-10-884-730-125	Sequence 125, Appl	321	4	16.7	89	6	US-10-884-730-30	Sequence 30, Appl
249	4	16.7	85	6	US-10-884-730-141	Sequence 141, Appl	322	4	16.7	89	6	US-10-884-730-31	Sequence 31, Appl
250	4	16.7	85	6	US-10-884-730-186	Sequence 186, Appl	323	4	16.7	89	6	US-10-884-730-34	Sequence 34, Appl
251	4	16.7	85	6	US-10-884-730-187	Sequence 187, Appl	324	4	16.7	89	6	US-10-884-730-37	Sequence 37, Appl
252	4	16.7	85	6	US-10-884-730-243	Sequence 243, Appl	325	4	16.7	89	6	US-10-884-730-59	Sequence 59, Appl
253	4	16.7	85	6	US-10-884-730-277	Sequence 277, Appl	326	4	16.7	89	6	US-10-884-730-60	Sequence 60, Appl
254	4	16.7	85	6	US-10-884-730-286	Sequence 286, Appl	327	4	16.7	89	6	US-10-884-730-64	Sequence 64, Appl
255	4	16.7	85	6	US-10-884-730-347	Sequence 347, Appl	328	4	16.7	89	6	US-10-884-730-65	Sequence 65, Appl
256	4	16.7	85	6	US-10-884-730-347	Sequence 347, Appl	329	4	16.7	89	6	US-10-884-730-66	Sequence 66, Appl
257	4	16.7	86	6	US-10-884-730-21	Sequence 21, Appl	330	4	16.7	89	6	US-10-884-730-67	Sequence 67, Appl
258	4	16.7	86	6	US-10-884-730-63	Sequence 63, Appl	331	4	16.7	89	6	US-10-884-730-72	Sequence 72, Appl
259	4	16.7	86	6	US-10-884-730-71	Sequence 71, Appl	332	4	16.7	89	6	US-10-884-730-73	Sequence 73, Appl
260	4	16.7	86	6	US-10-884-730-87	Sequence 87, Appl	333	4	16.7	89	6	US-10-884-730-74	Sequence 74, Appl
261	4	16.7	86	6	US-10-884-730-95	Sequence 95, Appl	334	4	16.7	89	6	US-10-884-730-78	Sequence 78, Appl
262	4	16.7	86	6	US-10-884-730-99	Sequence 99, Appl	335	4	16.7	89	6	US-10-884-730-91	Sequence 91, Appl
263	4	16.7	86	6	US-10-884-730-102	Sequence 102, Appl	336	4	16.7	89	6	US-10-884-730-92	Sequence 92, Appl
264	4	16.7	86	6	US-10-884-730-155	Sequence 155, Appl	337	4	16.7	89	6	US-10-884-730-97	Sequence 97, Appl
265	4	16.7	86	6	US-10-884-730-157	Sequence 157, Appl	338	4	16.7	89	6	US-10-884-730-98	Sequence 98, Appl
266	4	16.7	86	6	US-10-884-730-191	Sequence 191, Appl	339	4	16.7	89	6	US-10-884-730-100	Sequence 100, Appl
267	4	16.7	86	6	US-10-884-730-247	Sequence 247, Appl	340	4	16.7	89	6	US-10-884-730-104	Sequence 104, Appl
268	4	16.7	86	6	US-10-884-730-262	Sequence 262, Appl	341	4	16.7	89	6	US-10-884-730-106	Sequence 106, Appl
269	4	16.7	86	6	US-10-884-730-292	Sequence 292, Appl	342	4	16.7	89	6	US-10-884-730-108	Sequence 108, Appl
270	4	16.7	87	6	US-10-884-730-11	Sequence 11, Appl	343	4	16.7	89	6	US-10-884-730-109	Sequence 109, Appl
271	4	16.7	87	6	US-10-884-730-48	Sequence 48, Appl	344	4	16.7	89	6	US-10-884-730-110	Sequence 110, Appl
272	4	16.7	87	6	US-10-884-730-126	Sequence 126, Appl	345	4	16.7	89	6	US-10-884-730-111	Sequence 111, Appl
273	4	16.7	87	6	US-10-884-730-180	Sequence 180, Appl	346	4	16.7	89	6	US-10-884-730-118	Sequence 118, Appl
274	4	16.7	87	6	US-10-884-730-219	Sequence 219, Appl	347	4	16.7	89	6	US-10-884-730-119	Sequence 119, Appl
275	4	16.7	87	6	US-10-884-730-237	Sequence 237, Appl	348	4	16.7	89	6	US-10-884-730-133	Sequence 133, Appl
276	4	16.7	87	6	US-10-884-730-238	Sequence 238, Appl	349	4	16.7	89	6	US-10-884-730-137	Sequence 137, Appl
277	4	16.7	87	6	US-10-884-730-239	Sequence 239, Appl	350	4	16.7	89	6	US-10-884-730-146	Sequence 146, Appl
278	4	16.7	87	6	US-10-884-730-278	Sequence 278, Appl	351	4	16.7	89	6	US-10-884-730-149	Sequence 149, Appl
279	4	16.7	87	6	US-10-884-730-310	Sequence 310, Appl	352	4	16.7	89	6	US-10-884-730-150	Sequence 150, Appl
280	4	16.7	87	6	US-10-884-730-312	Sequence 312, Appl	353	4	16.7	89	6	US-10-884-730-151	Sequence 151, Appl
281	4	16.7	87	6	US-10-884-730-346	Sequence 346, Appl	354	4	16.7	89	6	US-10-884-730-152	Sequence 152, Appl
282	4	16.7	87	6	US-10-467-657-4732	Sequence 4732, Ap	355	4	16.7	89	6	US-10-884-730-154	Sequence 154, Appl
283	4	16.7	88	6	US-10-884-730-32	Sequence 32, Appl	356	4	16.7	89	6	US-10-884-730-156	Sequence 156, Appl
284	4	16.7	88	6	US-10-884-730-40	Sequence 40, Appl	357	4	16.7	89	6	US-10-884-730-158	Sequence 158, Appl
285	4	16.7	88	6	US-10-884-730-43	Sequence 43, Appl	358	4	16.7	89	6	US-10-884-730-159	Sequence 159, Appl
286	4	16.7	88	6	US-10-884-730-44	Sequence 44, Appl	359	4	16.7	89	6	US-10-884-730-160	Sequence 160, Appl
287	4	16.7	88	6	US-10-884-730-75	Sequence 75, Appl	360	4	16.7	89	6	US-10-884-730-161	Sequence 161, Appl
288	4	16.7	88	6	US-10-884-730-76	Sequence 76, Appl	361	4	16.7	89	6	US-10-884-730-164	Sequence 164, Appl
289	4	16.7	88	6	US-10-884-730-77	Sequence 77, Appl	362	4	16.7	89	6	US-10-884-730-176	Sequence 176, Appl
290	4	16.7	88	6	US-10-884-730-112	Sequence 112, Appl	363	4	16.7	89	6	US-10-884-730-182	Sequence 182, Appl
291	4	16.7	88	6	US-10-884-730-139	Sequence 139, Appl	364	4	16.7	89	6	US-10-884-730-184	Sequence 184, Appl
292	4	16.7	88	6	US-10-884-730-140	Sequence 140, Appl	365	4	16.7	89	6	US-10-884-730-185	Sequence 185, Appl
293	4	16.7	88	6	US-10-884-730-163	Sequence 163, Appl	366	4	16.7	89	6	US-10-884-730-188	Sequence 188, Appl
294	4	16.7	88	6	US-10-884-730-178	Sequence 178, Appl	367	4	16.7	89	6	US-10-884-730-189	Sequence 189, Appl
295	4	16.7	88	6	US-10-884-730-199	Sequence 199, Appl	368	4	16.7	89	6	US-10-884-730-190	Sequence 190, Appl
296	4	16.7	88	6	US-10-884-730-202	Sequence 202, Appl	369	4	16.7	89	6	US-10-884-730-193	Sequence 193, Appl
297	4	16.7	88	6	US-10-884-730-203	Sequence 203, Appl	370	4	16.7	89	6	US-10-884-730-197	Sequence 197, Appl
298	4	16.7	88	6	US-10-884-730-214	Sequence 214, Appl	371	4	16.7	89	6	US-10-884-730-205	Sequence 205, Appl
299	4	16.7	88	6	US-10-884-730-228	Sequence 228, Appl	372	4	16.7	89	6	US-10-884-730-206	Sequence 206, Appl
300	4	16.7	88	6	US-10-884-730-234	Sequence 234, Appl	373	4	16.7	89	6	US-10-884-730-208	Sequence 208, Appl
301	4	16.7	88	6	US-10-884-730-235	Sequence 235, Appl	374	4	16.7	89	6	US-10-884-730-210	Sequence 210, Appl
302	4	16.7	88	6	US-10-884-730-246	Sequence 246, Appl	375	4	16.7	89	6	US-10-884-730-211	Sequence 211, Appl
303	4	16.7	88	6	US-10-884-730-264	Sequence 264, Appl	376	4	16.7	89	6	US-10-884-730-215	Sequence 215, Appl
304	4	16.7	88	6	US-10-884-730-272	Sequence 272, Appl	377	4	16.7	89	6	US-10-884-730-216	Sequence 216, Appl
305	4	16.7	88	6	US-10-884-730-271	Sequence 271, Appl	378	4	16.7	89	6	US-10-884-730-218	Sequence 218, Appl
306	4	16.7	88	6	US-10-884-730-272	Sequence 272, Appl	379	4	16.7	89	6	US-10-884-730-220	Sequence 220, Appl
307	4	16.7	88	6	US-10-884-730-305	Sequence 305, Appl	380	4	16.7	89	6	US-10-884-730-221	Sequence 221, Appl
308	4	16.7	88	7	US-10-884-730-309	Sequence 309, Appl	381	4	16.7	89	6	US-10-884-730-222	Sequence 222, Appl
309	4	16.7	89	6	US-11-194-890-1	Sequence 1, Appl	382	4	16.7	89	6	US-10-884-730-223	Sequence 223, Appl
310	4	16.7	89	6	US-10-884-730-6	Sequence 6, Appl	383	4	16.7	89	6	US-10-884-730-225	Sequence 225, Appl
311	4	16.7	89	6	US-10-884-730-8	Sequence 7, Appl	384	4	16.7	89	6	US-10-884-730-226	Sequence 226, Appl
312	4	16.7	89	6	US-10-884-730-9	Sequence 8, Appl	385	4	16.7	89	6	US-10-884-730-227	Sequence 227, Appl
313	4	16.7	89	6	US-10-884-730-15	Sequence 9, Appl	386	4	16.7	89	6	US-10-884-730-233	Sequence 233, Appl
314	4	16.7	89	6	US-10-884-730-16	Sequence 15, Appl	387	4	16.7	89	6	US-10-884-730-251	Sequence 251, Appl
315	4	16.7	89	6	US-10-884-730-16	Sequence 16, Appl	388	4	16.7	89	6	US-10-884-730-252	Sequence 252, Appl
316	4	16.7	89	6	US-10-884-730-17	Sequence 17, Appl	389	4	16.7	89	6	US-10-884-730-255	Sequence 255, Appl
317	4	16.7	89	6	US-10-884-730-23	Sequence 23, Appl	390	4	16.7	89	6	US-10-884-730-256	Sequence 256, Appl

391	4	16.7	89	6	US-10-884-730-258	Sequence 258, App	464	4	16.7	122	6	US-10-678-790-60	Sequence 60, Appl
392	4	16.7	89	6	US-10-884-730-261	Sequence 261, App	465	4	16.7	122	6	US-10-746-909-9	Sequence 9, Appl
393	4	16.7	89	6	US-10-884-730-263	Sequence 263, App	466	4	16.7	123	6	US-10-793-626-1856	Sequence 1856, Ap
394	4	16.7	89	6	US-10-884-730-265	Sequence 265, App	467	4	16.7	124	6	US-10-467-657-1092	Sequence 1092, Ap
395	4	16.7	89	6	US-10-884-730-266	Sequence 266, App	468	4	16.7	125	6	US-10-516-768-11	Sequence 11, Appl
396	4	16.7	89	6	US-10-884-730-267	Sequence 267, App	469	4	16.7	127	6	US-10-516-768-11	Sequence 11, Appl
397	4	16.7	89	6	US-10-884-730-268	Sequence 268, App	470	4	16.7	127	6	US-10-467-657-4210	Sequence 4210, Ap
398	4	16.7	89	6	US-10-884-730-269	Sequence 269, App	471	4	16.7	127	6	US-10-467-657-5246	Sequence 5246, Ap
399	4	16.7	89	6	US-10-884-730-281	Sequence 281, App	472	4	16.7	127	6	US-10-467-657-6036	Sequence 6036, Ap
400	4	16.7	89	6	US-10-884-730-282	Sequence 282, App	473	4	16.7	128	6	US-10-467-657-5268	Sequence 5268, Ap
401	4	16.7	89	6	US-10-884-730-284	Sequence 284, App	474	4	16.7	128	7	US-11-116-144-147	Sequence 147, App
402	4	16.7	89	6	US-10-884-730-293	Sequence 293, App	475	4	16.7	129	6	US-11-116-144-147	Sequence 147, App
403	4	16.7	89	6	US-10-884-730-311	Sequence 311, App	476	4	16.7	131	6	US-10-873-528-51	Sequence 51, Appl
404	4	16.7	89	6	US-10-884-730-319	Sequence 319, App	477	4	16.7	132	6	US-10-689-742-192	Sequence 192, App
405	4	16.7	89	6	US-10-884-730-320	Sequence 320, App	478	4	16.7	133	7	US-11-141-642-5	Sequence 5, Appl
406	4	16.7	89	6	US-10-884-730-321	Sequence 321, App	479	4	16.7	133	6	US-10-793-626-1154	Sequence 1154, Ap
407	4	16.7	89	6	US-10-884-730-323	Sequence 323, App	480	4	16.7	134	7	US-11-091-643-2	Sequence 2, Appl
408	4	16.7	89	6	US-10-884-730-339	Sequence 339, App	481	4	16.7	134	7	US-11-084-591-2	Sequence 2, Appl
409	4	16.7	89	6	US-10-884-730-348	Sequence 348, App	482	4	16.7	136	6	US-10-467-657-6108	Sequence 6108, Ap
410	4	16.7	89	6	US-10-467-657-4576	Sequence 4576, Ap	483	4	16.7	138	6	US-10-793-626-2302	Sequence 2302, Ap
411	4	16.7	90	6	US-10-884-730-94	Sequence 94, Appl	484	4	16.7	139	6	US-10-793-626-1154	Sequence 1154, Ap
412	4	16.7	90	6	US-10-884-730-124	Sequence 124, App	485	4	16.7	139	6	US-10-878-556A-117	Sequence 117, App
413	4	16.7	90	6	US-10-884-730-201	Sequence 201, App	486	4	16.7	142	6	US-10-667-295-74	Sequence 74, Appl
414	4	16.7	90	6	US-10-884-730-248	Sequence 248, App	487	4	16.7	143	6	US-10-821-234-1408	Sequence 1408, Ap
415	4	16.7	93	6	US-10-884-730-135	Sequence 135, App	488	4	16.7	143	6	US-10-821-234-1408	Sequence 1408, Ap
416	4	16.7	94	6	US-10-884-730-39	Sequence 39, Appl	489	4	16.7	145	6	US-10-793-626-2328	Sequence 2328, Ap
417	4	16.7	94	6	US-10-884-730-42	Sequence 42, Appl	490	4	16.7	145	6	US-10-467-657-264	Sequence 264, App
418	4	16.7	94	6	US-10-884-730-122	Sequence 122, App	491	4	16.7	145	6	US-10-467-657-3600	Sequence 3600, Ap
419	4	16.7	94	6	US-10-884-730-134	Sequence 134, App	492	4	16.7	145	6	US-10-454-437-164	Sequence 164, App
420	4	16.7	94	6	US-10-884-730-229	Sequence 229, App	493	4	16.7	147	6	US-10-467-657-9020	Sequence 9020, Ap
421	4	16.7	94	6	US-10-884-730-231	Sequence 231, App	494	4	16.7	148	6	US-10-467-657-4330	Sequence 4330, Ap
422	4	16.7	94	6	US-10-884-730-232	Sequence 232, App	495	4	16.7	148	7	US-11-134-241-8	Sequence 8, Appl
423	4	16.7	96	6	US-10-884-730-253	Sequence 253, App	496	4	16.7	148	7	US-11-134-241-10	Sequence 10, Appl
424	4	16.7	96	6	US-10-467-657-3954	Sequence 3954, Ap	497	4	16.7	149	6	US-10-995-561-584	Sequence 584, App
425	4	16.7	96	7	US-11-000-463-762	Sequence 762, App	498	4	16.7	153	7	US-10-821-234-1355	Sequence 1355, Ap
426	4	16.7	97	7	US-11-054-669-50	Sequence 50, Appl	499	4	16.7	153	7	US-11-066-480-8	Sequence 8, Appl
427	4	16.7	97	7	US-11-134-241-18	Sequence 18, Appl	500	4	16.7	156	6	US-10-667-295-125	Sequence 125, App
428	4	16.7	98	6	US-10-884-730-276	Sequence 276, App	501	4	16.7	157	6	US-10-667-295-124	Sequence 124, App
429	4	16.7	98	7	US-11-082-381-11	Sequence 11, Appl	502	4	16.7	161	7	US-11-052-554A-86	Sequence 86, Appl
430	4	16.7	99	6	US-10-467-657-472	Sequence 472, App	503	4	16.7	162	6	US-10-516-768-21	Sequence 21, Appl
431	4	16.7	100	6	US-10-884-730-13	Sequence 13, Appl	504	4	16.7	162	6	US-10-793-626-1010	Sequence 1010, Ap
432	4	16.7	101	6	US-10-884-730-89	Sequence 89, Appl	505	4	16.7	162	6	US-10-793-626-2432	Sequence 2432, Ap
433	4	16.7	101	6	US-10-884-730-117	Sequence 117, App	506	4	16.7	162	7	US-11-055-822-788	Sequence 788, App
434	4	16.7	101	6	US-10-884-730-179	Sequence 179, App	507	4	16.7	163	6	US-10-667-295-123	Sequence 123, App
435	4	16.7	101	6	US-10-884-730-181	Sequence 181, App	508	4	16.7	164	6	US-10-793-626-252	Sequence 252, App
436	4	16.7	101	6	US-10-454-437-48	Sequence 48, Appl	509	4	16.7	165	7	US-11-055-822-678	Sequence 678, App
437	4	16.7	101	7	US-11-082-381-1	Sequence 1, Appl	510	4	16.7	167	6	US-10-884-730-342	Sequence 342, App
438	4	16.7	102	6	US-10-884-730-19	Sequence 19, Appl	511	4	16.7	167	7	US-11-055-822-676	Sequence 676, App
439	4	16.7	102	6	US-10-884-730-20	Sequence 20, Appl	512	4	16.7	172	6	US-10-793-626-2838	Sequence 2838, Ap
440	4	16.7	103	6	US-10-884-730-123	Sequence 123, App	513	4	16.7	175	7	US-11-058-384-2	Sequence 2, Appl
441	4	16.7	106	6	US-10-793-626-794	Sequence 794, App	514	4	16.7	176	6	US-10-467-657-1880	Sequence 1880, App
442	4	16.7	106	6	US-10-793-626-2140	Sequence 2140, Ap	515	4	16.7	176	6	US-10-467-657-1282	Sequence 1282, Ap
443	4	16.7	106	6	US-10-821-234-906	Sequence 906, App	516	4	16.7	177	6	US-10-467-657-7762	Sequence 7762, Ap
444	4	16.7	107	6	US-10-678-790-61	Sequence 61, Appl	517	4	16.7	177	6	US-10-623-155-165	Sequence 165, App
445	4	16.7	108	6	US-10-884-730-198	Sequence 198, App	518	4	16.7	177	6	US-10-623-155-166	Sequence 166, App
446	4	16.7	108	6	US-10-467-657-3054	Sequence 3054, Ap	519	4	16.7	177	6	US-11-035-826-16	Sequence 16, Appl
447	4	16.7	110	6	US-10-524-647-140	Sequence 140, App	520	4	16.7	179	6	US-10-467-962B-39	Sequence 39, Appl
448	4	16.7	110	7	US-11-134-241-4	Sequence 4, Appl	521	4	16.7	179	6	US-10-884-730-84	Sequence 84, Appl
449	4	16.7	111	6	US-10-467-657-980	Sequence 980, App	522	4	16.7	181	6	US-10-746-959C-10	Sequence 10, Appl
450	4	16.7	112	6	US-10-884-730-138	Sequence 138, App	523	4	16.7	183	6	US-10-884-730-86	Sequence 86, Appl
451	4	16.7	113	7	US-11-144-242-20	Sequence 20, Appl	524	4	16.7	183	6	US-10-467-657-8825	Sequence 8825, Ap
452	4	16.7	113	7	US-11-144-222-20	Sequence 20, Appl	525	4	16.7	186	7	US-11-134-241-12	Sequence 12, Appl
453	4	16.7	114	6	US-10-884-730-196	Sequence 196, App	526	4	16.7	186	7	US-10-884-730-88	Sequence 88, Appl
454	4	16.7	117	6	US-10-884-730-378	Sequence 378, App	527	4	16.7	188	6	US-10-884-730-322	Sequence 322, App
455	4	16.7	117	6	US-10-467-657-2282	Sequence 2282, Ap	528	4	16.7	189	6	US-10-995-561-806	Sequence 806, App
456	4	16.7	118	6	US-10-821-234-1247	Sequence 1247, Ap	529	4	16.7	189	6	US-10-467-657-638	Sequence 638, App
457	4	16.7	118	7	US-11-000-463-274	Sequence 274, App	530	4	16.7	191	6	US-10-793-626-330	Sequence 330, Appl
458	4	16.7	118	7	US-11-000-463-746	Sequence 746, App	531	4	16.7	191	6	US-10-624-932-4	Sequence 4, Appl
459	4	16.7	119	6	US-10-884-730-200	Sequence 200, App	532	4	16.7	193	6	US-11-194-246-301	Sequence 301, App
460	4	16.7	120	6	US-10-884-730-153	Sequence 153, App	533	4	16.7	194	7	US-11-186-284-175	Sequence 175, App
461	4	16.7	120	6	US-10-467-657-8851	Sequence 8851, Ap	534	4	16.7	195	7	US-10-467-657-3296	Sequence 3296, Ap
462	4	16.7	121	6	US-10-793-626-3214	Sequence 3214, Ap	535	4	16.7	196	6	US-10-467-657-3296	Sequence 3296, Ap
463	4	16.7	121	6	US-10-678-790-63	Sequence 63, Appl	536	4	16.7	198	6	US-10-131-826A-550	Sequence 550, App

537	4	16.7	198	6	US-10-798-532-6	Sequence 6, Appli	610	4	16.7	244	6	US-10-793-626-566	Sequence 566, App
538	4	16.7	198	7	US-11-179-411-29	Sequence 29, Appl	611	4	16.7	246	7	US-11-124-368A-170	Sequence 170, App
539	4	16.7	198	7	US-11-175-766-29	Sequence 29, Appl	612	4	16.7	247	7	US-11-054-515-2076	Sequence 2076, Ap
540	4	16.7	198	7	US-11-052-554A-34	Sequence 34, Appl	613	4	16.7	248	6	US-10-467-557-6046	Sequence 6046, Ap
541	4	16.7	199	6	US-10-454-437-162	Sequence 162, App	614	4	16.7	249	7	US-11-054-515-1838	Sequence 1838, Ap
542	4	16.7	203	6	US-10-467-557-3492	Sequence 3492, Ap	615	4	16.7	250	7	US-11-113-837-2	Sequence 2, Appli
543	4	16.7	203	6	US-11-038-284-21	Sequence 21, Appl	616	4	16.7	252	7	US-11-054-515-1772	Sequence 1772, Ap
544	4	16.7	204	6	US-10-793-626-692	Sequence 692, App	617	4	16.7	254	7	US-11-054-515-1625	Sequence 1625, Ap
545	4	16.7	206	6	US-10-467-557-2550	Sequence 2550, Ap	618	4	16.7	255	6	US-10-467-557-6148	Sequence 6148, Ap
546	4	16.7	210	6	US-11-055-822-1026	Sequence 1026, Ap	619	4	16.7	255	6	US-10-467-557-7562	Sequence 7562, Ap
547	4	16.7	211	6	US-10-467-557-8728	Sequence 8728, Ap	620	4	16.7	257	6	US-10-821-234-1484	Sequence 1484, Ap
548	4	16.7	213	7	US-11-038-284-22	Sequence 22, Appl	621	4	16.7	258	6	US-10-995-561-583	Sequence 583, App
549	4	16.7	214	7	US-11-067-425A-73	Sequence 73, Appl	622	4	16.7	260	6	US-10-055-877-163	Sequence 163, App
550	4	16.7	214	7	US-11-134-241-16	Sequence 16, Appl	623	4	16.7	261	6	US-10-467-557-4282	Sequence 4282, Ap
551	4	16.7	215	7	US-11-119-212-9	Sequence 9, Appli	624	4	16.7	262	6	US-10-884-730-289	Sequence 289, App
552	4	16.7	217	6	US-10-821-234-1568	Sequence 1568, Ap	625	4	16.7	262	6	US-10-793-626-1568	Sequence 1568, Ap
553	4	16.7	217	7	US-11-080-991-58	Sequence 58, Appl	626	4	16.7	263	6	US-10-793-626-2750	Sequence 2750, Ap
554	4	16.7	217	7	US-11-206-746-2	Sequence 2, Appli	627	4	16.7	264	6	US-10-884-730-35	Sequence 35, Appl
555	4	16.7	218	6	US-10-995-561-830	Sequence 830, App	628	4	16.7	265	7	US-11-134-241-6	Sequence 6, Appli
556	4	16.7	218	7	US-11-156-084-96	Sequence 96, Appl	629	4	16.7	266	6	US-10-884-730-1	Sequence 1, Appli
557	4	16.7	219	6	US-10-793-626-2526	Sequence 2526, Ap	630	4	16.7	266	6	US-10-884-730-4	Sequence 4, Appli
558	4	16.7	219	6	US-10-883-512-92	Sequence 92, Appl	631	4	16.7	266	6	US-10-884-730-33	Sequence 33, Appl
559	4	16.7	220	6	US-10-620-787-31	Sequence 31, Appl	632	4	16.7	266	6	US-10-884-730-38	Sequence 38, Appl
560	4	16.7	221	5	US-09-978-360A-436	Sequence 436, App	633	4	16.7	266	6	US-10-884-730-47	Sequence 47, Appl
561	4	16.7	221	6	US-10-467-557-3194	Sequence 3194, Ap	634	4	16.7	266	6	US-10-884-730-79	Sequence 79, Appl
562	4	16.7	221	6	US-10-620-787-30	Sequence 30, Appl	635	4	16.7	266	6	US-10-884-730-85	Sequence 85, Appl
563	4	16.7	221	7	US-11-102-978-11	Sequence 11, Appl	636	4	16.7	266	6	US-10-884-730-116	Sequence 116, App
564	4	16.7	222	7	US-11-067-425A-74	Sequence 74, Appl	637	4	16.7	266	6	US-10-884-730-121	Sequence 121, App
565	4	16.7	222	6	US-10-467-557-7990	Sequence 7990, App	638	4	16.7	266	6	US-10-884-730-270	Sequence 270, App
566	4	16.7	222	6	US-10-454-437-380	Sequence 380, App	639	4	16.7	266	6	US-10-884-730-285	Sequence 285, App
567	4	16.7	222	7	US-11-019-711-81	Sequence 81, Appl	640	4	16.7	266	6	US-10-884-730-287	Sequence 287, App
568	4	16.7	224	6	US-10-857-780-25	Sequence 25, Appl	641	4	16.7	266	6	US-10-884-730-306	Sequence 306, App
569	4	16.7	225	6	US-10-884-730-5	Sequence 5, Appli	642	4	16.7	266	6	US-10-884-730-345	Sequence 345, App
570	4	16.7	226	6	US-10-980-388-86	Sequence 86, Appl	643	4	16.7	266	6	US-10-502-972-8	Sequence 8, Appli
571	4	16.7	227	6	US-10-670-009-4	Sequence 4, Appli	644	4	16.7	266	7	US-11-000-463-381	Sequence 381, App
572	4	16.7	228	5	US-09-978-360A-475	Sequence 475, App	645	4	16.7	266	7	US-11-000-463-853	Sequence 853, App
573	4	16.7	228	6	US-10-467-557-156	Sequence 156, App	646	4	16.7	266	7	US-11-156-084-187	Sequence 187, App
574	4	16.7	229	6	US-10-467-557-1754	Sequence 1754, Ap	647	4	16.7	267	6	US-10-623-155-352	Sequence 352, App
575	4	16.7	229	6	US-10-873-528-131	Sequence 131, App	648	4	16.7	267	6	US-10-524-647-86	Sequence 86, Appl
576	4	16.7	230	6	US-10-884-730-372	Sequence 372, App	649	4	16.7	267	7	US-11-194-890-11	Sequence 11, Appl
577	4	16.7	230	6	US-10-884-730-373	Sequence 373, App	650	4	16.7	269	6	US-10-793-626-2472	Sequence 2472, Ap
578	4	16.7	230	6	US-10-884-730-374	Sequence 374, App	651	4	16.7	270	7	US-11-052-554A-315	Sequence 315, App
579	4	16.7	230	6	US-10-884-730-375	Sequence 375, App	652	4	16.7	271	7	US-11-074-176-104	Sequence 104, App
580	4	16.7	230	6	US-10-884-730-376	Sequence 376, App	653	4	16.7	272	6	US-10-793-626-1308	Sequence 1308, Ap
581	4	16.7	230	6	US-10-454-437-294	Sequence 294, App	654	4	16.7	273	5	US-09-978-360A-709	Sequence 709, App
582	4	16.7	230	6	US-10-873-528-187	Sequence 187, App	655	4	16.7	273	7	US-11-196-475-98	Sequence 98, Appl
583	4	16.7	233	6	US-10-467-557-8268	Sequence 8268, Ap	656	4	16.7	273	7	US-11-196-475-101	Sequence 9, Appli
584	4	16.7	234	7	US-11-052-554A-348	Sequence 348, App	657	4	16.7	274	7	US-11-196-475-86	Sequence 86, Appl
585	4	16.7	236	7	US-11-156-084-284	Sequence 284, App	658	4	16.7	274	7	US-11-196-475-138	Sequence 138, App
586	4	16.7	237	6	US-10-884-730-2	Sequence 2, Appli	659	4	16.7	274	7	US-11-156-062-2	Sequence 2, Appli
587	4	16.7	237	6	US-10-884-730-10	Sequence 10, Appl	660	4	16.7	274	7	US-11-156-062-4	Sequence 4, Appli
588	4	16.7	237	6	US-10-884-730-12	Sequence 12, Appl	661	4	16.7	274	7	US-11-156-062-6	Sequence 6, Appli
589	4	16.7	237	6	US-10-884-730-22	Sequence 22, Appl	662	4	16.7	274	7	US-11-156-062-8	Sequence 8, Appli
590	4	16.7	237	6	US-10-884-730-36	Sequence 36, Appl	663	4	16.7	274	7	US-11-156-062-10	Sequence 10, Appl
591	4	16.7	237	6	US-10-884-730-41	Sequence 41, Appl	664	4	16.7	274	7	US-11-156-062-12	Sequence 12, Appl
592	4	16.7	237	6	US-10-884-730-113	Sequence 113, App	665	4	16.7	274	7	US-11-156-062-14	Sequence 14, Appl
593	4	16.7	237	6	US-10-884-730-120	Sequence 120, App	666	4	16.7	274	7	US-11-156-062-16	Sequence 16, Appl
594	4	16.7	237	6	US-10-884-730-175	Sequence 175, App	667	4	16.7	274	7	US-11-156-062-18	Sequence 18, Appl
595	4	16.7	237	6	US-10-884-730-177	Sequence 177, App	668	4	16.7	274	7	US-10-467-557-1544	Sequence 1544, Ap
596	4	16.7	237	6	US-10-884-730-203	Sequence 203, App	669	4	16.7	275	6	US-11-110-977-2	Sequence 2, Appli
597	4	16.7	237	6	US-10-884-730-307	Sequence 307, App	670	4	16.7	275	7	US-11-091-100-16	Sequence 16, Appl
598	4	16.7	237	6	US-10-884-730-317	Sequence 317, App	671	4	16.7	276	7	US-11-091-100-16	Sequence 16, Appl
599	4	16.7	237	6	US-10-884-730-318	Sequence 318, App	672	4	16.7	277	6	US-10-793-626-94	Sequence 94, Appl
600	4	16.7	237	6	US-10-884-730-336	Sequence 336, App	673	4	16.7	277	7	US-11-156-084-180	Sequence 180, App
601	4	16.7	237	6	US-10-884-730-355	Sequence 355, App	674	4	16.7	277	6	US-10-883-512-105	Sequence 105, App
602	4	16.7	237	6	US-10-884-730-356	Sequence 356, App	675	4	16.7	280	6	US-10-485-517-240	Sequence 240, App
603	4	16.7	237	6	US-10-884-730-357	Sequence 357, App	676	4	16.7	280	7	US-11-170-653-66	Sequence 66, Appl
604	4	16.7	237	6	US-10-884-730-358	Sequence 358, App	677	4	16.7	284	7	US-11-089-551A-36	Sequence 36, Appl
605	4	16.7	237	6	US-10-884-730-360	Sequence 360, App	678	4	16.7	285	7	US-11-179-843-3	Sequence 3, Appli
606	4	16.7	237	6	US-10-884-730-361	Sequence 361, App	679	4	16.7	289	6	US-10-793-626-3254	Sequence 3254, Ap
607	4	16.7	237	6	US-10-884-730-362	Sequence 362, App	680	4	16.7	291	7	US-11-096-070-36	Sequence 36, Appl
608	4	16.7	238	6	US-10-467-557-1308	Sequence 1308, Ap	681	4	16.7	295	6	US-10-467-557-1604	Sequence 1604, Ap
609	4	16.7	238	7	US-11-194-890-12	Sequence 12, Appl	682	4	16.7	295	6	US-10-995-561-581	Sequence 581, App

683	4	16.7	298	7	US-11-025-834A-14	Sequence 14, Appl	756	4	16.7	346	7	US-11-118-809-8	Sequence 8, Appl
684	4	16.7	299	6	US-10-623-155-354	Sequence 354, App	757	4	16.7	347	6	US-10-793-626-462	Sequence 462, App
685	4	16.7	300	7	US-11-156-084-339	Sequence 339, App	758	4	16.7	347	6	US-10-793-626-1268	Sequence 1268, Ap
686	4	16.7	301	7	US-11-025-834A-21	Sequence 21, Appl	759	4	16.7	347	6	US-10-821-234-1136	Sequence 1136, Ap
687	4	16.7	302	7	US-11-152-569-10	Sequence 10, Appl	760	4	16.7	347	6	US-10-821-234-1379	Sequence 1379, Ap
688	4	16.7	303	7	US-11-119-212-13	Sequence 13, Appl	761	4	16.7	347	6	US-10-512-277-3	Sequence 3, Appl
689	4	16.7	302	7	US-11-119-212-25	Sequence 25, Appl	762	4	16.7	348	6	US-10-512-277-3	Sequence 4, Appl
690	4	16.7	303	6	US-10-467-962B-16	Sequence 16, Appl	763	4	16.7	348	6	US-10-674-767-4	Sequence 4, Appl
691	4	16.7	303	6	US-10-467-962B-45	Sequence 45, Appl	764	4	16.7	348	6	US-10-667-295-121	Sequence 121, App
692	4	16.7	303	6	US-10-878-556A-74	Sequence 74, Appl	765	4	16.7	348	6	US-10-512-277-1	Sequence 1, Appl
693	4	16.7	303	7	US-11-134-241-2	Sequence 2, Appl	766	4	16.7	348	7	US-11-102-497-3	Sequence 3, Appl
694	4	16.7	304	6	US-11-156-084-291	Sequence 291, App	767	4	16.7	348	7	US-11-102-497-11	Sequence 11, Appl
695	4	16.7	305	6	US-10-995-561-582	Sequence 582, App	768	4	16.7	349	7	US-11-182-946-13	Sequence 13, Appl
696	4	16.7	306	6	US-10-793-626-382	Sequence 382, App	769	4	16.7	349	7	US-11-055-822-186	Sequence 186, App
697	4	16.7	306	6	US-10-467-657-1318	Sequence 1318, Ap	770	4	16.7	350	6	US-10-667-295-120	Sequence 120, App
698	4	16.7	308	6	US-11-156-084-304	Sequence 304, App	771	4	16.7	350	6	US-10-517-939-176	Sequence 176, App
699	4	16.7	309	6	US-10-793-626-1608	Sequence 1608, Ap	772	4	16.7	350	6	US-10-517-939-192	Sequence 192, App
700	4	16.7	309	7	US-11-138-642-1	Sequence 1, Appl	773	4	16.7	351	6	US-11-132-285-41	Sequence 41, Appl
701	4	16.7	309	7	US-11-138-882-1	Sequence 1, Appl	774	4	16.7	351	6	US-10-729-121-2	Sequence 2, Appl
702	4	16.7	310	6	US-10-131-826A-538	Sequence 538, App	775	4	16.7	351	7	US-11-118-809-6	Sequence 6, Appl
703	4	16.7	310	7	US-11-000-463-357	Sequence 357, App	776	4	16.7	352	7	US-11-122-849-2	Sequence 2, Appl
704	4	16.7	310	7	US-11-025-834A-13	Sequence 13, Appl	777	4	16.7	352	7	US-11-037-243-95	Sequence 95, Appl
705	4	16.7	310	7	US-11-025-834A-15	Sequence 15, Appl	778	4	16.7	354	7	US-11-052-554A-156	Sequence 156, App
706	4	16.7	310	7	US-11-156-084-301	Sequence 301, App	779	4	16.7	355	7	US-11-082-389-6	Sequence 6, Appl
707	4	16.7	311	6	US-10-467-657-3740	Sequence 3740, Ap	780	4	16.7	355	7	US-11-182-946-14	Sequence 14, Appl
708	4	16.7	311	7	US-11-000-463-345	Sequence 345, App	781	4	16.7	355	7	US-11-205-109-31	Sequence 31, Appl
709	4	16.7	311	7	US-11-000-463-829	Sequence 829, App	782	4	16.7	356	6	US-10-793-626-2054	Sequence 2054, Ap
710	4	16.7	311	7	US-11-156-084-176	Sequence 176, App	783	4	16.7	356	7	US-11-143-986-8	Sequence 8, Appl
711	4	16.7	311	7	US-11-156-084-330	Sequence 330, App	784	4	16.7	356	7	US-11-143-986-9	Sequence 9, Appl
712	4	16.7	312	6	US-10-527-500-11	Sequence 11, Appl	785	4	16.7	358	6	US-10-838-616-12	Sequence 12, Appl
713	4	16.7	312	7	US-11-156-084-331	Sequence 331, App	786	4	16.7	358	7	US-11-129-143-111	Sequence 111, App
714	4	16.7	313	7	US-11-099-691-4	Sequence 4, Appl	787	4	16.7	359	7	US-11-205-460-4	Sequence 4, Appl
715	4	16.7	314	7	US-11-143-980-56	Sequence 56, Appl	788	4	16.7	359	7	US-11-129-143-71	Sequence 71, Appl
716	4	16.7	315	6	US-10-454-437-220	Sequence 220, App	789	4	16.7	360	6	US-10-467-962B-75	Sequence 75, Appl
717	4	16.7	315	7	US-11-156-084-313	Sequence 313, App	790	4	16.7	360	6	US-10-878-556A-134	Sequence 134, App
718	4	16.7	315	7	US-11-156-084-353	Sequence 353, App	791	4	16.7	360	6	US-10-878-556A-137	Sequence 137, App
719	4	16.7	319	6	US-10-467-657-640	Sequence 640, App	792	4	16.7	361	7	US-11-186-284-115	Sequence 115, App
720	4	16.7	319	6	US-10-467-657-1760	Sequence 1760, Ap	793	4	16.7	361	7	US-11-129-143-108	Sequence 108, App
721	4	16.7	319	6	US-10-467-657-2324	Sequence 2324, Ap	794	4	16.7	362	6	US-10-821-234-1148	Sequence 1148, Ap
722	4	16.7	319	6	US-10-467-657-6604	Sequence 6604, Ap	795	4	16.7	363	6	US-10-995-561-804	Sequence 804, App
723	4	16.7	320	6	US-10-793-626-2988	Sequence 2988, Ap	796	4	16.7	363	6	US-10-055-877-14	Sequence 14, Appl
724	4	16.7	321	6	US-10-055-877-338	Sequence 338, App	797	4	16.7	363	7	US-11-055-822-1156	Sequence 1156, Ap
725	4	16.7	322	6	US-10-454-437-218	Sequence 218, App	798	4	16.7	363	7	US-11-156-084-199	Sequence 199, App
726	4	16.7	322	7	US-11-055-822-66	Sequence 66, App	799	4	16.7	363	7	US-11-156-084-347	Sequence 347, App
727	4	16.7	324	7	US-11-119-212-15	Sequence 15, Appl	800	4	16.7	365	6	US-10-821-234-1575	Sequence 1575, Ap
728	4	16.7	324	7	US-11-063-343-20	Sequence 20, Appl	801	4	16.7	365	7	US-11-024-959-403	Sequence 403, App
729	4	16.7	326	7	US-11-119-212-19	Sequence 19, Appl	802	4	16.7	366	7	US-11-000-463-457	Sequence 457, App
730	4	16.7	326	7	US-11-156-084-239	Sequence 239, App	803	4	16.7	369	7	US-11-024-959-485	Sequence 485, App
731	4	16.7	326	7	US-11-156-084-28	Sequence 28, Appl	804	4	16.7	372	7	US-11-143-986-5	Sequence 5, Appl
732	4	16.7	329	7	US-11-156-084-46	Sequence 46, Appl	805	4	16.7	372	7	US-11-143-986-6	Sequence 6, Appl
733	4	16.7	329	7	US-11-156-084-171	Sequence 171, App	806	4	16.7	372	7	US-11-024-959-362	Sequence 362, App
734	4	16.7	329	7	US-11-156-084-243	Sequence 243, App	807	4	16.7	374	7	US-11-000-463-453	Sequence 453, App
735	4	16.7	330	6	US-10-453-372-516	Sequence 516, App	808	4	16.7	375	6	US-10-667-295-119	Sequence 119, App
736	4	16.7	330	7	US-11-205-460-2	Sequence 2, Appl	809	4	16.7	375	7	US-11-139-406-3	Sequence 3, Appl
737	4	16.7	331	6	US-10-453-372-508	Sequence 508, App	810	4	16.7	376	6	US-10-467-657-6138	Sequence 6138, Ap
738	4	16.7	331	7	US-11-129-143-87	Sequence 87, Appl	811	4	16.7	377	6	US-10-793-626-3014	Sequence 3014, Ap
739	4	16.7	331	7	US-11-149-403-4	Sequence 4, Appl	812	4	16.7	377	6	US-10-821-234-1436	Sequence 1436, Ap
740	4	16.7	332	6	US-10-793-626-540	Sequence 540, App	813	4	16.7	378	6	US-10-485-517-410	Sequence 410, App
741	4	16.7	332	6	US-10-793-626-2562	Sequence 2562, Ap	814	4	16.7	378	6	US-10-793-626-1428	Sequence 1428, App
742	4	16.7	333	7	US-11-024-959-349	Sequence 349, App	815	4	16.7	378	6	US-10-995-561-891	Sequence 891, App
743	4	16.7	335	6	US-10-453-372-512	Sequence 512, App	816	4	16.7	379	7	US-11-152-892-7	Sequence 7, Appl
744	4	16.7	336	6	US-10-793-626-1858	Sequence 1858, Ap	817	4	16.7	379	6	US-10-793-626-2810	Sequence 2810, Ap
745	4	16.7	336	6	US-10-453-372-510	Sequence 510, App	818	4	16.7	379	7	US-11-109-156-16	Sequence 16, Appl
746	4	16.7	337	6	US-10-467-962B-97	Sequence 97, Appl	819	4	16.7	379	7	US-11-156-062-23	Sequence 23, Appl
747	4	16.7	337	7	US-11-102-497-5	Sequence 5, Appl	820	4	16.7	380	6	US-10-793-626-702	Sequence 702, App
748	4	16.7	337	7	US-11-102-497-12	Sequence 12, Appl	821	4	16.7	380	7	US-11-089-551A-25	Sequence 25, Appl
749	4	16.7	338	6	US-10-821-234-1565	Sequence 1565, Ap	822	4	16.7	381	7	US-11-194-246-340	Sequence 340, App
750	4	16.7	338	7	US-11-055-822-830	Sequence 830, App	823	4	16.7	384	6	US-11-052-554A-299	Sequence 299, App
751	4	16.7	339	7	US-11-043-542-40	Sequence 40, Appl	824	4	16.7	384	6	US-10-838-616-28	Sequence 28, Appl
752	4	16.7	344	7	US-11-083-800-10	Sequence 10, Appl	825	4	16.7	385	7	US-11-060-029-2	Sequence 2, Appl
753	4	16.7	344	7	US-11-108-172-1085	Sequence 1085, Ap	826	4	16.7	386	7	US-11-143-986-2	Sequence 2, Appl
754	4	16.7	345	7	US-11-100-352-4	Sequence 4, Appl	827	4	16.7	386	7	US-11-143-986-3	Sequence 3, Appl
755	4	16.7	346	7	US-11-157-930-2	Sequence 2, Appl	828	4	16.7	387	7	US-11-092-140-17	Sequence 17, Appl

829	4	16.7	388	6	US-10-527-500-17	Sequence 17, Appl	902	4	16.7	447	7	US-11-024-959-505	Sequence 505, App
830	4	16.7	388	7	US-11-046-668-7	Sequence 7, Appli	903	4	16.7	448	6	US-10-793-626-1728	Sequence 1728, Ap
831	4	16.7	388	7	US-11-082-389-220	Sequence 220, App	904	4	16.7	448	6	US-10-763-712A-69	Sequence 69, Appl
832	4	16.7	388	7	US-11-129-143-47	Sequence 47, Appl	905	4	16.7	448	6	US-10-763-712A-112	Sequence 112, App
833	4	16.7	389	7	US-11-074-176-324	Sequence 324, App	906	4	16.7	448	6	US-10-995-561-793	Sequence 793, App
834	4	16.7	389	7	US-11-060-008-11	Sequence 11, Appl	907	4	16.7	448	7	US-11-055-822-826	Sequence 826, App
835	4	16.7	393	6	US-10-485-517-316	Sequence 316, App	908	4	16.7	448	7	US-11-052-554A-230	Sequence 230, App
836	4	16.7	394	6	US-10-793-626-300	Sequence 300, App	909	4	16.7	449	6	US-10-763-712A-73	Sequence 73, Appl
837	4	16.7	395	6	US-10-838-616-26	Sequence 26, Appl	910	4	16.7	451	6	US-10-793-626-2908	Sequence 2908, Ap
838	4	16.7	397	6	US-10-793-626-644	Sequence 644, App	911	4	16.7	451	6	US-10-821-234-1491	Sequence 1491, Ap
839	4	16.7	397	7	US-11-022-562-223	Sequence 223, App	912	4	16.7	451	6	US-10-641-678-56	Sequence 56, Appl
840	4	16.7	398	6	US-10-382-234A-4	Sequence 4, Appli	913	4	16.7	451	6	US-10-641-678-57	Sequence 57, Appl
841	4	16.7	398	6	US-10-517-939-210	Sequence 210, App	914	4	16.7	452	7	US-11-024-959-451	Sequence 451, App
842	4	16.7	398	7	US-11-046-668-9	Sequence 9, Appli	915	4	16.7	453	6	US-10-793-626-3260	Sequence 3260, Ap
843	4	16.7	398	7	US-11-052-554A-252	Sequence 252, App	916	4	16.7	453	7	US-11-082-389-198	Sequence 198, App
844	4	16.7	399	6	US-10-392-234A-10	Sequence 10, Appl	917	4	16.7	453	7	US-11-052-554A-224	Sequence 224, App
845	4	16.7	399	6	US-10-821-234-1031	Sequence 1031, Ap	918	4	16.7	454	7	US-11-089-551A-35	Sequence 35, Appl
846	4	16.7	400	6	US-10-454-437-306	Sequence 306, App	919	4	16.7	454	7	US-11-196-475-160	Sequence 160, App
847	4	16.7	401	6	US-10-641-678-33	Sequence 33, Appl	920	4	16.7	455	6	US-10-793-626-718	Sequence 718, App
848	4	16.7	401	6	US-10-838-616-18	Sequence 18, Appl	921	4	16.7	455	6	US-10-880-881-4	Sequence 4, Appli
849	4	16.7	401	7	US-11-097-749-3	Sequence 3, Appli	922	4	16.7	458	7	US-11-069-642-3	Sequence 3, Appli
850	4	16.7	401	7	US-11-134-795-28	Sequence 28, Appl	923	4	16.7	458	7	US-11-020-486-2	Sequence 2, Appli
851	4	16.7	401	7	US-11-052-554A-66	Sequence 66, Appl	924	4	16.7	466	6	US-10-467-657-2360	Sequence 2360, Ap
852	4	16.7	402	7	US-11-052-554A-184	Sequence 184, App	925	4	16.7	466	7	US-11-074-176-58	Sequence 58, Appl
853	4	16.7	403	6	US-10-528-031-7	Sequence 7, Appli	926	4	16.7	467	6	US-11-127-877-41	Sequence 41, Appl
854	4	16.7	404	6	US-10-667-295-112	Sequence 112, App	927	4	16.7	467	6	US-10-519-238-2	Sequence 2, Appli
855	4	16.7	404	6	US-10-793-626-398	Sequence 398, App	928	4	16.7	467	7	US-11-000-463-452	Sequence 452, App
856	4	16.7	405	7	US-11-089-551A-29	Sequence 29, Appl	929	4	16.7	467	7	US-11-000-463-924	Sequence 924, App
857	4	16.7	405	7	US-11-089-551A-50	Sequence 50, Appl	930	4	16.7	467	7	US-11-000-463-925	Sequence 925, App
858	4	16.7	406	7	US-11-074-176-92	Sequence 92, Appl	931	4	16.7	468	6	US-10-957-569-28	Sequence 28, Appl
859	4	16.7	410	6	US-10-513-759-14	Sequence 14, Appl	932	4	16.7	468	6	US-10-793-626-1648	Sequence 1648, Ap
860	4	16.7	411	7	US-11-119-212-17	Sequence 17, Appl	933	4	16.7	469	6	US-10-063-703-58	Sequence 58, Appl
861	4	16.7	412	7	US-11-074-176-24	Sequence 24, Appl	934	4	16.7	469	7	US-11-102-240-58	Sequence 58, Appl
862	4	16.7	412	7	US-11-168-874-12	Sequence 12, Appl	935	4	16.7	469	7	US-11-024-959-398	Sequence 398, App
863	4	16.7	413	7	US-11-060-029-4	Sequence 4, Appli	936	4	16.7	471	7	US-11-156-084-23	Sequence 23, Appl
864	4	16.7	413	7	US-11-119-212-21	Sequence 21, Appl	937	4	16.7	472	6	US-10-793-626-658	Sequence 658, App
865	4	16.7	414	6	US-10-995-561-803	Sequence 803, App	938	4	16.7	472	6	US-10-793-626-1902	Sequence 1902, Ap
866	4	16.7	415	6	US-10-793-626-1406	Sequence 1406, Ap	939	4	16.7	480	6	US-10-793-626-2852	Sequence 2852, Ap
867	4	16.7	416	6	US-10-793-626-196	Sequence 196, App	940	4	16.7	480	6	US-10-793-626-2986	Sequence 2986, Ap
868	4	16.7	417	6	US-10-613-744-2	Sequence 2, Appli	941	4	16.7	480	7	US-11-080-991-76	Sequence 76, Appl
869	4	16.7	419	6	US-10-793-626-2516	Sequence 2516, Ap	942	4	16.7	480	7	US-11-132-142-6	Sequence 6, Appli
870	4	16.7	420	6	US-10-520-820-14	Sequence 14, Appl	943	4	16.7	483	7	US-11-037-829A-5	Sequence 5, Appli
871	4	16.7	421	6	US-10-793-626-144	Sequence 144, App	944	4	16.7	484	6	US-10-467-657-6816	Sequence 6816, Ap
872	4	16.7	422	6	US-10-467-657-212	Sequence 212, App	945	4	16.7	485	6	US-10-485-517-136	Sequence 136, App
873	4	16.7	422	6	US-10-467-657-6516	Sequence 6516, Ap	946	4	16.7	486	6	US-10-821-234-1063	Sequence 1063, Ap
874	4	16.7	422	6	US-10-873-528-25	Sequence 25, Appl	947	4	16.7	489	6	US-10-793-626-3088	Sequence 3088, Ap
875	4	16.7	422	6	US-10-873-528-77	Sequence 77, Appl	948	4	16.7	491	6	US-10-793-626-3178	Sequence 3178, Ap
876	4	16.7	423	6	US-10-995-561-794	Sequence 794, App	949	4	16.7	491	7	US-11-069-642-137	Sequence 137, App
877	4	16.7	423	6	US-10-995-561-795	Sequence 795, App	950	4	16.7	491	7	US-11-069-642-191	Sequence 191, App
878	4	16.7	423	7	US-10-454-437-304	Sequence 304, App	951	4	16.7	491	7	US-11-212-443-191	Sequence 1558, Ap
879	4	16.7	423	7	US-11-156-084-22	Sequence 22, Appl	952	4	16.7	500	6	US-10-793-626-1558	Sequence 1558, Ap
880	4	16.7	424	6	US-10-485-517-264	Sequence 264, App	953	4	16.7	501	6	US-10-957-569-18	Sequence 18, Appl
881	4	16.7	424	6	US-10-485-517-281	Sequence 281, App	954	4	16.7	501	6	US-11-167-856-22	Sequence 22, Appl
882	4	16.7	424	6	US-10-880-881-6	Sequence 6, Appli	955	4	16.7	504	6	US-10-507-928-6	Sequence 6, Appli
883	4	16.7	425	6	US-10-821-234-990	Sequence 990, App	956	4	16.7	504	6	US-11-029-465-6	Sequence 6, Appli
884	4	16.7	430	6	US-10-793-626-130	Sequence 130, App	957	4	16.7	505	6	US-10-507-928-8	Sequence 8, Appli
885	4	16.7	430	6	US-10-467-657-2346	Sequence 2346, Ap	958	4	16.7	505	7	US-11-029-465-8	Sequence 8, Appli
886	4	16.7	430	7	US-11-126-313-35	Sequence 35, Appl	959	4	16.7	507	7	US-11-033-039-96	Sequence 96, Appl
887	4	16.7	430	7	US-11-126-313-36	Sequence 36, Appl	960	4	16.7	510	6	US-10-485-517-320	Sequence 320, App
888	4	16.7	431	7	US-11-169-013-2	Sequence 2, Appli	961	4	16.7	510	7	US-11-093-814-1	Sequence 1, Appli
889	4	16.7	436	6	US-10-131-826A-404	Sequence 404, App	962	4	16.7	512	6	US-10-467-657-4870	Sequence 4870, Ap
890	4	16.7	437	6	US-10-821-234-1608	Sequence 1608, Ap	963	4	16.7	513	6	US-10-131-826A-192	Sequence 192, App
891	4	16.7	438	6	US-10-821-234-1051	Sequence 1051, Ap	964	4	16.7	513	6	US-10-485-517-233	Sequence 233, App
892	4	16.7	438	7	US-11-074-176-152	Sequence 152, App	965	4	16.7	513	6	US-10-995-561-566	Sequence 566, App
893	4	16.7	439	7	US-11-034-569-16	Sequence 16, Appl	966	4	16.7	514	6	US-10-840-688-2	Sequence 2, Appli
894	4	16.7	439	7	US-11-093-814-2	Sequence 2, Appli	967	4	16.7	514	6	US-10-840-688-3	Sequence 3, Appli
895	4	16.7	446	6	US-10-667-295-111	Sequence 111, App	968	4	16.7	514	6	US-10-840-688-4	Sequence 4, Appli
896	4	16.7	446	7	US-11-108-172-1121	Sequence 1121, Ap	969	4	16.7	514	6	US-10-840-688-5	Sequence 5, Appli
897	4	16.7	447	6	US-10-467-657-364	Sequence 364, App	970	4	16.7	514	6	US-10-840-688-6	Sequence 6, Appli
898	4	16.7	447	6	US-10-467-657-4034	Sequence 4034, Ap	971	4	16.7	514	6	US-10-840-688-7	Sequence 7, Appli
899	4	16.7	447	6	US-10-467-657-7050	Sequence 7050, Ap	972	4	16.7	514	6	US-10-840-688-8	Sequence 8, Appli
900	4	16.7	447	7	US-11-196-475-162	Sequence 162, App	973	4	16.7	514	6	US-10-840-688-9	Sequence 9, Appli
901	4	16.7	447	7	US-11-024-959-452	Sequence 452, App	974	4	16.7	514	6	US-10-840-688-10	Sequence 10, Appli

```
975      4 16.7 514 6 US-10-840-688-11
976      4 16.7 514 6 US-10-840-688-12
977      4 16.7 514 6 US-10-840-688-13
978      4 16.7 514 6 US-10-840-688-21
979      4 16.7 518 6 US-10-821-234-1165
980      4 16.7 521 7 US-11-105-268-58
981      4 16.7 522 6 US-10-793-626-604
982      4 16.7 522 6 US-10-517-939-286
983      4 16.7 523 6 US-10-453-372-1006
984      4 16.7 523 6 US-10-453-372-1008
985      4 16.7 524 6 US-10-878-556A-131
986      4 16.7 525 6 US-10-878-556A-171
987      4 16.7 527 7 US-11-120-543-18
988      4 16.7 528 6 US-10-467-657-1042
989      4 16.7 529 6 US-10-632-150-44
990      4 16.7 529 7 US-11-073-457-44
991      4 16.7 529 7 US-11-073-460-44
992      4 16.7 531 7 US-11-096-070-4
993      4 16.7 532 6 US-10-793-626-546
994      4 16.7 533 7 US-11-145-035-15
995      4 16.7 534 7 US-11-089-551A-52
996      4 16.7 537 6 US-10-504-364-6
997      4 16.7 537 6 US-10-504-364-7
998      4 16.7 537 7 US-11-129-442-47
999      4 16.7 540 7 US-11-045-802-35
1000     4 16.7 546 6 US-10-520-820-8
```

ALIGNMENTS

```
RESULT 1
US-10-821-234-1266
; Sequence 1266, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1266
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1266
```

```
Query Match      100.0%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LRFDSQTKSIFEQETNNNSSFTT 24
      |||||
Db      35 LRFDSQTKSIFEQETNNNSSFTT 58
```

```
RESULT 2
US-11-052-554A-58
; Sequence 58, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
```

```
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-58

Query Match      25.0%; Score 6; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTKS 9
      |||||
Db      99 DSQTKS 104

RESULT 3
US-11-089-551A-4
; Sequence 4, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT APPLICATION NUMBER: US/11/089,551A
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/559,286
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-4

Query Match      25.0%; Score 6; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNSS 21
      |||||
Db      47 NNNSS 52

RESULT 4
US-10-467-962B-95
; Sequence 95, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 95
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-95
```

```
Query Match          25.0%; Score 6; DB 6; Length 592;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20
Db 13 TNNNS 18

RESULT 5
US-10-524-647-112
; Sequence 112, Application US/10524647
; Publication No. US20050281909A1
; GENERAL INFORMATION:
; APPLICANT: Flachmann, Ralf
; APPLICANT: Sauer, Matt
; APPLICANT: Schopfer, Christel R.
; APPLICANT: Klebsattel, Martin
; APPLICANT: Pfeiffer, Angelika-Maria
; APPLICANT: Luck, Thomas
; APPLICANT: Voeste, Dirk
; TITLE OF INVENTION: Use of astaxanthin-containing plants or parts of plants of the
; TITLE OF INVENTION: genus Tagetes as feedstuffs
; FILE REFERENCE: 13173-00004-US
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/009109
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: DE 102 38 980.2
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 38 978.0
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 38 979.9
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 53 112.9
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: DE 102 58 971.2
; PRIOR FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 112
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-524-647-112

Query Match          25.0%; Score 6; DB 6; Length 592;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20
Db 13 TNNNS 18

RESULT 6
US-11-087-227-24
; Sequence 24, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-24

Query Match          25.0%; Score 6; DB 7; Length 1531;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FDSQTK 8
Db 373 FDSQTK 378

RESULT 7
US-11-186-284-211
; Sequence 211, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-211

Query Match          25.0%; Score 6; DB 7; Length 1531;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FDSQTK 8
Db 373 FDSQTK 378

RESULT 8
US-11-108-528-84
; Sequence 84, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
```

```
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 1613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-528-84

Query Match          25.0%; Score 6; DB 7; Length 1613;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 ETNNNN 19
Db      648 ETNNNN 653

RESULT 9
US-11-108-528-86
; Sequence 86, Application US/11/108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 1613
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-86

Query Match          25.0%; Score 6; DB 7; Length 1613;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 ETNNNN 19
Db      648 ETNNNN 653

RESULT 10
US-11-013-759-9
; Sequence 9, Application US/11/013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:jb

; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 1613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-528-84

Query Match          25.0%; Score 6; DB 7; Length 1613;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 ETNNNN 19
Db      648 ETNNNN 653

RESULT 11
US-11-045-024-616
; Sequence 616, Application US/11/045024
; Publication No. US20050271876A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-616

Query Match          20.8%; Score 5; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNNS 20
Db      3 NNNNS 7
```

```
RESULT 12
US-11-045-024-770
; Sequence 770, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007 US/11/045,024
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-770

Query Match          20.8%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 20
DB 4 NNNNS 8

RESULT 13
US-10-467-657-8871
; Sequence 8871, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8871
; LENGTH: 10
; TYPE: PRT
; ORGANISM: NEISSERIA GONORRHOEA
US-10-467-657-8871

Query Match          20.8%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFYT 24
DB 14 SSFYT 18

RESULT 14
US-10-467-657-6884
; Sequence 6884, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6884
; LENGTH: 56
; TYPE: PRT
; ORGANISM: NEISSERIA GONORRHOEA
US-10-467-657-6884

Query Match          20.8%; Score 5; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFYT 24
DB 14 SSFYT 18

RESULT 15
US-09-978-360A-737
; Sequence 737, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
```

```
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8871

Query Match          20.8%; Score 5; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TKSIF 11
DB 18 TKSIF 22

RESULT 14
US-10-467-657-6884
; Sequence 6884, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6884
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6884

Query Match          20.8%; Score 5; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFYT 24
DB 14 SSFYT 18

RESULT 15
US-09-978-360A-737
; Sequence 737, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
```

```

; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 737
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18..-1
US-09-978-360A-737

```

```

Query Match      20.8%; Score 5; DB 5; Length 78;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 TKSIF 11
        |||||
Db      48 TKSIF 52

```

Search completed: January 20, 2006, 17:47:39
Job time : 4.53846 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:35:41 ; Search time 5.53846 Seconds
(without alignments)
416.939 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58
Perfect score: 24
Sequence: 1 LRFDSTQKSI FEQETNNNSSFYT 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

```
Database :      PIR_80:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	24	100.0	228	1	A40402	CD9 antigen [valid	
2	24	100.0	228	1	A42329	CD9 antigen - gree	
3	16	66.7	226	1	S3262	CD9 antigen - rat	
4	14	58.3	226	1	JX0221	CD9 antigen - bovi	
5	14	58.3	226	2	I49589	antigen - mouse	
6	8	33.3	680	2	H84774	probable homeodoma	
7	7	29.2	279	2	A96913	ABC-type sulfate t	
8	7	29.2	419	2	T18420	hypothetical prote	
9	7	29.2	1274	2	S59405	probable membrane	
10	6	25.0	69	1	A48180	small acid-soluble	
11	6	25.0	92	2	B85911	hypothetical prote	
12	6	25.0	107	2	S52508	probable membrane	
13	6	25.0	131	2	B91067	hypothetical lipop	
14	6	25.0	136	2	T17640	hypothetical prote	
15	6	25.0	150	2	D95131	hypothetical prote	
16	6	25.0	183	2	T48609	hypothetical prote	
17	6	25.0	180	2	B45613	surface antigen FU	
18	6	25.0	194	2	AH3405	hypothetical cytos	
19	6	25.0	208	2	T46896	merozoite surface	
20	6	25.0	213	2	B65019	hypothetical prote	
21	6	25.0	229	2	F84685	hypothetical prote	
22	6	25.0	234	2	S14469	asparagine-rich pr	
23	6	25.0	241	2	T06067	hypothetical prote	
24	6	25.0	257	2	G87473	transcription regu	
25	6	25.0	272	2	G71618	merozoite surface	
26	6	25.0	274	1	JQ0957	myb-related protei	
27	6	25.0	274	2	A45632	merozoite surface	
28	6	25.0	278	2	S9310	merozoite surface	
29	6	25.0	280	2	T19362	hypothetical prote	

merozoite surface
merozoite 45K surf
hypothetical prote
merozoite 45K surf
merozoite 45K surf
merozoite 45K surf
merozoite protein A
merozoite 45K surf
glutathione transfe
probable DOF zinc
aspartate kinase (
hypothetical prote
heat shock transcr
Knox protein 1 - g
trehalase-6-phosph
ERD1 protein - yea
ecdysone-inducible
KNAT1 homeobox-li
homeotic protein S
hypothetical prote
variant-specific s
weakly methyltrans
SUF1 protein - yea
hypothetical prote
hypothetical prote
SIN3 protein-bindin
hypothetical prote
cyclin A-type (Glo
cyclin A-type (Glo
cyclin, A-type - c
Abd-B protein - fr
homeotic protein A
steroid 17 alpha-h
steroid 17alpha-mo
fork head domain p
hypothetical prote
hypothetical prote
PHD finger protein
phosphoprotein pho
hypothetical prote
hypothetical prote
phosphoprotein pho
probable homeodoma
DNA polymerase III
PSP2 protein - yea
DNA polymerase III
hydroxymethylgluta
hypothetical prote
probable transcrip
probable GT-like t
hypothetical prote
homeotic protein B
homeotic protein B
protein kinase (8C
hypothetical prote
hypothetical prote
hypothetical threo
probable membrane
transcription fact
hypothetical prote
hypothetical prote
envelope protein E
hypothetical prote
ODV-B6 orf46 - Bo
occlusion-derived
BRCore-NS-23 prote
uncharacterized co
GIN3 protein - yea
tyrosine kinase-re
hypothetical prote
box A-binding fact
hypothetical prote
hypothetical prote
aconitate hydratase
ecdysone-inducible
hypothetical prote
finger protein AZF
protein phosphatas

103	6	25.0	932	2	S09151	176	5	20.8	67	1	B48180	small acid-soluble
104	6	25.0	941	2	T49136	177	5	20.8	68	1	A24033	small acid-soluble
105	6	25.0	947	2	T08605	178	5	20.8	70	1	A61028	small acid-soluble
106	6	25.0	950	1	PH6V81	179	5	20.8	72	1	C48180	SLA class II DR-be
107	6	25.0	959	2	D71619	180	5	20.8	72	2	I47166	HLA-DRB sigma anti
108	6	25.0	960	1	A39651	181	5	20.8	72	2	PH0164	HLA-DRB sigma anti
109	6	25.0	969	2	S54594	182	5	20.8	72	2	PH0154	HLA-DRB sigma anti
110	6	25.0	970	2	F64230	183	5	20.8	72	2	T70169	DRB1 transplanta
111	6	25.0	980	2	H64593	184	5	20.8	73	2	I79651	hypothetical prote
112	6	25.0	1061	2	T18085	185	5	20.8	73	2	AB1810	MHC protein - cott
113	6	25.0	1074	2	G96504	186	5	20.8	76	2	I68908	hypothetical prote
114	6	25.0	1111	1	A42640	187	5	20.8	76	2	S70428	hypothetical prote
115	6	25.0	1113	2	S28925	188	5	20.8	77	2	B30849	unknown protein en
116	6	25.0	1121	2	S54504	189	5	20.8	77	2	H85706	calcium-binding pr
117	6	25.0	1123	2	T28139	190	5	20.8	79	1	KLPGI	MHC HLA-DR-beta-1
118	6	25.0	1138	2	A48944	191	5	20.8	80	2	I54469	MHC HLA-DR-beta-1
119	6	25.0	1140	2	S73786	192	5	20.8	80	2	I68777	HLA DRB1*1202 - hu
120	6	25.0	1154	2	S69206	193	5	20.8	81	2	I54550	apovitellenin I -
121	6	25.0	1178	2	S54073	194	5	20.8	82	1	VLDK1	apovitellenin I -
122	6	25.0	1228	2	S37621	195	5	20.8	82	2	I61810	gene MHC DQ-beta 1
123	6	25.0	1244	2	S25327	196	5	20.8	82	2	I51147	MHC class II beta
124	6	25.0	1256	2	S14556	197	5	20.8	82	2	I51147	apovitellenin I -
125	6	25.0	1314	1	TNBYR6	198	5	20.8	84	1	VLEU1	ubiquinol-cytochro
126	6	25.0	1397	2	T10466	199	5	20.8	85	2	T41058	class II histocomp
127	6	25.0	1402	2	T24664	200	5	20.8	87	2	S03117	myosin - human (fr
128	6	25.0	1403	2	S24548	201	5	20.8	87	2	I61696	MHC class II anti
129	6	25.0	1435	2	T32930	202	5	20.8	88	2	I59656	MHC class II histo
130	6	25.0	1436	2	D71618	203	5	20.8	89	2	S38676	myosin - human (fr
131	6	25.0	1447	2	S02160	204	5	20.8	89	2	I61699	MHC class II histo
132	6	25.0	1462	2	T06819	205	5	20.8	89	2	I68555	H-2 class II histo
133	6	25.0	1464	2	T13716	206	5	20.8	89	2	PL0126	myosin - human (fr
134	6	25.0	1473	2	S53599	207	5	20.8	90	2	I61691	C15L protein - vac
135	6	25.0	1475	2	A60026	208	5	20.8	91	2	H42502	HLA-DRB1 protein -
136	6	25.0	1485	1	IS2PT2	209	5	20.8	94	2	T01409	probable membrane
137	6	25.0	1520	2	T23620	210	5	20.8	94	2	C97352	hypothetical prote
138	6	25.0	1526	2	JN0598	211	5	20.8	100	2	A70424	hypothetical prote
139	6	25.0	1526	2	A44406	212	5	20.8	101	2	T14780	thioredoxin [impor
140	6	25.0	1528	2	JS0703	213	5	20.8	103	2	A11228	thioredoxin [impor
141	6	25.0	1530	2	A04093	214	5	20.8	103	2	AC1582	hypothetical prote
142	6	25.0	1532	2	T18438	215	5	20.8	103	2	T28354	hypothetical prote
143	6	25.0	1572	2	T00027	216	5	20.8	103	2	S64759	thioredoxin [impor
144	6	25.0	1584	2	T18276	217	5	20.8	104	2	H95206	thioredoxin-disulf
145	6	25.0	1589	2	T13606	218	5	20.8	104	2	H98071	hypothetical prote
146	6	25.0	1612	2	S59969	219	5	20.8	104	2	E71048	hypothetical prote
147	6	25.0	1613	2	JE0272	220	5	20.8	107	2	C69354	hypothetical prote
148	6	25.0	1613	2	JE0273	221	5	20.8	109	2	S77444	hypothetical prote
149	6	25.0	1626	2	A39242	222	5	20.8	109	2	T49551	conserved hypoteth
150	6	25.0	1655	2	T13398	223	5	20.8	109	2	B95043	tcpi protein - Vib
151	6	25.0	1664	2	T18216	224	5	20.8	113	2	S37091	conserved hypoteth
152	6	25.0	1677	2	T43021	225	5	20.8	113	2	D97913	hypothetical prote
153	6	25.0	1737	2	A59235	226	5	20.8	115	2	H64030	MHC class II histo
154	6	25.0	1855	2	S41649	227	5	20.8	116	2	I38898	hypothetical prote
155	6	25.0	1891	2	T13394	228	5	20.8	117	2	C64378	hypothetical prote
156	6	25.0	1920	2	T13893	229	5	20.8	117	2	C90556	ORF MSV220 hypot
157	6	25.0	2023	2	T13154	230	5	20.8	120	2	T28381	MHC class II histo
158	6	25.0	2038	2	T18397	231	5	20.8	121	2	A46561	hypothetical prote
159	6	25.0	2109	2	T13352	232	5	20.8	122	2	S64834	transcription regu
160	6	25.0	2150	2	S71629	233	5	20.8	123	2	H81130	hypothetical prote
161	6	25.0	2167	2	S06558	234	5	20.8	123	2	C39777	conserved hypoteth
162	6	25.0	2175	1	S03170	235	5	20.8	124	2	E95372	hypothetical prote
163	6	25.0	2269	2	T18472	236	5	20.8	125	2	T24592	hypothetical prote
164	6	25.0	2359	2	T03094	237	5	20.8	126	2	T15993	conserved hypoteth
165	6	25.0	3130	2	T13828	238	5	20.8	128	2	G95409	conserved hypoteth
166	6	25.0	3973	2	B71612	239	5	20.8	129	2	F82515	iron-sulfur cluste
167	5	20.8	20	2	I59073	240	5	20.8	131	2	H69397	hypothetical prote
168	5	20.8	57	2	I68900	241	5	20.8	134	2	S42040	hypothetical prote
169	5	20.8	57	2	I35057	242	5	20.8	135	2	C90527	chitinase (EC 3.2.
170	5	20.8	57	2	B43603	243	5	20.8	138	2	T14185	hypothetical prote
171	5	20.8	57	2	D71096	244	5	20.8	139	2	T28243	hypothetical prote
172	5	20.8	62	2	AH3059	245	5	20.8	140	2	B28756	class II histocomp
173	5	20.8	64	2	F97143	246	5	20.8	142	2	T00616	probable nucleic a
174	5	20.8	65	2	T17665	247	5	20.8	143	2	F82186	hypothetical prote
175	5	20.8	66	2	H84489	248	5	20.8	144	2	G72056	nucleoside diphosp

249	5	20.8	144	2	H86567	nucleoside-2-P kin	322	5	20.8	217	2	H71566	probable ribonucle
250	5	20.8	144	2	G70023	hypothetical prote	323	5	20.8	219	2	B49181	beta B2-crystallin
251	5	20.8	148	2	H90424	conserved hypotet	324	5	20.8	219	2	AF1525	probable transcrip
252	5	20.8	151	2	C95069	hypothetical prote	325	5	20.8	220	2	JC2337	T-cell receptor al
253	5	20.8	151	2	B97937	hypothetical prote	326	5	20.8	220	2	T27980	hypothetical prote
254	5	20.8	153	2	A36079	insulin-like growt	327	5	20.8	224	2	A64599	hydrogenase (BC 1.
255	5	20.8	153	2	C30405	hypothetical prote	328	5	20.8	224	2	D71915	hydrogenase, cytoc
256	5	20.8	154	2	A36591	superoxide dismuta	329	5	20.8	224	2	T19959	hypothetical prote
257	5	20.8	156	2	H94689	hypothetical prote	330	5	20.8	226	2	T28268	hypothetical prote
258	5	20.8	158	2	S47140	pathogenesis-relat	331	5	20.8	227	2	JG0176	EBF-2 precursor pr
259	5	20.8	158	2	E87723	protein R06A10.3 [332	5	20.8	229	2	JQ0928	coat protein - tom
260	5	20.8	158	2	T13738	hypothetical prote	333	5	20.8	230	2	S71747	DAG protein precu
261	5	20.8	160	2	C69900	hypothetical prote	334	5	20.8	231	2	S73469	probable lipoprote
262	5	20.8	160	2	B86614	CR832 hypotetical	335	5	20.8	231	2	AI3632	transcription regu
263	5	20.8	160	2	F72010	CR832 hypotetical	336	5	20.8	232	1	HLMS82	H-2 class II histo
264	5	20.8	163	2	C55582	unknown protein en	337	5	20.8	232	2	H98807	exotoxin 12 (impor
265	5	20.8	163	2	H90731	hypothetical prote	338	5	20.8	232	2	E89807	glucosamine-6-phos
266	5	20.8	163	2	B81530	N utilization subs	339	5	20.8	233	2	H95184	MHC class II prote
267	5	20.8	164	2	T26534	hypothetical prote	340	5	20.8	233	2	I55654	3-oxoacyl-l-acyl-ca
268	5	20.8	166	2	F66898	single-strand bind	341	5	20.8	236	2	T11638	MHC class II histo
269	5	20.8	167	2	T39286	probable ubiquitin	342	5	20.8	237	2	B28043	H-2 class II histo
270	5	20.8	168	2	T47054	hypothetical prote	343	5	20.8	237	2	A21200	hypothetical prote
271	5	20.8	169	2	A21489	hypothetical prote	344	5	20.8	237	2	T04913	pur operon repress
272	5	20.8	169	2	S66862	probable membrane	345	5	20.8	237	2	F75185	beta-crystallin B1
273	5	20.8	172	2	S24397	stellate protein -	346	5	20.8	238	1	CYCEB1	dye resistance pro
274	5	20.8	172	2	S24398	hypothetical prote	347	5	20.8	238	2	AF0607	arginine transport
275	5	20.8	174	2	F85028	hypothetical prote	348	5	20.8	238	2	F64824	arginine transport
276	5	20.8	174	2	D83309	probable transcrip	349	5	20.8	238	2	E85597	arginine 3rd trans
277	5	20.8	176	2	F66881	conserved hypotet	350	5	20.8	238	2	A90747	arginine 3rd trans
278	5	20.8	177	2	T37212	hypothetical prote	351	5	20.8	238	2	AH0164	arginine transport
279	5	20.8	177	2	A86735	transcription regu	352	5	20.8	238	2	AF1076	global response re
280	5	20.8	179	2	T06962	hypothetical prote	353	5	20.8	238	2	G91298	dye resistance pro
281	5	20.8	180	2	H95260	transcription regu	354	5	20.8	238	2	H86140	dye resistance pro
282	5	20.8	180	2	E98126	conserved hypotet	355	5	20.8	238	2	H82084	aerobic respiratio
283	5	20.8	183	2	A41351	multidrug resistan	356	5	20.8	238	2	AG0056	glucosamine-6-phos
284	5	20.8	184	2	D42118	ribosomal protein	357	5	20.8	240	2	G98030	probable zinc fing
285	5	20.8	184	2	AD0232	hypothetical prote	358	5	20.8	240	2	T09602	I-E (beta) protei
286	5	20.8	184	2	T17446	hypothetical 21.1K	359	5	20.8	241	2	I48657	hypothetical prote
287	5	20.8	184	2	S35751	lex10 protein - le	360	5	20.8	241	2	S63458	hypothetical prote
288	5	20.8	185	2	S37479	T-cell receptor al	361	5	20.8	242	2	T40458	hypothetical prote
289	5	20.8	186	2	T51412	bZIP DNA-binding p	362	5	20.8	243	2	A99387	SAW-dependent meth
290	5	20.8	187	2	S69466	hypothetical prote	363	5	20.8	243	2	T24981	hypothetical prote
291	5	20.8	187	2	H89981	hypothetical prote	364	5	20.8	244	2	G91093	type III secretion
292	5	20.8	188	2	G69225	hypothetical prote	365	5	20.8	245	2	AI0634	conserved hypotet
293	5	20.8	190	2	T39622	probable phosphate	366	5	20.8	245	2	C90805	hypothetical prote
294	5	20.8	192	2	A45836	MHC class II histo	367	5	20.8	245	2	H85664	hypothetical prote
295	5	20.8	193	2	T00595	hypothetical prote	368	5	20.8	245	2	AE0248	conserved hypotet
296	5	20.8	193	2	C86334	hypothetical prote	369	5	20.8	245	2	G64845	ycdX protein - Esc
297	5	20.8	195	2	AF2496	hypothetical prote	370	5	20.8	246	2	E82908	hypothetical prote
298	5	20.8	198	2	F70371	hypothetical prote	371	5	20.8	249	2	T05424	hypothetical prote
299	5	20.8	199	2	H89781	hypothetical prote	372	5	20.8	249	2	B71024	probable lipote p
300	5	20.8	201	2	S54475	hypothetical prote	373	5	20.8	251	2	T52370	homeobox protein H
301	5	20.8	202	2	T29252	hypothetical prote	374	5	20.8	251	2	T49950	homeobox-leucine z
302	5	20.8	204	2	T51669	myb-related trans	375	5	20.8	251	2	F89929	hypothetical prote
303	5	20.8	205	1	CYBOB	beta-crystallin B2	376	5	20.8	252	1	HLMSBF	H-2 class II histo
304	5	20.8	205	2	JC2009	beta-crystallin B2	377	5	20.8	253	2	B69098	phosphate transpor
305	5	20.8	205	2	JC4964	beta-B2-crystallin	378	5	20.8	253	2	D86839	phosphate ABC tran
306	5	20.8	205	2	S05015	beta-crystallin B2	379	5	20.8	253	2	E64852	conserved hypotet
307	5	20.8	206	2	B82095	probable lipoprote	380	5	20.8	256	2	E72427	oxidoreductase, sh
308	5	20.8	207	2	A39757	beta-crystallin B2	381	5	20.8	256	2	A84437	probable PHD-type
309	5	20.8	207	2	S32124	B2 protein - carro	382	5	20.8	257	2	E70330	conserved hypotet
310	5	20.8	207	2	D97190	hypothetical prote	383	5	20.8	257	2	B75038	soj protein homolo
311	5	20.8	208	2	A97011	probable Zn-finger	384	5	20.8	257	2	A84848	probable C2H2-type
312	5	20.8	208	2	C89804	hypothetical prote	385	5	20.8	257	2	T00406	hypothetical prote
313	5	20.8	209	2	S65300	hypothetical prote	386	5	20.8	258	2	A86618	protein ZKS20.2 [i
314	5	20.8	210	2	JH0603	beta-crystallin A4	387	5	20.8	258	2	I64070	cyclase hisP HI047
315	5	20.8	210	2	A64394	hypothetical prote	388	5	20.8	258	2	T05194	hypothetical prote
316	5	20.8	214	2	S49599	probable permease	389	5	20.8	259	1	PWBV3	H+-transporting tw
317	5	20.8	215	2	A49758	chloramphenicol O-	390	5	20.8	259	1	PWBVJ6	H+-transporting tw
318	5	20.8	215	2	JQ1951	probable CMAAT-box	391	5	20.8	259	2	G84685	probable DOF zinc
319	5	20.8	215	2	F84508	hypothetical prote	392	5	20.8	259	2	AB1718	ferrichrome ABC tr
320	5	20.8	216	2	E86154	hypothetical prote	393	5	20.8	259	2	AF1347	ferrichrome ABC tr
321	5	20.8	216	2	T20186	hypothetical prote	394	5	20.8	261	2	A60404	MHC class II histo

395	5	20.8	261	2	B60404	MHC class II histo	468	5	20.8	294	2	T08408	transcription fact
396	5	20.8	261	2	D90123	hypothetical prote	469	5	20.8	295	2	A11795	ABC transporter, A
397	5	20.8	262	2	H84152	hypothetical prote	470	5	20.8	296	2	T34910	hypothetical prote
398	5	20.8	262	2	B85939	hypothetical prote	471	5	20.8	296	2	S47594	cyclophilin B-bind
399	5	20.8	263	1	HLMSBS	H-2 class II histo	472	5	20.8	296	2	B40257	RNA5 protein - ye
400	5	20.8	263	1	HLMSBU	MHC class II histo	473	5	20.8	297	1	NBR7	lipoprotein H p
401	5	20.8	263	2	T11469	cytochrome-c oxida	474	5	20.8	297	2	S06267	surface antigen H
402	5	20.8	263	2	A61389	MHC class II histo	475	5	20.8	297	2	T51005	hypothetical prote
403	5	20.8	263	2	A25911	H-2 class II histo	476	5	20.8	299	2	S60529	envelope polyprote
404	5	20.8	263	2	F85986	probable FADA-type	477	5	20.8	299	2	S60528	envelope polyprote
405	5	20.8	263	2	C91141	probable transcript	478	5	20.8	300	2	S60546	envelope polyprote
406	5	20.8	263	2	D65114	hypothetical prote	479	5	20.8	300	2	S60547	envelope polyprote
407	5	20.8	263	2	T38635	hypothetical prote	480	5	20.8	300	2	S60556	envelope polyprote
408	5	20.8	264	1	HLMSB1	H-2 class II histo	481	5	20.8	300	2	S60555	envelope polyprote
409	5	20.8	264	1	HLMSB	H-2 class II histo	482	5	20.8	300	2	S60555	envelope polyprote
410	5	20.8	264	2	F27579	T-cell receptor al	483	5	20.8	301	2	S60548	envelope polyprote
411	5	20.8	264	2	S11650	class II histocomp	484	5	20.8	303	2	AG1443	protein gp49 homol
412	5	20.8	264	2	A30529	H-2 class II histo	485	5	20.8	304	2	A40368	mrr protein - Esch
413	5	20.8	264	2	I56056	MHC E-beta-f - mou	486	5	20.8	304	2	C71637	rod shape-determin
414	5	20.8	264	2	T06601	hypothetical prote	487	5	20.8	306	2	S38183	probable purine nu
415	5	20.8	264	2	T05594	hypothetical prote	488	5	20.8	307	2	C95171	thiamin biosynthes
416	5	20.8	264	2	T24327	hypothetical prote	489	5	20.8	307	2	A45600	asparagine-rich bl
417	5	20.8	265	2	AF1890	WD-repeat protein	490	5	20.8	307	2	C98037	thiamin biosynthes
418	5	20.8	265	2	F75506	conserved hypothet	491	5	20.8	307	2	S37252	homeotic protein H
419	5	20.8	266	2	T31264	cis-1,2-dihydro-1,	492	5	20.8	310	2	S60425	probable membrane
420	5	20.8	266	2	I54295	lymphocyte antigen	493	5	20.8	310	2	C90277	hypothetical prote
421	5	20.8	266	2	I68733	MHC HLA-DR-beta ch	494	5	20.8	312	2	T32678	hypothetical prote
422	5	20.8	266	2	B39260	MHC class II histo	495	5	20.8	313	2	E81356	hypothetical prote
423	5	20.8	268	2	S57542	hypothetical prote	496	5	20.8	313	2	T29691	hypothetical prote
424	5	20.8	268	2	C70139	conserved hypothet	497	5	20.8	314	2	G64324	hypothetical prote
425	5	20.8	269	2	S57494	T-cell receptor al	498	5	20.8	315	2	H31090	H+-transporting tw
426	5	20.8	270	2	B70817	probable oxidoredu	499	5	20.8	315	2	D82559	riboflavin biosynt
427	5	20.8	272	2	S23684	erythrocyte membra	500	5	20.8	315	2	T13654	synthasin homolog -
428	5	20.8	273	2	PL0063	T-cell receptor al	501	5	20.8	315	2	C29624	spherulin 2a - sli
429	5	20.8	273	2	S21731	signal recognition	502	5	20.8	315	2	JC7572	somite Maf1 protei
430	5	20.8	273	2	S60751	homeotic protein s	503	5	20.8	315	2	T34528	hypothetical prote
431	5	20.8	274	2	AB1821	hypothetical prote	504	5	20.8	316	2	E84636	NAM (no apical mer
432	5	20.8	275	1	RHWUAC	T-cell receptor al	505	5	20.8	316	2	A83588	streptogramin lyas
433	5	20.8	275	2	A82257	oxidoreductase, sh	506	5	20.8	318	2	AB1792	transcription regu
434	5	20.8	275	2	B75479	conserved hypothet	507	5	20.8	318	2	S51261	probable beta-glyc
435	5	20.8	276	2	C82084	conserved hypothet	508	5	20.8	319	2	H81903	probable acetyl-Co
436	5	20.8	277	2	AG1983	hypothetical prote	509	5	20.8	319	2	B81119	acetyl-CoA carboxy
437	5	20.8	277	2	AB2461	hypothetical prote	510	5	20.8	319	2	C81390	hypothetical prote
438	5	20.8	277	2	T16020	hypothetical prote	511	5	20.8	319	2	S48355	STSL protein - yea
439	5	20.8	277	2	T24329	hypothetical prote	512	5	20.8	320	1	QQEV3M	MTV superantigen -
440	5	20.8	278	2	AD3253	chromosome partiti	513	5	20.8	320	2	T02987	myb-related protei
441	5	20.8	279	2	D97026	nicotinate-nucleot	514	5	20.8	321	2	T23758	hypothetical prote
442	5	20.8	279	2	E97849	rod shape-determin	515	5	20.8	323	2	T06506	glutenin low molec
443	5	20.8	279	2	T16047	hypothetical prote	516	5	20.8	323	2	F86192	hypothetical prote
444	5	20.8	280	2	H70089	hypothetical prote	517	5	20.8	323	2	AG3381	glycosyltransferas
445	5	20.8	280	2	A35872	steroid hormone re	518	5	20.8	324	2	AB1364	protein gp49 [Bact
446	5	20.8	281	2	G82201	hypothetical prote	519	5	20.8	325	2	I65354	stem cell antigen
447	5	20.8	284	2	A84682	probable zinc-fing	520	5	20.8	325	2	C90703	SfmH protein [impo
448	5	20.8	284	2	B84146	transglutaminase t	521	5	20.8	325	2	F85553	protein involved i
449	5	20.8	285	2	C86423	unknown protein, 1	522	5	20.8	325	2	D64785	SfmH protein precu
450	5	20.8	286	2	H96706	probable transcript	523	5	20.8	327	2	S57121	hypothetical prote
451	5	20.8	286	2	T12522	hypothetical prote	524	5	20.8	328	2	G84826	hypothetical prote
452	5	20.8	287	2	B96717	unknown protein, 3	525	5	20.8	328	2	T07726	hypothetical prote
453	5	20.8	288	2	AE0056	probable right ori	526	5	20.8	329	2	T18615	hypothetical prote
454	5	20.8	288	2	T21770	hypothetical prote	527	5	20.8	329	2	T13016	hypothetical prote
455	5	20.8	289	2	AB1075	right origin-bindi	528	5	20.8	330	2	T02525	probable DOF zinc
456	5	20.8	289	2	JU0158	right oriC-binding	529	5	20.8	330	2	T25939	hypothetical prote
457	5	20.8	289	2	B91298	right oriC-binding	530	5	20.8	332	2	T10886	iron utilization p
458	5	20.8	289	2	D86139	right origin-bindi	531	5	20.8	332	2	T42370	probable glucan 1,
459	5	20.8	289	2	F97322	uncharacterized co	532	5	20.8	332	2	H84443	homeodomain transc
460	5	20.8	290	2	G72203	sugar ABC transpor	533	5	20.8	332	2	B71606	probable integrat
461	5	20.8	290	2	T05009	hypothetical prote	534	5	20.8	333	2	C41080	glyceraldhyde-3-p
462	5	20.8	291	2	T51668	myb-related transc	535	5	20.8	333	2	T27883	hypothetical prote
463	5	20.8	292	2	S28832	microtubule-associ	536	5	20.8	334	1	A40166	gap junction prote
464	5	20.8	292	2	F82385	hypothetical prote	537	5	20.8	334	1	B34575	gap junction prote
465	5	20.8	293	2	T24165	hypothetical prote	538	5	20.8	334	2	C22735	hypothetical nox2
466	5	20.8	294	2	C64048	major ferric iron-	539	5	20.8	334	2	AH0300	conserved hypothet
467	5	20.8	294	2	H84591	hypothetical prote	540	5	20.8	334	2	T23444	hypothetical prote

541	5	20.8	336	2	T17370	NADH2 dehydrogenas	614	5	20.8	381	2	T43517	dnaJ protein homol
542	5	20.8	336	2	D88102	protein w10G11.9 [615	5	20.8	381	2	A46358	steroid/thyroid ho
543	5	20.8	337	2	T18431	hypothetical prote	616	5	20.8	382	1	A35853	gap junction prote
544	5	20.8	338	2	T17366	NADH2 dehydrogenas	617	5	20.8	382	2	E64866	myosin-like protei
545	5	20.8	338	2	T17114	NADH2 dehydrogenas	618	5	20.8	382	2	I52565	stem cell antigen
546	5	20.8	338	2	T14130	NADH2 dehydrogenas	619	5	20.8	382	2	AH2728	glycosyl transfera
547	5	20.8	338	2	T17112	NADH2 dehydrogenas	620	5	20.8	382	2	S51651	cyclin delta-2 - A
548	5	20.8	338	2	T17371	NADH2 dehydrogenas	621	5	20.8	384	2	T10187	S-locus-specific g
549	5	20.8	338	2	T17374	NADH2 dehydrogenas	622	5	20.8	385	2	E86797	hypothetical prote
550	5	20.8	339	2	T17113	NADH2 dehydrogenas	623	5	20.8	385	2	H90083	protein C10G8.8 [i
551	5	20.8	339	2	T17375	NADH2 dehydrogenas	624	5	20.8	385	2	E89046	hypothetical prote
552	5	20.8	339	2	T17376	NADH2 dehydrogenas	625	5	20.8	386	2	T24324	hypothetical prote
553	5	20.8	339	2	T46713	hypothetical prote	626	5	20.8	387	2	T27287	dnaJ related prote
554	5	20.8	340	2	AF0867	probable regulator	627	5	20.8	389	2	B82479	D-alanyl-D-alanine
555	5	20.8	340	2	D70615	antigen fbpc2 - My	628	5	20.8	389	2	H90083	polyadenylate-bind
556	5	20.8	340	2	T02120	hypothetical prote	629	5	20.8	389	2	S53612	gene MSP-2 protei
557	5	20.8	340	2	A44019	membrane protein S	630	5	20.8	390	2	T49619	hypothetical prote
558	5	20.8	340	2	T23567	hypothetical prote	631	5	20.8	391	2	S14577	asparagine-rich pr
559	5	20.8	341	2	T04050	hypothetical prote	632	5	20.8	391	2	E64474	hypothetical prote
560	5	20.8	341	2	T24954	hypothetical prote	633	5	20.8	392	2	T13722	NADH2 dehydrogenas
561	5	20.8	342	2	T01735	homeobox protein N	634	5	20.8	392	2	B86549	polymorphic outer
562	5	20.8	344	2	T23028	hypothetical prote	635	5	20.8	392	2	B72075	polymorphic outer
563	5	20.8	345	2	S07114	MHC class I histoc	636	5	20.8	393	2	T13501	NADH2 dehydrogenas
564	5	20.8	345	2	D91201	type III secretion	637	5	20.8	393	2	T13565	NADH2 dehydrogenas
565	5	20.8	345	2	H86047	escu [imported] -	638	5	20.8	393	2	T12630	NADH2 dehydrogenas
566	5	20.8	345	2	AB1813	hypothetical prote	639	5	20.8	393	2	T12609	NADH2 dehydrogenas
567	5	20.8	348	2	S29990	histocompatibility	640	5	20.8	393	2	B84758	probable katanin [
568	5	20.8	348	2	D84922	probable sugar tra	641	5	20.8	393	2	A97510	probable hexosyltr
569	5	20.8	348	2	S19873	single-stranded DN	642	5	20.8	394	1	BWH1XD	bexD protein - Hae
570	5	20.8	349	1	E64442	probable arsenical	643	5	20.8	395	2	T13756	NADH2 dehydrogenas
571	5	20.8	352	2	AG0762	probable membrane	644	5	20.8	395	2	T22751	hypothetical prote
572	5	20.8	352	2	T33433	hypothetical prote	645	5	20.8	395	2	A95860	hypothetical prote
573	5	20.8	353	2	C85572	hypothetical prote	646	5	20.8	395	2	A43700	hypothetical prote
574	5	20.8	353	2	E90721	hypothetical prote	647	5	20.8	396	1	AJNZRB	BN51 protein - hum
575	5	20.8	353	2	T24010	hypothetical prote	648	5	20.8	396	1	BMH02	argininosuccinate
576	5	20.8	355	2	T04317	homeobox protein L	649	5	20.8	396	2	AF3168	bone morphogenetic
577	5	20.8	357	2	S33144	leucoanthocyanidin	650	5	20.8	397	2	F72072	conserved hypothet
578	5	20.8	357	2	JQ2174	hypothetical 39.2K	651	5	20.8	397	2	C86552	probable transamin
579	5	20.8	357	2	S27909	hypothetical prote	652	5	20.8	397	2	T36119	aspartate aminotra
580	5	20.8	358	1	PKWKG	H+-transporting tw	653	5	20.8	397	2	E88533	hypothetical prote
581	5	20.8	358	2	B81302	probable alcohol d	654	5	20.8	397	2	T17008	probable zinc fing
582	5	20.8	358	2	AB2041	hypothetical prote	655	5	20.8	398	1	R3BYM1	ribosomal protein
583	5	20.8	358	2	T10244	G-Box binding prot	656	5	20.8	400	2	D71520	knotted-like home
584	5	20.8	358	2	D96579	hypothetical prote	657	5	20.8	401	2	T00897	probable transamin
585	5	20.8	360	2	S06287	fragmin - aline mo	658	5	20.8	402	2	A84581	probable disease r
586	5	20.8	361	2	C84613	probable cyclin D	659	5	20.8	402	2	T13614	N-acetyltransferas
587	5	20.8	362	2	A60384	MHC class I histoc	660	5	20.8	403	2	S47659	CDC2/CDC13 suppres
588	5	20.8	362	2	C81453	flagellar biosynth	661	5	20.8	404	2	A46165	envelope surface g
589	5	20.8	362	2	C64807	ybgO protein - Esc	662	5	20.8	405	2	F89930	hypothetical prote
590	5	20.8	364	2	A81261	probable periplasm	663	5	20.8	406	2	D86895	membrane protein l
591	5	20.8	365	2	S62542	hypothetical coile	664	5	20.8	406	2	AG3021	hypothetical prote
592	5	20.8	365	2	F88449	protein P54D8.4 [i	665	5	20.8	406	2	C98263	hypothetical prote
593	5	20.8	366	2	S53898	probable membrane	666	5	20.8	407	2	T32882	probable exo-beta-
594	5	20.8	366	2	AH0445	conserved hypothet	667	5	20.8	407	2	S49890	regulatory protein
595	5	20.8	366	2	F27203	probable heat choc	668	5	20.8	409	2	C45600	asparagine-rich bl
596	5	20.8	369	1	PABY21	phosphoprotein pho	669	5	20.8	409	2	B87262	2-octaprenyl-6-met
597	5	20.8	369	2	T24205	hypothetical prote	670	5	20.8	409	2	H90096	eukaryotic release
598	5	20.8	370	2	G97277	glycosyltransferas	671	5	20.8	409	2	S74704	hypothetical prote
599	5	20.8	371	2	T07938	probable acetyl-Co	672	5	20.8	409	2	T25935	hypothetical prote
600	5	20.8	372	2	A64176	hypothetical prote	673	5	20.8	413	1	S03631	homotetic protein S
601	5	20.8	372	2	I38042	single-stranded DN	674	5	20.8	413	2	S70874	tapC protein - Aer
602	5	20.8	373	2	S63262	hypothetical prote	675	5	20.8	413	2	H88481	protein let-756 [i
603	5	20.8	373	2	S72368	single-stranded DN	676	5	20.8	413	2	A62205	sensory transducti
604	5	20.8	375	2	T06096	hypothetical prote	677	5	20.8	414	2	A86229	hypothetical prote
605	5	20.8	376	2	E85435	cysteine proteinas	678	5	20.8	414	2	F29826	hypothetical prote
606	5	20.8	376	2	G71828	hypothetical prote	679	5	20.8	416	2	A99996	probable ammonium
607	5	20.8	377	1	S01615	site-specific DNA-	680	5	20.8	417	2	S34433	site-specific DNA-
608	5	20.8	377	2	F84473	hypothetical prote	681	5	20.8	418	2	T25368	hypothetical prote
609	5	20.8	378	2	A44443	basic helix-loop-h	682	5	20.8	419	2	S14508	asparagine-rich pr
610	5	20.8	380	2	T51647	myb-related transc	683	5	20.8	422	2	T20588	hypothetical prote
611	5	20.8	380	2	T20269	hypothetical prote	684	5	20.8	423	2	A99242	hypothetical prote
612	5	20.8	380	2	T24678	hypothetical prote	685	5	20.8	423	2	AC3044	hypothetical prote
613	5	20.8	381	2	T13701	NADH2 dehydrogenas	686	5	20.8	426	2	E83981	pyruvate dehydroge

687	5	20.8	426	2	S58304	hypothetical prote	760	5	20.8	483	2	A11665	glutamyl-tRNA(Gln)
688	5	20.8	427	2	AF0839	4-aminobutyrate tr	761	5	20.8	485	2	S48650	catalase [EC 1.11.
689	5	20.8	428	2	PC4163	toxin-co-regulated	762	5	20.8	486	2	S66097	cell-cycle protein
690	5	20.8	429	1	JCS861	endo-1,4-beta-xyla	763	5	20.8	486	2	D64474	hypothetical prote
691	5	20.8	429	2	S24705	probable segment i	764	5	20.8	486	2	E85433	SCARECROW-like pro
692	5	20.8	431	2	T07812	S-locus-specific g	765	5	20.8	487	2	F84727	hypothetical prote
693	5	20.8	431	2	T47528	hypothetical prote	766	5	20.8	487	2	T49351	hypothetical prote
694	5	20.8	431	2	E86236	protein F14N23.7 [767	5	20.8	488	2	A59291	myosin-14 - malari
695	5	20.8	433	2	S63143	cell division cont	768	5	20.8	490	2	A35546	muscarinic acetyl
696	5	20.8	434	2	T37350	probable 49.8K pro	769	5	20.8	490	2	A46391	CAMP receptor subt
697	5	20.8	434	2	A72159	ISR protein - vari	770	5	20.8	490	2	S52830	HMS1 protein - yea
698	5	20.8	434	2	S33082	G5R protein - vari	771	5	20.8	492	1	CS5V	catalase [EC 1.11.
699	5	20.8	434	2	T28505	hypothetical prote	772	5	20.8	492	2	T16969	catalase [EC 1.11.
700	5	20.8	434	2	C82885	membrane nuclease	773	5	20.8	492	2	S52079	catalase [EC 1.11.
701	5	20.8	436	2	I51237	inosine-guanosine	774	5	20.8	492	2	T12300	catalase [EC 1.11.
702	5	20.8	436	2	S20060	translation elonga	775	5	20.8	492	2	S10770	catalase [EC 1.11.
703	5	20.8	436	2	A30145	translation elonga	776	5	20.8	492	2	S17493	catalase [EC 1.11.
704	5	20.8	437	2	S60957	invariant surface	777	5	20.8	492	2	S10395	catalase [EC 1.11.
705	5	20.8	437	2	S05357	transcription modu	778	5	20.8	492	2	T05779	catalase [EC 1.11.
706	5	20.8	437	2	S05357	transcription modu	779	5	20.8	492	2	S46297	catalase [EC 1.11.
707	5	20.8	438	2	E84922	hypothetical prote	780	5	20.8	492	2	S46298	catalase [EC 1.11.
708	5	20.8	439	2	T52291	probable DNA-bind	781	5	20.8	492	2	T10902	catalase [EC 1.11.
709	5	20.8	439	2	F85189	disease resistance	782	5	20.8	492	2	T28025	hypothetical prote
710	5	20.8	441	2	T32350	hypothetical prote	783	5	20.8	492	1	S39532	aldehyde dehydroge
711	5	20.8	442	2	G83672	6-phospho-beta-glu	784	5	20.8	493	2	T07911	catalase [EC 1.11.
712	5	20.8	442	2	H86276	F14L17.4 protein -	785	5	20.8	493	2	S51450	probable membrane
713	5	20.8	443	2	H84449	hypothetical prote	786	5	20.8	493	2	S50625	GLO3 protein - yea
714	5	20.8	443	2	A54813	CAMP receptor CAR4	787	5	20.8	494	1	CSPM	catalase [EC 1.11.
715	5	20.8	446	2	C87130	sugar transport pe	788	5	20.8	495	2	S31493	env polyprotein -
716	5	20.8	447	2	A84718	hypothetical prote	789	5	20.8	498	2	F83523	probable colicin-1
717	5	20.8	448	2	S07711	larvicidal toxin 5	790	5	20.8	500	1	S00364	aldehyde dehydroge
718	5	20.8	448	2	A28211	larvicidal toxin 5	791	5	20.8	500	2	S59795	hypothetical prote
719	5	20.8	448	2	C28211	mosquitocidal toxi	792	5	20.8	501	2	T43047	retrovirus-related
720	5	20.8	448	2	T01570	hypothetical prote	793	5	20.8	503	1	VCVDA	transforming prote
721	5	20.8	448	2	S60961	hypothetical prote	794	5	20.8	505	2	B88206	protein F21D12.3 [
722	5	20.8	451	2	A23535	clustered asparagi	795	5	20.8	505	2	AF1214	hypothetical prote
723	5	20.8	452	2	JC2459	gastrin/cholecysto	796	5	20.8	506	2	T02400	probable beta-gluc
724	5	20.8	452	2	S77436	sigma factor sibG	797	5	20.8	507	2	S05542	hypothetical prote
725	5	20.8	452	2	T33049	hypothetical prote	798	5	20.8	508	2	T11513	usp protein - frui
726	5	20.8	454	2	A43501	sucrose-6-phosphat	799	5	20.8	508	2	T13737	steroid hormone re
727	5	20.8	457	2	I54340	DNA-binding protei	800	5	20.8	509	1	I51281	steroid 17alpha-mo
728	5	20.8	458	2	T49114	hypothetical prote	801	5	20.8	509	2	T31706	hypothetical prote
729	5	20.8	459	2	I64224	aromatic amino aci	802	5	20.8	512	2	T02498	probable WRKY-type
730	5	20.8	460	1	YKBYC	citrates (si)-synth	803	5	20.8	512	2	T04708	hypothetical prote
731	5	20.8	460	2	C27311	NADH2 dehydrogenas	804	5	20.8	513	2	B96524	monosaccharide tra
732	5	20.8	462	2	S65570	dihydrofolate redu	805	5	20.8	514	2	S25009	hypothetical prote
733	5	20.8	462	2	B48326	cytb intron la pro	806	5	20.8	514	2	D81952	type I site-specif
734	5	20.8	462	2	T19652	hypothetical prote	807	5	20.8	514	2	F81152	type I site-specif
735	5	20.8	466	2	T41375	probable phosphogl	808	5	20.8	514	2	T15338	hypothetical prote
736	5	20.8	467	2	T41053	triglyceride lipas	809	5	20.8	517	1	S26606	myb-related protei
737	5	20.8	467	2	T51574	hypothetical prote	810	5	20.8	518	2	D69813	ABC transporter (A
738	5	20.8	468	1	A41242	interleukin-6 rece	811	5	20.8	520	2	S02166	type I site-specif
739	5	20.8	469	2	H97064	putative sugar-pro	812	5	20.8	521	1	A44267	protein-tyrosine-p
740	5	20.8	469	2	E90105	NAC2-like protein	813	5	20.8	521	2	T27192	hypothetical prote
741	5	20.8	469	2	T46230	6-phospho-beta-gal	814	5	20.8	522	2	H86248	protein T23J18.22
742	5	20.8	470	2	C95055	6-phospho-beta-gal	815	5	20.8	522	2	S25015	monosaccharide tra
743	5	20.8	470	2	H97924	hypothetical prote	816	5	20.8	523	2	G90109	T-complex protein
744	5	20.8	471	2	T49175	hypothetical prote	817	5	20.8	525	1	KGHUGH	histidine-rich gly
745	5	20.8	471	2	T32788	hypothetical prote	818	5	20.8	525	2	F97305	spore germination
746	5	20.8	472	2	T20454	hypothetical prote	819	5	20.8	528	2	C85056	probable DNA-bind
747	5	20.8	472	2	S34955	gene 10 protein -	820	5	20.8	529	1	YRHU1	monophenol monooxy
748	5	20.8	472	2	S28026	nuclear pore compl	821	5	20.8	531	2	JT0531	muscarinic acetyl
749	5	20.8	472	2	A26357	homeotic protein C	822	5	20.8	531	2	AH1491	hypothetical prote
750	5	20.8	473	2	T04799	hypothetical prote	823	5	20.8	532	2	JT0530	muscarinic acetyl
751	5	20.8	475	2	A87396	sensor histidine k	824	5	20.8	533	1	YRMSCS	monophenol monooxy
752	5	20.8	475	2	T39486	hypothetical prote	825	5	20.8	533	2	S63270	probable membrane
753	5	20.8	476	2	AG2868	succinoglycan bios	826	5	20.8	533	2	D96710	F24J5.16 imported
754	5	20.8	479	2	T02623	hypothetical prote	827	5	20.8	534	2	G50925	hypothetical prote
755	5	20.8	480	2	E81407	probable membrane	828	5	20.8	534	2	C85774	hypothetical prote
756	5	20.8	480	2	E86656	protein F56D6.2 [1	829	5	20.8	535	2	D64924	hypothetical prote
757	5	20.8	482	2	H71400	hypothetical prote	830	5	20.8	535	2	S53957	VAN1 protein - yea
758	5	20.8	482	2	S55950	hypothetical prote	831	5	20.8	536	2	A45409	atrial natriuretic
759	5	20.8	483	2	AC1294	glutamyl-tRNA(Gln)	832	5	20.8	536	2	H71563	hypothetical prote

833	5	20.8	537	1	A28111	natriuretic peptid	906	5	20.8	610	2	T18441	asparagine synthas
834	5	20.8	537	2	D86520	CTP synthetase [im	907	5	20.8	610	2	S05807	SAN1 protein - yea
835	5	20.8	537	2	E81568	CTP synthase CP052	908	5	20.8	612	2	T13616	hypothetical prote
836	5	20.8	537	2	A72103	ctp synthetase - C	909	5	20.8	613	2	T47483	receptor like prot
837	5	20.8	537	2	A23770	asparagine-rich pr	910	5	20.8	613	2	JC7762	SOX-3 protein - gu
838	5	20.8	537	2	B97013	and cellulose-bind	911	5	20.8	614	2	T29902	hypothetical prote
839	5	20.8	538	2	T40298	membrane transport	912	5	20.8	614	2	S58306	WD-40 repeat regul
840	5	20.8	538	2	H86329	F6F9.25 protein -	913	5	20.8	614	2	T29937	hypothetical prote
841	5	20.8	539	2	T00149	hypothetical prote	914	5	20.8	616	2	C95861	probable ABC trans
842	5	20.8	540	1	VGN2B3	cell fusion glycop	915	5	20.8	617	2	A72123	hypothetical prote
843	5	20.8	540	2	B83121	probable AMP-bindl	916	5	20.8	618	2	T04237	hypothetical prote
844	5	20.8	541	2	S73383	probable lipoprote	917	5	20.8	620	2	D82274	toxin co-regulated
845	5	20.8	542	2	S45557	resB protein - Bac	918	5	20.8	621	1	S59632	endo-1,4-beta-xyla
846	5	20.8	542	2	A98021	hypothetical prote	919	5	20.8	622	2	T18737	hypothetical prote
847	5	20.8	543	2	B93369	homeotic protein B	920	5	20.8	622	2	A90570	lipoprotein [impor
848	5	20.8	544	2	S65231	tRNA-pseudouridine	921	5	20.8	623	1	S33167	gene pointed prote
849	5	20.8	544	2	H84790	hypothetical prote	922	5	20.8	623	1	G86860	serine/threonine p
850	5	20.8	546	2	B97645	integral membrane	923	5	20.8	627	2	T02415	probable homeodoma
851	5	20.8	547	1	ERADP4	60.5K fiber protei	924	5	20.8	628	2	S51422	probable membrane
852	5	20.8	547	2	S15028	chromatin-binding	925	5	20.8	631	2	S70908	transferin-bindin
853	5	20.8	547	2	S41618	probable DNA-direc	926	5	20.8	632	2	A25784	hypothetical 70K p
854	5	20.8	547	2	T03901	hypothetical prote	927	5	20.8	633	2	S13352	amino acid transpo
855	5	20.8	548	2	T06266	germacrene C synth	928	5	20.8	633	2	T14612	hypothetical prote
856	5	20.8	548	2	G82286	phosphate ABC tran	929	5	20.8	633	2	T04835	probable serine/th
857	5	20.8	550	2	A41585	J-kappa recombinat	930	5	20.8	635	2	F71621	hypothetical prote
858	5	20.8	551	2	T39092	hypothetical ser-p	931	5	20.8	635	2	JCS896	killer cell inhibi
859	5	20.8	552	2	T29114	probable secreted	932	5	20.8	638	2	S67605	hypothetical prote
860	5	20.8	553	2	B91120	probable membrane	933	5	20.8	639	1	VCNWSA	env polyprotein pr
861	5	20.8	553	2	E85965	probable membrane	934	5	20.8	639	2	S20887	actA protein precu
862	5	20.8	553	2	A65093	hypothetical prote	935	5	20.8	639	2	AE1100	actin-assembly ind
863	5	20.8	554	2	S24949	pollen-specific pr	936	5	20.8	640	2	T07923	acetyl-CoA carboxy
864	5	20.8	554	2	JQ2010	transcription fact	937	5	20.8	642	2	D96777	hypothetical prote
865	5	20.8	559	1	AF0891	probable exported	938	5	20.8	645	1	VCNWS	env polyprotein pr
866	5	20.8	561	2	S57784	4-coumarate-CoA li	939	5	20.8	646	2	T02398	hypothetical prote
867	5	20.8	562	1	ERADN2	60.5K fiber protei	940	5	20.8	647	2	T35141	hypothetical prote
868	5	20.8	563	2	S70196	kfiB protein - Bac	941	5	20.8	647	2	S06450	steroid hormone re
869	5	20.8	567	2	T01032	hypothetical prote	942	5	20.8	649	2	T32967	hypothetical prote
870	5	20.8	567	2	T15574	hypothetical prote	943	5	20.8	650	2	S16706	transcription acti
871	5	20.8	567	2	A71619	membrane transport	944	5	20.8	651	2	T03889	Na+/Ca2+, K+-exch
872	5	20.8	567	2	T18462	hypothetical prote	945	5	20.8	655	2	S51884	probable protein k
873	5	20.8	570	1	S50933	myb-related protei	946	5	20.8	656	2	T10568	probable serine/th
874	5	20.8	570	1	G89123	protein K07C11.4 [947	5	20.8	657	2	S64073	hypothetical prote
875	5	20.8	572	2	A87156	unknown permease [948	5	20.8	659	2	C96730	probable ABC trans
876	5	20.8	572	2	B89782	hypothetical prote	949	5	20.8	659	2	A36664	S59/2 homeotic pro
877	5	20.8	575	2	AF2374	hypothetical prote	950	5	20.8	661	2	S21221	hemocyanin chain c
878	5	20.8	576	2	S69214	deformed epidermal	951	5	20.8	663	2	S55164	hypothetical prote
879	5	20.8	577	2	D75406	aspartyl-tRNA synt	952	5	20.8	664	2	B85122	serine/threonine k
880	5	20.8	577	2	S34785	catechol oxidase (953	5	20.8	666	2	T10573	probable serine/th
881	5	20.8	583	2	S30930	probable myosin he	954	5	20.8	666	2	S50452	hypothetical prote
882	5	20.8	583	2	C84788	excinuclease ABC s	955	5	20.8	666	2	S36218	hepatocyte nuclear
883	5	20.8	584	2	H82898	hypothetical prote	956	5	20.8	667	2	B84018	two-component sens
884	5	20.8	584	2	T39704	topoisomerase I-re	957	5	20.8	668	2	S39836	hypothetical prote
885	5	20.8	584	2	S51882	hypothetical prote	958	5	20.8	669	1	DNMUU5	NADH2 dehydrogenas
886	5	20.8	587	2	D96578	methyl-accepting c	959	5	20.8	669	2	S64795	suppressor protein
887	5	20.8	587	2	E82431	catechol oxidase (960	5	20.8	669	2	S14535	asparagine-rich pr
888	5	20.8	588	2	S30929	homeotic protein D	961	5	20.8	672	2	S61463	p83/100 protein -
889	5	20.8	588	2	T25638	hypothetical prote	962	5	20.8	674	2	S63043	MEF4 protein - yea
890	5	20.8	590	2	A42770	Suppressor of Hair	963	5	20.8	674	2	S75662	sensory transducti
891	5	20.8	594	2	T17590	probable glutamine	964	5	20.8	675	2	D85065	receptor protein k
892	5	20.8	595	2	G84825	probable dual spec	965	5	20.8	678	2	S62939	hypothetical prote
893	5	20.8	597	2	T51889	related to clathri	966	5	20.8	679	2	S48939	hypothetical prote
894	5	20.8	597	2	T15324	hypothetical prote	967	5	20.8	679	2	S37842	hypothetical prote
895	5	20.8	602	2	F84432	probable C2H2-type	968	5	20.8	679	2	G71615	phospholipase A2-1
896	5	20.8	603	2	B83022	transport protein	969	5	20.8	684	2	D71683	proteinase II (ptr
897	5	20.8	604	2	T51936	probable 9-cis-epo	970	5	20.8	686	2	E71895	probable heavy-met
898	5	20.8	604	2	S05447	finger protein gla	971	5	20.8	686	2	A71607	Mtn3/RAG1p-like p
899	5	20.8	605	2	T07123	nine-cis-epoxycaro	972	5	20.8	688	2	H83070	conserved hypothet
900	5	20.8	610	2	H71612	asparagine-tRNA li	973	5	20.8	693	2	S61464	p83/100 protein -
901	5	20.8					974	5	20.8	693	2	I40090	p93 protein - Lyme
902	5	20.8					975	5	20.8	695	2	E75099	hypothetical prote
903	5	20.8					976	5	20.8	698	2	JH0163	No-on-transient A
904	5	20.8					977	5	20.8	699	1	QRHUUT	lutropin-choriogon
905	5	20.8					978	5	20.8	699	2	T12163	NADH2 dehydrogenas

```
979      5 20.8 699 2 T12169 NADH2 dehydrogenas
980      5 20.8 699 2 T12170 NADH2 dehydrogenas
981      5 20.8 699 2 T12167 NADH2 dehydrogenas
982      5 20.8 699 2 T12172 NADH2 dehydrogenas
983      5 20.8 699 2 T12164 NADH2 dehydrogenas
984      5 20.8 699 2 T12173 NADH2 dehydrogenas
985      5 20.8 699 2 T12168 NADH2 dehydrogenas
986      5 20.8 699 2 S67773 hypothetical prote
987      5 20.8 700 2 I77463 lutropinizing hormon
988      5 20.8 700 2 A42395 lutropin-choriogon
989      5 20.8 700 2 A49744 probable serine/th
990      5 20.8 700 2 T10566 No-on-transient A
991      5 20.8 700 2 JH0162 Na+/H+ antiporter
992      5 20.8 701 2 F70155 hypothetical prote
993      5 20.8 702 2 T34313 probable protein k
994      5 20.8 704 2 T38117 NADH2 dehydrogenas
995      5 20.8 707 2 T12759 NADH2 dehydrogenas
996      5 20.8 707 2 T12658 NADH2 dehydrogenas
997      5 20.8 707 2 T12664 NADH2 dehydrogenas
998      5 20.8 707 2 T12665 NADH2 dehydrogenas
999      5 20.8 707 2 T12668 NADH2 dehydrogenas
1000     5 20.8 707 2 T12671 NADH2 dehydrogenas

ALIGNMENTS

RESULT 1
A40402
C99 antigen [validated] - human
N:Alternate names: motility-related protein-1
C:Species: Homo sapiens (man)
C:Date: 06-Dec-1991 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A46123; A40402; JH0555; A39029; S10564
R:Rubinstein, E.; Benoit, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouchei
Genomics 16, 132-138, 1993
A:Title: Organization of the human CD9 gene.
A:Reference number: A46123; MUID:93252369; PMID:8486348
A:Accession: A46123
A:Molecule type: DNA
A:Residues: 1-228 <RUB>
A:Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:g300112; PIDN:
A:Experimental source: leukocyte
A:Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,
R:Rianza, F.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.;
J. Biol. Chem. 266, 10638-10645, 1991
A:Title: cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of m
A:Reference number: A40402; MUID:91244846; PMID:2037603
A:Accession: A40402
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-228 <RUB>
A:Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:g508495; PIDN:AAA59
A:Note: parts of this sequence, including the amino end of the mature protein, were conf
R:Miyake, M.; Koyama, M.; Seno, M.; Ikeyama, S.
J. Exp. Med. 174, 1347-1354, 1991
A:Title: Identification of the motility-related protein (MRP-1), recognized by monoclonal
A:Reference number: JH0555; MUID:92078843; PMID:1720807
A:Accession: JH0555
A:Molecule type: mRNA
A:Residues: 1-228 <MIY>
A:Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:g34768; PIDN:CAA42708.1; PID:9
A:Experimental source: breast carcinoma
A:Note: This protein has the epitope defined by cell motility-inhibiting monoclonal anti
R:Bouchaix, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uza
J. Biol. Chem. 266, 117-122, 1991
A:Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.
A:Reference number: A39029; MUID:91093112; PMID:1840589
A:Accession: A39029
A:Molecule type: mRNA
A:Residues: 1-8,'S',10-66,'A',68-193,195-228 <BOU>
A:Cross-references: UNIPARC:UPI000017414B; GB:M38690
A:Note: parts of this sequence, including the amino end of the mature protein, were conf
```

```
R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.
FEBS Lett. 264, 270-274, 1990
A:Title: Purification and partial characterization of CD9 antigen of human platelets.
A:Reference number: S10564; MUID:90292223; PMID:2358073
A:Accession: S10564
A:Molecule type: protein
A:Residues: 2-8,'X',10-21 <HIG>
A:Cross-references: UNIPARC:UPI000017414C
C:Genetics:
A:Gene: GDB:CD9; MIC3
A:Cross-references: GDB:120582; OMIM:143030
A:Map position: 12p13-12p13
A:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status experimental <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTQKSIPEQETNNNSSFYT 24
DB 35 LRFDSTQKSIPEQETNNNSSFYT 58

RESULT 2
A42929
CD9 antigen - green monkey
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A42929
R:Miyamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
eptors on toxin-sensitive cells.
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-228 <MIT>
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:g218565; PIDN:
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52.53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTQKSIPEQETNNNSSFYT 24
DB 35 LRFDSTQKSIPEQETNNNSSFYT 58
```



```
RESULT 3
S39262
CD9 antigen - rat
N/Alternate names: platelet cell surface glycoprotein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: I56562; S39262
R:Kapielarian, Z.; Cho, K.O.; Hadjiarygrou, M.; Patterson, P.H.
J: Neurosci. 15, 562-573, 1995
A:Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed in the placenta.
A:Reference number: I56562; MUID:95123481; PMID:7823164
A:Accession: I56562
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:g434314; PID:
C:Gene: CD9
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-11/Domain: intracellular #status predicted <CV1>
F:12-35/Domain: transmembrane #status predicted <EX1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-80/Domain: transmembrane #status predicted <EX2>
F:81-84/Domain: intracellular #status predicted <CV2>
F:85-109/Domain: transmembrane #status predicted <EX3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <EX4>
F:220-226/Domain: intracellular #status predicted <CV3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.7%; Score 16; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQETN 16
|||||
Db 35 LRFDSQTKSIFQETN 50

RESULT 4
JX0221
CD9 antigen - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: JX0221
R:Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J: Biochem. 112, 63-67, 1992
A:Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell
A:Reference number: JX0221; MUID:93054422; PMID:1339429
A:Accession: JX0221
A:Molecule type: mRNA
A:Residues: 1-226 <MAR>
A:Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:g162820; PID:
A:Experimental source: ocular ciliary epithelial cell
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-226/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CV1>
F:12-35/Domain: transmembrane #status predicted <EX1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-76/Domain: transmembrane #status predicted <EX2>
F:77-80/Domain: intracellular #status predicted <CV2>
F:81-109/Domain: transmembrane #status predicted <EX3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <EX4>
F:220-226/Domain: intracellular #status predicted <CV3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 14; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQETN 16
|||||
Db 35 LRFDSQTKSIFQETN 50

RESULT 5
I49589
antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49589
R:Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A:Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A:Reference number: I49589; MUID:94054345; PMID:8236164
A:Accession: I49589
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g398911; PID:
C:Superfamily: CD9 antigen

Query Match 58.3%; Score 14; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQ 14
|||||
Db 35 LRFDSQTKSIFQEQ 48

RESULT 6
H84774
probable homeodomain transcription factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84774
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: H84420; MUID:20083487; PMID:10617197
A:Accession: H84774
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-680 <STO>
A:Cross-references: UNIPROT:Q9SJ56; UNIPARC:UPI000009E071; GB:AE002093; NID:g4510375; P
C:Genetics:
A:Gene: At2g35940
A:Map position: 2

Query Match 33.3%; Score 8; DB 2; Length 680;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNSSP 22
|||||
Db 59 TNNNNSSP 66

RESULT 7
A96913
ABC-type sulfate transporter, ATPase component CAC0107 [imported] - Clostridium acetobu
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C:Accession: A96913
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
```

```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQ 14
|||||
Db 35 LRFDSQTKSIFQEQ 48

RESULT 5
I49589
antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49589
R:Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A:Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A:Reference number: I49589; MUID:94054345; PMID:8236164
A:Accession: I49589
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g398911; PID:
C:Superfamily: CD9 antigen

Query Match 58.3%; Score 14; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFQEQ 14
|||||
Db 35 LRFDSQTKSIFQEQ 48

RESULT 6
H84774
probable homeodomain transcription factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84774
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: H84420; MUID:20083487; PMID:10617197
A:Accession: H84774
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-680 <STO>
A:Cross-references: UNIPROT:Q9SJ56; UNIPARC:UPI000009E071; GB:AE002093; NID:g4510375; P
C:Genetics:
A:Gene: At2g35940
A:Map position: 2

Query Match 33.3%; Score 8; DB 2; Length 680;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNSSP 22
|||||
Db 59 TNNNNSSP 66

RESULT 7
A96913
ABC-type sulfate transporter, ATPase component CAC0107 [imported] - Clostridium acetobu
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C:Accession: A96913
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
```

A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A96913
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <KUR>
A;Cross-references: UNIPROT:Q97MT4; UNIPARC:UPI00000C9D67; GB:AE001437; PIDN:AAK78092.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0107

Query Match 29.2%; Score 7; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTKSI 10
|||
Db 165 DSQTKSI 171

RESULT 8
T18420
hypothetical protein C0130c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18420
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z18934
A;Accession: T18420
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-419 <LAW>
A;Cross-references: UNIPROT:O77316; UNIPARC:UPI0000076B8E; EMBL:Z97348; NID:e1323671; PID
C;Genetics:
A;Note: C0130c

Query Match 29.2%; Score 7; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 NNNNSF 22
|||
Db 394 NNNNSF 400

RESULT 9
S59405
probable membrane protein YLR436c - Yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9753.7
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S59405
R;Du, Z.

submitted to the EMBL Data Library, February 1995
A;Description: The sequence of S. cerevisiae cosmid 9753.
A;Reference number: S59401
A;Accession: S59405
A;Molecule type: DNA
A;Residues: 1-1274 <DUZ>
A;Cross-references: UNIPROT:Q06673; UNIPARC:UPI0000052EAF; EMBL:U21094; NID:g665967; PID
A;Experimental source: strain S288C (AB972)
C;Genetics:

A;Gene: SGD:ECW30
A;Cross-references: SGD:S0004428; MIPS:YLR436c
A;Map position: 12R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YLR436c
C;Keywords: transmembrane protein
F;117-133/Domain: transmembrane #status predicted <TM1>
F;242-258/Domain: transmembrane #status predicted <TM2>
F;529-545/Domain: transmembrane #status predicted <TM3>
F;710-726/Domain: transmembrane #status predicted <TM4>

Query Match 29.2%; Score 7; DB 2; Length 1274;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ETNNNS 20
|||
Db 1134 ETNNNS 1140

RESULT 10
A48180
small acid-soluble spore protein 1 - Sporosarcina ureae
C;Species: Sporosarcina ureae
C;Date: 10-Mar-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: A48180
R;Magill, N.G.; Loshon, C.A.; Setlow, P.
FEMS Microbiol. Lett. 72, 293-298, 1990
A;Title: Small, acid-soluble, spore proteins and their genes from two species of Sporos
A;Reference number: A48180
A;Accession: A48180
A;Molecule type: DNA
A;Residues: 1-69 <MAG>
A;Cross-references: UNIPROT:P52968; UNIPARC:UPI000004AB1B; GB:X55158; NID:947971; PIDN:
C;Comment: Saturation of DNA with this alpha/beta-type small acid-soluble spore protein
dly during the first minutes of germination, after an initial cleavage by the spore prot
C;Superfamily: alpha/beta-type small acid-soluble spore protein
C;Keywords: DNA binding; germination; sporulation; storage protein
F;2-69/Product: small acid-soluble spore protein 1 #status predicted <MAT>
F;27-28/Cleavage site: Glu-Ile (spore-specific proteinase) #status predicted

Query Match 25.0%; Score 6; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TNNNS 20
|||
Db 2 TNNNS 7

RESULT 11
B85911
hypothetical protein Z3937 [imported] - Escherichia coli (strain O157:H7, substrain EDL5
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85911
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: B85911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-92 <STO>
A;Cross-references: UNIPROT:Q8X978; UNIPARC:UPI00001658D6; GB:AE005174; NID:g12517070; F;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3937

Query Match 25.0%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTKS 9
|||
Db 60 DSQTKS 65

RESULT 12
S52508
probable membrane protein YDL011c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2885
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S52508; S67543
R;Andre, B.; Vissers, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV
A;Reference number: S52492
A;Accession: S52508
A;Molecule type: DNA
A;Residues: 1-107 <AND>
A;Cross-references: UNIPROT:Q12023; UNIPARC:UPI000006C1A5; EMBL:Z48432; NID:g683669; PID:11258796
R;Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67535
A;Accession: S67543
A;Molecule type: DNA
A;Residues: 1-107 <URR>
A;Cross-references: UNIPARC:UPI000006C1A5; EMBL:Z74059; NID:g1430970; PID:g1430971; MIPS:11258796
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0002169
A;Map position: 4L
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YDL011c
C;Keywords: transmembrane protein
F;50-66/Domain: transmembrane #status predicted <TM1>
F;86-102/Domain: transmembrane #status predicted <TM2>
Query Match 25.0%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TNNNS 20
Db 80 TNNNS 85
RESULT 13
B91067
hypothetical lipoprotein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B91067
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <HAY>
A;Cross-references: UNIPROT:Q8X978; UNIPARC:UPI00000D085E; GB:BA000007; PIDN:BA036929.1;
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: EC83506
Query Match 25.0%; Score 6; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTKS 9
Db 99 DSQTKS 104
RESULT 14
T17640
hypothetical protein a149L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17640
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806

A;Accession: T17640
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <GRA>
A;Cross-references: UNIPROT:Q84469; UNIPARC:UPI00000F0AAC; EMBL:U42580; NID:g4028896; P
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: a149L
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A149L
Query Match 25.0%; Score 6; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RFDSTQ 7
Db 89 RFDSTQ 94
RESULT 15
D95131
hypothetical protein SP1135 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95131
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hel
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: D95131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <KUR>
A;Cross-references: UNIPROT:Q97QR5; UNIPARC:UPI000005170C; GB:AE005672; PIDN:AAK75245.1
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1135
Query Match 25.0%; Score 6; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SQTQSI 10
Db 37 SQTQSI 42
Search completed: January 20, 2006, 17:44:35
Job time : 18.5385 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:34:35 ; Search time 30.2308 Seconds
(without alignments)
560.114 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24

Sequence: 1 LRFDQTKSIFQETNNNSPYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	182	2	Q56CY1 homo sapien
2	24	100.0	227	1	CD9 CERAE
3	24	100.0	227	1	CD9 HUMAN
4	24	100.0	228	2	Q5J7W6 HUMAN
5	16	66.7	225	1	CD9 RAT
6	14	58.3	225	1	CD9 BOVIN
7	14	58.3	225	1	CD9 MOUSE
8	14	58.3	225	1	CD9 PIG
9	14	58.3	226	2	Q8MJ48 PIG
10	13	54.2	225	1	CD9 FELCA
11	8	33.3	228	2	Q8AV92 PETWA
12	8	33.3	228	2	Q6GQES XENLA
13	8	33.3	607	2	Q56F04 9CAUD
14	8	33.3	607	2	Q6U9U5 9CAUD
15	8	33.3	607	2	Q76XL0 9CAUD
16	8	33.3	680	2	Q94KL4 ARATH
17	8	33.3	680	2	Q9SU56 ARATH
18	7	29.2	77	2	Q70905 9HIV1
19	7	29.2	88	2	Q69744 9HIV1
20	7	29.2	88	2	Q70907 9HIV1
21	7	29.2	89	2	Q70906 9HIV1
22	7	29.2	89	2	Q70908 9HIV1
23	7	29.2	91	2	Q70904 9HIV1
24	7	29.2	91	2	Q70910 9HIV1
25	7	29.2	92	2	Q70909 9HIV1
26	7	29.2	110	2	Q9BADI FUCVE
27	7	29.2	131	2	Q7PX92 ANOGA
28	7	29.2	133	2	Q4YMU0 FLABE
29	7	29.2	137	2	Q8R7G8 THETN
30	7	29.2	166	2	Q5CDE4 CRYHO
31	7	29.2	224	2	Q9IBC9 CHICK

32	7	29.2	234	2	Q6TBF6 9ROSI	Q6tbf6 trigonia ni
33	7	29.2	271	2	Q4NR07 BACCE	Q4nr07 bacillus ce
34	7	29.2	271	2	Q72V61 BACCI	Q72v61 bacillus ce
35	7	29.2	271	2	Q6HBN7 BACHK	Q6hbn7 bacillus th
36	7	29.2	271	2	Q631V1 BACCZ	Q631v1 bacillus ce
37	7	29.2	271	2	Q81XHS BACAN	Q81xhs bacillus an
38	7	29.2	272	2	Q6VSA5 9APIC	Q6vsa5 plasmodium
39	7	29.2	279	2	Q97MT4 CIOAB	Q97mt4 clostridium
40	7	29.2	309	2	Q9P4W5 KLULA	Q9p4w5 kluyveromyc
41	7	29.2	320	2	Q66078 9LACT	Q66078 lactococcus
42	7	29.2	331	2	Q7SEL4 NEUCR	Q7sel4 neurospora
43	7	29.2	333	2	Q8T986 DROME	Q8t986 drosophila
44	7	29.2	336	2	Q5XWK5 SOLTU	Q5xwk5 solanum tub
45	7	29.2	363	2	Q93ZD2 ARATH	Q93zd2 arabidopsis
46	7	29.2	363	2	Q9CSA2 ARATH	Q9csa2 arabidopsis
47	7	29.2	402	2	Q54JN3 DICDI	Q54jn3 dictyosteli
48	7	29.2	419	2	Q77316 PLAF7	Q77316 plasmodium
49	7	29.2	469	2	Q5RHM6 BRARE	Q5rhm6 brachydanio
50	7	29.2	479	2	Q54CR0 DICDI	Q54cr0 dictyosteli
51	7	29.2	487	2	Q5GRL4 WOLTR	Q5grl4 wolbachia s
52	7	29.2	524	2	Q54N32 DICDI	Q54n32 dictyosteli
53	7	29.2	539	2	Q4RW38 TETNG	Q4rw38 tetraodon n
54	7	29.2	544	2	Q70147 9HIV1	Q70147 human immun
55	7	29.2	556	2	Q59LE2 CANAL	Q59le2 candida alb
56	7	29.2	606	2	Q7Y5D4 BPR69	Q7y5d4 bacterioph
57	7	29.2	608	2	Q4YJS0 PLABE	Q4yjs0 plasmodium
58	7	29.2	647	2	Q869Q4 DICDI	Q869q4 dictyosteli
59	7	29.2	674	2	Q55513 DICDI	Q55513 dictyosteli
60	7	29.2	688	2	Q55FD6 DICDI	Q55fd6 dictyosteli
61	7	29.2	779	2	Q7YY75 CRYPV	Q7yy75 cryptospori
62	7	29.2	824	2	Q54JC5 DICDI	Q54jc5 dictyosteli
63	7	29.2	824	2	Q54JC5 DICDI	Q54jc5 dictyosteli
64	7	29.2	846	2	Q54WR0 DICDI	Q54wr0 dictyosteli
65	7	29.2	851	2	Q70145 9HIV1	Q70145 human immun
66	7	29.2	858	2	Q6BC37 9HIV1	Q6bc37 human immun
67	7	29.2	864	2	Q9YP39 9HIV1	Q9yp39 human immun
68	7	29.2	879	2	Q54P37 DICDI	Q54p37 dictyosteli
69	7	29.2	981	2	Q54SW0 DICDI	Q54sw0 dictyosteli
70	7	29.2	1016	2	Q54DM8 DICDI	Q54dm8 dictyosteli
71	7	29.2	1043	2	Q8SSW7 DICDI	Q8ssw7 dictyosteli
72	7	29.2	1056	2	Q6YHU9 SCHNA	Q6yhu9 schistosoma
73	7	29.2	1264	2	Q7S9R1 NEUCR	Q7s9r1 neurospora
74	7	29.2	1274	1	ECM30 YEAST	Q06673 saccharomyc
75	7	29.2	1304	2	Q9VBE5 DROME	Q9vbe5 drosophila
76	7	29.2	1333	2	Q54XA8 DICDI	Q54xa8 dictyosteli
77	7	29.2	1480	2	Q54VW9 DICDI	Q54vw9 dictyosteli
78	7	29.2	1550	2	Q54GSI DICDI	Q54gsi dictyosteli
79	7	29.2	1861	2	Q55F12 DICDI	Q55f12 dictyosteli
80	7	29.2	1964	2	Q81IX6 PLAF7	Q81ix6 plasmodium
81	7	29.2	1992	2	Q55BR0 DICDI	Q55br0 dictyosteli
82	7	29.2	2825	2	Q81D16 PLAF7	Q81d16 plasmodium
83	7	29.2	3078	2	Q81KH4 PLAF7	Q81kh4 plasmodium
84	7	29.2	5222	2	Q54L33 DICDI	Q54l33 dictyosteli
85	6	25.0	44	2	Q53IG5 PLAPA	Q53ig5 plasmodium
86	6	25.0	46	2	Q53IG7 PLAPA	Q53ig7 plasmodium
87	6	25.0	48	2	Q54VH6 DICDI	Q54vh6 dictyosteli
88	6	25.0	49	2	Q53IG9 PLAPA	Q53ig9 plasmodium
89	6	25.0	52	2	Q4XPC5 PLACH	Q4xpc5 plasmodium
90	6	25.0	52	2	Q53IH0 PLAPA	Q53ih0 plasmodium
91	6	25.0	53	2	Q53IG8 PLAPA	Q53ig8 plasmodium
92	6	25.0	55	2	Q53IG6 PLAPA	Q53ig6 plasmodium
93	6	25.0	67	2	Q4L388 STAHJ	Q4l388 staphylococ
94	6	25.0	67	2	Q7YVP7 9TRYP	Q7yvp7 trypanosoma
95	6	25.0	69	1	SASI SPOUR	P52968 sporosarcin
96	6	25.0	78	2	Q61M90 CAEBR	Q61m90 caenorhabdi
97	6	25.0	78	2	Q8TIK3 METAC	Q8tik3 methanosarc
98	6	25.0	82	2	Q55F08 DICDI	Q55f08 dictyosteli
99	6	25.0	90	2	Q81FL5 PLAF7	Q81fl5 plasmodium
100	6	25.0	91	2	Q61T84 ONCFA	Q61t84 oncopeltus
101	6	25.0	91	2	Q8HCF8 EUSO	Q8hcf8 eusosta sol
102	6	25.0	92	2	Q8X978 ECO57	Q8x978 escherichia
103	6	25.0	96	2	Q5YK64 MYCGE	Q5yk64 mycoplasma
104	6	25.0	97	2	Q8TF84 YEAST	Q8tf84 saccharomyc

105	6	25.0	98	2	Q4YP43_PLABE	Q4YP43 plasmodium	178	6	25.0	176	2	Q7XXZ9_MIMGU	Q7xxz9 mimulus gut
106	6	25.0	102	2	Q5AFP2_DICDI	Q5AFP2 dictyosteli	179	6	25.0	176	2	Q7XY01_MIMGU	Q7xy01 mimulus gut
107	6	25.0	104	2	Q5AD14_CANAL	Q5AD14 candida alb	180	6	25.0	177	2	Q764J4_PLABE	Q764j4 plasmodium
108	6	25.0	107	2	Q12023_YEAST	Q12023 saccharomyc	181	6	25.0	177	2	Q4YTW4_PLABE	Q4ytw4 plasmodium
109	6	25.0	109	2	Q24542_DROME	Q24542 drosophila	182	6	25.0	177	2	Q7X611_MIMNA	Q7x611 mimulus nas
110	6	25.0	110	2	Q57VW7_TRYTP	Q57vw7 trypanosoma	183	6	25.0	177	2	Q7X7K4_MIMNA	Q7x7k4 mimulus nas
111	6	25.0	113	2	Q54R21_DICDI	Q54r21 dictyosteli	184	6	25.0	177	2	Q7XXV6_MIMNA	Q7xxv6 mimulus nas
112	6	25.0	115	2	Q5DDF3_SCHJA	Q5ddf3 schistosoma	185	6	25.0	177	2	Q7XXM4_MIMGU	Q7xxm4 mimulus gut
113	6	25.0	118	2	Q9U9Z1_LINUN	Q9u9z1 lingua ung	186	6	25.0	177	2	Q7X6X6_MIMPL	Q7x6x6 mimulus pia
114	6	25.0	120	2	Q8EN11_OCEIH	Q8en11 oceanobacil	187	6	25.0	178	2	Q7XXU9_MIMNA	Q7xxu9 mimulus nas
115	6	25.0	122	2	Q54NI2_DICDI	Q54ni2 dictyosteli	188	6	25.0	178	2	Q7XXV1_MIMNA	Q7xxv1 mimulus nas
116	6	25.0	124	2	Q36886_SCHJA	Q36886 schistosoma	189	6	25.0	178	2	Q7XXW6_MIMGU	Q7xxw6 mimulus gut
117	6	25.0	126	2	Q7YX21_CABEL	Q7yx21 caenorhabdi	190	6	25.0	178	2	Q7XXZ6_MIMGU	Q7xxz6 mimulus gut
118	6	25.0	126	2	Q6Y9V5_9SOLA	Q6y9v5 schizanthus	191	6	25.0	179	2	Q9XZ40_PLABE	Q9xz40 plasmodium
119	6	25.0	127	2	Q6Y9V4_9SOLA	Q6y9v4 schizanthus	192	6	25.0	179	2	Q7XXU6_MIMNA	Q7xxu6 mimulus nas
120	6	25.0	128	2	Q5ARF1_DICDI	Q5arf1 dictyosteli	193	6	25.0	179	2	Q7XXV7_MIMGU	Q7xxv7 mimulus gut
121	6	25.0	129	2	Q69QZ5_ORYSA	Q69qz5 oryza sativ	194	6	25.0	180	2	Q25945_PLABE	Q25945 plasmodium
122	6	25.0	131	2	Q65XW5_ORYSA	Q65xw5 oryza sativ	195	6	25.0	180	2	Q25945_PLABE	Q25945 plasmodium
123	6	25.0	131	2	Q7ABG0_ECO57	Q7abg0 escherichia	196	6	25.0	180	2	Q9TXC4_PLABE	Q9txc4 plasmodium
124	6	25.0	133	1	RBFA_CHLMU	Q9pkul chlamydia m	197	6	25.0	180	2	Q7XXU8_MIMNA	Q7xxu8 mimulus nas
125	6	25.0	134	2	Q88F39_9TREM	Q88f39 schistosoma	198	6	25.0	180	2	Q7XXV9_MIMGU	Q7xxv9 mimulus gut
126	6	25.0	136	2	Q84469_CHVP1	Q84469 paramecium	199	6	25.0	180	2	Q7XXZ0_MIMGU	Q7xxz0 mimulus gut
127	6	25.0	137	2	Q6U5F8_PLABE	Q6u5f8 plasmodium	200	6	25.0	181	2	Q7X6G8_MIMGU	Q7x6g8 mimulus gut
128	6	25.0	137	2	Q55DG1_DICDI	Q55dg1 dictyosteli	201	6	25.0	181	2	Q7XXV4_MIMNA	Q7xxv4 mimulus nas
129	6	25.0	137	2	Q4YX33_PLABE	Q4yx33 plasmodium	202	6	25.0	181	2	Q7XXW9_MIMGU	Q7xxw9 mimulus gut
130	6	25.0	138	2	Q5C585_SCHJA	Q5c585 schistosoma	203	6	25.0	182	2	Q8IR78_DROME	Q8irt8 drosophila
131	6	25.0	138	2	Q95T66_DROME	Q95t66 drosophila	204	6	25.0	182	2	Q4YTW8_PLABE	Q4ytw8 plasmodium
132	6	25.0	138	2	Q98K76_RHITO	Q98k76 rhizobium l	205	6	25.0	182	2	Q7X6N7_MIMNA	Q7x6n7 mimulus nas
133	6	25.0	139	2	Q6WHX9_BPKV4	Q6whx9 bacterioph	206	6	25.0	182	2	Q7X706_MIMGU	Q7x706 mimulus gut
134	6	25.0	141	2	Q94HJ6_ORYSA	Q94hj6 oryza sativ	207	6	25.0	182	2	Q7XXU4_MIMLA	Q7xxu4 mimulus lac
135	6	25.0	142	2	Q5C2K3_SCHJA	Q5c2k3 schistosoma	208	6	25.0	182	2	Q7XXU5_MIMNA	Q7xxu5 mimulus nas
136	6	25.0	143	2	Q59X66_CANAL	Q59x66 candida alb	209	6	25.0	182	2	Q7XXZ0_MIMGU	Q7xxz0 mimulus gut
137	6	25.0	144	2	Q59XB4_CANAL	Q59xb4 candida alb	210	6	25.0	183	2	Q6U9A7_PLABE	Q6ua97 plasmodium
138	6	25.0	146	2	Q25711_PLABE	Q25711 plasmodium	211	6	25.0	183	2	Q86QX1_PLABE	Q86qx1 plasmodium
139	6	25.0	146	2	Q7TU06_RHOBA	Q7tu06 rhodopirell	212	6	25.0	183	2	Q9U0B5_PLABE	Q9u0b5 plasmodium
140	6	25.0	147	2	Q15805_PLABE	Q15805 plasmodium	213	6	25.0	183	2	Q9U0B6_PLABE	Q9u0b6 plasmodium
141	6	25.0	147	2	Q6U5F7_PLABE	Q6u5f7 plasmodium	214	6	25.0	183	2	Q7X7H2_MIMGU	Q7x7h2 mimulus gut
142	6	25.0	150	2	Q97QR5_STRPN	Q97qr5 streptococ	215	6	25.0	184	2	Q5DEB3_SCHJA	Q5ded3 schistosoma
143	6	25.0	151	2	Q6U9A9_PLABE	Q6ua99 plasmodium	216	6	25.0	184	2	Q86QX2_PLABE	Q86qx2 plasmodium
144	6	25.0	152	2	Q25697_PLABE	Q25697 plasmodium	217	6	25.0	184	2	Q9TY34_PLABE	Q9ty34 plasmodium
145	6	25.0	155	2	Q6U5F5_PLABE	Q6u5f5 plasmodium	218	6	25.0	184	2	Q9U0B8_PLABE	Q9u0b8 plasmodium
146	6	25.0	155	2	Q6U9A8_PLABE	Q6ua98 plasmodium	219	6	25.0	184	2	Q9U0B9_PLABE	Q9u0b9 plasmodium
147	6	25.0	157	2	Q25713_PLABE	Q25713 plasmodium	220	6	25.0	184	2	Q7XXW1_MIMGU	Q7xxw1 mimulus gut
148	6	25.0	159	2	Q6U5F3_PLABE	Q6u5f3 plasmodium	221	6	25.0	185	2	Q6U9A9_PLABE	Q6ua99 plasmodium
149	6	25.0	161	2	Q59I16_CANAL	Q59i16 candida alb	222	6	25.0	185	2	Q4G402_MACMU	Q4g402 macaca mula
150	6	25.0	161	2	Q6U9A0_PLABE	Q6ua90 plasmodium	223	6	25.0	185	2	Q35069_MOUSE	Q35069 mus musculus
151	6	25.0	162	2	Q25702_PLABE	Q25702 plasmodium	224	6	25.0	185	2	Q80RK5_PRRSV	Q80rk5 porcine rep
152	6	25.0	162	2	Q25714_PLABE	Q25714 plasmodium	225	6	25.0	186	2	Q764J5_PLABE	Q764j5 plasmodium
153	6	25.0	162	2	Q6QV33_9RETR	Q6qv33 equine infe	226	6	25.0	186	2	Q86QX3_PLABE	Q86qx3 plasmodium
154	6	25.0	163	2	Q9LY93_ARATH	Q9ly93 arabidopsis	227	6	25.0	186	2	Q55EQ1_DICDI	Q55eq1 dictyosteli
155	6	25.0	163	2	Q7XXW5_MIMGU	Q7xxw5 mimulus gut	228	6	25.0	186	2	Q7XXU2_MIMNU	Q7xxu2 mimulus nud
156	6	25.0	166	2	Q25698_PLABE	Q25698 plasmodium	229	6	25.0	187	2	Q6U5G0_PLABE	Q6u5g0 plasmodium
157	6	25.0	166	2	Q86QX0_PLABE	Q86qx0 plasmodium	230	6	25.0	187	2	Q9XZ39_PLABE	Q9xz39 plasmodium
158	6	25.0	167	2	Q27911_POIMI	Q27911 polyandroca	231	6	25.0	188	2	Q6XJ05_DROYA	Q6xj05 drosophila
159	6	25.0	168	2	Q6U5E9_PLABE	Q6u5e9 plasmodium	232	6	25.0	188	2	Q7XXW7_MIMGU	Q7xxw7 mimulus gut
160	6	25.0	168	2	Q5C7B4_SCHJA	Q5c7b4 schistosoma	233	6	25.0	188	2	Q7XXY3_MIMGU	Q7xyy3 mimulus gut
161	6	25.0	169	2	Q5HRZ4_STABEQ	Q5hrz4 staphylococ	234	6	25.0	189	2	Q7X781_MIMNA	Q7x781 mimulus nas
162	6	25.0	169	2	Q8CQP5_STAEP	Q8cp5 staphylococ	235	6	25.0	189	2	Q7X782_MIMGU	Q7x782 mimulus gut
163	6	25.0	170	2	Q4L341_STAEP	Q4l341 staphylococ	236	6	25.0	189	2	Q7X7R0_MIMNA	Q7x7r0 mimulus nas
164	6	25.0	171	2	Q4XDB7_PLACH	Q4xdb7 plasmodium	237	6	25.0	189	2	Q7XXW3_MIMGU	Q7xxw3 mimulus gut
165	6	25.0	171	2	Q7XXU3_MIMLA	Q7xxu3 mimulus lac	238	6	25.0	189	2	Q7XXX1_MIMGU	Q7xxx1 mimulus gut
166	6	25.0	171	2	Q6UDP0_9HIV1	Q6udp0 human immun	239	6	25.0	189	2	Q7XXX3_MIMGU	Q7xxx3 mimulus gut
167	6	25.0	172	2	Q7XXZ7_MIMGU	Q7xxz7 mimulus gut	240	6	25.0	189	2	Q7XXY2_MIMGU	Q7xyy2 mimulus gut
168	6	25.0	173	2	Q9BJP5_PLABE	Q9bjp5 plasmodium	241	6	25.0	189	2	Q7XXY4_MIMGU	Q7xyy4 mimulus gut
169	6	25.0	173	2	Q8IGK9_DROME	Q8igk9 drosophila	242	6	25.0	189	2	Q7XXY7_MIMGU	Q7xyy7 mimulus gut
170	6	25.0	173	2	Q7XXX6_MIMGU	Q7xxx6 mimulus gut	243	6	25.0	189	2	Q7XXZ2_MIMGU	Q7xxz2 mimulus gut
171	6	25.0	174	2	Q9U0C4_PLABE	Q9u0c4 plasmodium	244	6	25.0	190	2	Q7X827_MIMGU	Q7x827 mimulus gut
172	6	25.0	175	2	Q7XXV2_MIMNA	Q7xxv2 mimulus nas	245	6	25.0	190	2	Q7X8S8_MIMGU	Q7x8s8 mimulus gut
173	6	25.0	175	2	Q7XXV5_MIMNA	Q7xxv5 mimulus nas	246	6	25.0	190	2	Q7XXW8_MIMGU	Q7xxw8 mimulus gut
174	6	25.0	176	2	Q6U5F0_PLABE	Q6u5f0 plasmodium	247	6	25.0	190	2	Q7XXX4_MIMGU	Q7xxx4 mimulus gut
175	6	25.0	176	2	Q7X6J7_MIMNA	Q7x6j7 mimulus nas	248	6	25.0	190	2	Q7XXX7_MIMGU	Q7xxx7 mimulus gut
176	6	25.0	176	2	Q7XXV0_MIMNA	Q7xxv0 mimulus nas	249	6	25.0	190	2	Q7XXX8_MIMGU	Q7xxx8 mimulus gut
177	6	25.0	176	2	Q7XXV3_MIMNA	Q7xxv3 mimulus nas	250	6	25.0	190	2	Q7XXY5_MIMGU	Q7xyy5 mimulus gut

251	6	25.0	190	2	Q7XXZ5_MIMGU	Q7xxz5 mimulus gut	324	6	25.0	223	2	Q8IT84_PLAFA	Q8it84 plasmodium
252	6	25.0	190	2	Q7XY00_MIMGU	Q7xy00 mimulus gut	325	6	25.0	223	2	Q5XZ56_PLAFA	Q5xz56 plasmodium
253	6	25.0	191	2	Q6QYL1_PLAFA	Q6qyl1 plasmodium	326	6	25.0	225	2	Q5CXM1_CRYPV	Q5cxm1 cryptospori
254	6	25.0	191	2	Q9UOC1_PLAFA	Q9uoc1 plasmodium	327	6	25.0	226	2	Q9UOB2_PLAFA	Q9uob2 plasmodium
255	6	25.0	191	2	Q7X664_MIMGU	Q7x664 mimulus gut	328	6	25.0	227	2	Q4X4K4_PLACH	Q4x4k4 plasmodium
256	6	25.0	191	2	Q7X7A2_MIMGU	Q7x7a2 mimulus gut	329	6	25.0	228	2	Q24166_DROME	Q24166 drosophila
257	6	25.0	191	2	Q7XXW6_MIMGU	Q7xxw6 mimulus gut	330	6	25.0	228	2	Q9VD73_DROME	Q9vd73 drosophila
258	6	25.0	191	2	Q7XXX2_MIMGU	Q7xxx2 mimulus gut	331	6	25.0	229	1	LBD11_ARATH	Q9xk08 arabidopsis
259	6	25.0	191	2	Q7XXX5_MIMGU	Q7xxx5 mimulus gut	332	6	25.0	230	2	Q95N16_TRICA	Q95n16 tribolium c
260	6	25.0	191	2	Q7XXY1_MIMGU	Q7xxy1 mimulus gut	333	6	25.0	230	2	Q4YAS3_PLABE	Q4yas3 plasmodium
261	6	25.0	191	2	Q7XXY6_MIMGU	Q7xxy6 mimulus gut	334	6	25.0	231	2	Q8LLY1_ORYSA	Q8lly1 oryza sativ
262	6	25.0	192	2	Q4Y612_PLACH	Q4y612 plasmodium	335	6	25.0	233	2	Q9UOC2_PLAFA	Q9uoc2 plasmodium
263	6	25.0	192	2	Q7X7C6_MIMNA	Q7x7c6 mimulus nas	336	6	25.0	233	2	Q6E769_SAPPE	Q6e769 saprolegnia
264	6	25.0	193	2	Q7XXU7_MIMNA	Q7xxu7 mimulus nas	337	6	25.0	234	2	Q25769_PLAFA	Q25769 plasmodium
265	6	25.0	193	2	Q5ALZ1_CANAL	Q5alz1 candida alb	338	6	25.0	234	2	Q8XI71_CLOPE	Q8xi71 clostridium
266	6	25.0	193	2	Q4HFN2_CAMCO	Q4hfn2 campylobact	339	6	25.0	235	2	Q8IGN6_DROME	Q8ign6 drosophila
267	6	25.0	193	2	Q6U5G1_PLAFA	Q6u5g1 plasmodium	340	6	25.0	237	2	Q6G0E7_BARQU	Q6g0e7 bartonella
268	6	25.0	194	2	Q764J6_PLAFA	Q764j6 plasmodium	341	6	25.0	238	2	Q5AAD1_CANAL	Q5aad1 candida alb
269	6	25.0	194	2	Q9FIP6_ARATH	Q9fip6 arabidopsis	342	6	25.0	238	2	Q54T68_DICDI	Q54t68 dictyosteli
270	6	25.0	194	2	Q82W50_NITEU	Q82w50 nitrosomona	343	6	25.0	238	2	Q8T174_DICDI	Q8t174 dictyosteli
271	6	25.0	194	2	Q8YGC9_BRUME	Q8ygc9 brucella me	344	6	25.0	240	2	Q6B923_GRATL	Q6b923 gracilaria
272	6	25.0	195	2	Q25694_PLAFA	Q25694 plasmodium	345	6	25.0	240	2	Q94F99_MINNA	Q94f99 mimulus nas
273	6	25.0	195	2	Q25715_PLAFA	Q25715 plasmodium	346	6	25.0	241	2	Q4TM29_PLABE	Q4ym29 plasmodium
274	6	25.0	195	2	Q25948_PLAFA	Q25948 plasmodium	347	6	25.0	241	2	Q9SV16_ARATH	Q9sv16 arabidopsis
275	6	25.0	196	2	Q25947_PLAFA	Q25947 plasmodium	348	6	25.0	242	2	Q54P36_DICDI	Q54p36 dictyosteli
276	6	25.0	196	2	Q25951_PLAFA	Q25951 plasmodium	349	6	25.0	242	2	Q8GMF3_ARATH	Q8gmf3 arabidopsis
277	6	25.0	196	2	Q764J7_PLAFA	Q764j7 plasmodium	350	6	25.0	243	2	Q4X4S5_PLACH	Q4x4s5 plasmodium
278	6	25.0	196	2	Q9GQY7_PLAFA	Q9gqy7 plasmodium	351	6	25.0	245	2	Q54I25_DICDI	Q54i25 dictyosteli
279	6	25.0	196	2	Q9UOB7_PLAFA	Q9uob7 plasmodium	352	6	25.0	245	2	Q7ZXI4_XENLA	Q7zxy4 xenopus lae
280	6	25.0	196	2	Q54XLS_DICDI	Q54xls dictyosteli	353	6	25.0	246	1	YOR4_ANATH	Q4408 anaerocellu
281	6	25.0	196	2	Q57E21_BRUAB	Q57e21 brucella ab	354	6	25.0	247	2	Q95Z54_PLAFA	Q95z54 plasmodium
282	6	25.0	196	2	Q5GT34_WOLTR	Q5gt34 wolbachia s	355	6	25.0	249	2	Q4PGL0_USTMA	Q4pgl0 ustilago ma
283	6	25.0	197	2	Q8G1J3_BRUSU	Q8g1j3 brucella su	356	6	25.0	249	2	Q54YG3_DICDI	Q54yg3 dictyosteli
284	6	25.0	197	2	Q6U5F6_PLAFA	Q6u5f6 plasmodium	357	6	25.0	249	2	Q9VPM8_DROME	Q9vpm8 drosophila
285	6	25.0	200	2	Q513H2_PRESV	Q513h2 porcine rep	358	6	25.0	249	2	Q90S11_9HIV1	Q90s11 human immun
286	6	25.0	201	2	Q9YNP3_9HIV1	Q9ynp3 human immun	359	6	25.0	251	2	Q51351_9RETR	Q51351 equine infe
287	6	25.0	202	2	Q25952_PLAFA	Q25952 plasmodium	360	6	25.0	251	2	Q51359_9RETR	Q51359 equine infe
288	6	25.0	202	2	Q7SKT8_9HIV1	Q7skt8 human immun	361	6	25.0	252	2	Q9FY93_ARATH	Q9fy93 arabidopsis
289	6	25.0	203	2	Q15806_PLAFA	Q15806 plasmodium	362	6	25.0	252	2	Q4SGB0_TETNG	Q4sgb0 tetraodon n
290	6	25.0	203	2	Q9UOC0_PLAFA	Q9uoc0 plasmodium	363	6	25.0	253	2	Q51362_9RETR	Q51362 equine infe
291	6	25.0	203	2	Q736D0_BACCI	Q736d0 bacillus ce	364	6	25.0	254	2	Q53IP8_GBPFU	Q53ip8 gibberella
292	6	25.0	204	2	Q9UOB4_PLAFA	Q9uob4 plasmodium	365	6	25.0	254	2	Q51372_9RETR	Q51372 equine infe
293	6	25.0	204	2	Q54MC8_DICDI	Q54mc8 dictyosteli	366	6	25.0	255	2	Q6MTG2_MYCMA	Q6mtg2 mycoplasma
294	6	25.0	205	2	Q25944_PLAFA	Q25944 plasmodium	367	6	25.0	256	2	Q6R795_9HERP	Q6r795 ostreid her
295	6	25.0	205	2	Q25946_PLAFA	Q25946 plasmodium	368	6	25.0	257	2	Q6FJBA_CANGA	Q6fjba candida gla
296	6	25.0	205	2	Q9TXC5_PLAFA	Q9txc5 plasmodium	369	6	25.0	257	2	Q54H93_DICDI	Q54h93 dictyosteli
297	6	25.0	205	2	Q54MI7_DICDI	Q54mi7 dictyosteli	370	6	25.0	257	2	Q54HH8_DICDI	Q54hn8 dictyosteli
298	6	25.0	206	2	Q9UOC3_PLAFA	Q9uoc3 plasmodium	371	6	25.0	257	2	Q8SWV1_DROME	Q8swv1 drosophila
299	6	25.0	206	2	Q86L16_DICDI	Q86l16 dictyosteli	372	6	25.0	257	2	Q9A7B3_CAUCR	Q9a7b3 caulobacter
300	6	25.0	206	2	Q95Z57_PLAFA	Q95z57 plasmodium	373	6	25.0	257	2	Q6W987_9PERC	Q6w987 spheeroides
301	6	25.0	207	2	Q25701_PLAFA	Q25701 plasmodium	374	6	25.0	258	2	Q68LB3_9DIPT	Q68lb3 drosophila
302	6	25.0	208	2	Q25949_PLAFA	Q25949 plasmodium	375	6	25.0	258	2	Q512Z4_9RETR	Q512z4 equine infe
303	6	25.0	208	2	Q9UOA0_PLAFA	Q9uoa0 plasmodium	376	6	25.0	258	2	Q512Z5_9RETR	Q512z5 equine infe
304	6	25.0	209	2	Q86JH2_DICDI	Q86jh2 dictyosteli	377	6	25.0	258	2	Q512Z6_9RETR	Q512z6 equine infe
305	6	25.0	210	2	Q707X1_CANGA	Q707x1 candida gla	378	6	25.0	258	2	Q512Z7_9RETR	Q512z7 equine infe
306	6	25.0	212	2	Q95Z55_PLAFA	Q95z55 plasmodium	379	6	25.0	258	2	Q51304_9RETR	Q51304 equine infe
307	6	25.0	213	1	YFEL_ECOLI	P76543 escherichia	380	6	25.0	258	2	Q51310_9RETR	Q51310 equine infe
308	6	25.0	213	2	Q5ABQ6_CANAL	Q5abq6 candida alb	381	6	25.0	258	2	Q51315_9RETR	Q51315 equine infe
309	6	25.0	213	2	Q4XB89_PLACH	Q4xb89 plasmodium	382	6	25.0	258	2	Q51317_9RETR	Q51317 equine infe
310	6	25.0	214	2	Q5TNZ3_ANOGA	Q5tnz3 anopheles g	383	6	25.0	258	2	Q51320_9RETR	Q51320 equine infe
311	6	25.0	214	2	Q9V9Y2_DROME	Q9v9y2 drosophila	384	6	25.0	258	2	Q51338_9RETR	Q51338 equine infe
312	6	25.0	216	2	Q9U099_PLAFA	Q9u099 plasmodium	385	6	25.0	258	2	Q51342_9RETR	Q51342 equine infe
313	6	25.0	216	2	Q4IS91_AZOVI	Q4is91 azotobacter	386	6	25.0	258	2	Q51363_9RETR	Q51363 equine infe
314	6	25.0	217	2	Q81FN2_PLAP7	Q81fn2 plasmodium	387	6	25.0	258	2	Q51364_9RETR	Q51364 equine infe
315	6	25.0	217	2	Q8ACZ2_9HIV1	Q8acz2 human immun	388	6	25.0	258	2	Q51368_9RETR	Q51368 equine infe
316	6	25.0	218	2	Q9XY03_DUGJA	Q9xy03 dugesia jap	389	6	25.0	258	2	Q51370_9RETR	Q51370 equine infe
317	6	25.0	218	2	Q50HP5_TAV	Q50hp5 tomato aspe	390	6	25.0	258	2	Q51371_9RETR	Q51371 equine infe
318	6	25.0	219	2	Q88WK7_LACPL	Q88wk7 lactobacill	391	6	25.0	258	2	Q51374_9RETR	Q51374 equine infe
319	6	25.0	220	2	Q9UOB3_PLAFA	Q9uob3 plasmodium	392	6	25.0	258	2	Q51375_9RETR	Q51375 equine infe
320	6	25.0	221	2	Q8VZS8_ARATH	Q8vzs8 arabidopsis	393	6	25.0	258	2	Q51376_9RETR	Q51376 equine infe
321	6	25.0	221	2	Q6SU90_MANSM	Q6su90 manheimia	394	6	25.0	258	2	Q51377_9RETR	Q51377 equine infe
322	6	25.0	222	2	Q9UOB1_PLAFA	Q9uob1 plasmodium	395	6	25.0	258	2	Q51378_9RETR	Q51378 equine infe
323	6	25.0	223	2	Q25788_PLAFA	Q25788 plasmodium	396	6	25.0	259	2	Q51321_9RETR	Q51321 equine infe

397	6	25.0	2	Q81T83_PLAFA	Q81t83 plasmodium	470	6	25.0	2	Q52GI9_MAGGR	Q52gi9 magnaporthe
398	6	25.0	262	MSA2_PLAFC	Q99317 plasmodium	471	6	25.0	287	Q7KPY4_PLAFA	Q7kpy4 plasmodium
399	6	25.0	264	Q5ALP1_CANAL	Q5alp1 candida alb	472	6	25.0	287	Q25954_PLAFA	Q25954 plasmodium
400	6	25.0	264	Q06920_PLAFA	Q06920 plasmodium	473	6	25.0	287	Q52953_BACSU	Q52953 bacillus su
401	6	25.0	266	Q68LB8_9DIPT	Q68lb8 drosophila	474	6	25.0	288	Q8LF29_ARATH	Q8lf29 arabidopsis
402	6	25.0	267	Q7RDF2_PLAYO	Q7rdf2 plasmodium	475	6	25.0	288	Q8FJ33_ARATH	Q8fj33 arabidopsis
403	6	25.0	267	Q84RB7_LINUV	Q84rb7 linaria vul	476	6	25.0	289	Q86L26_9DIPT	Q86l26 drosophila
404	6	25.0	267	Q04FAP1_MINGU	Q04fal mimulus gut	477	6	25.0	290	Q54GM4_DICDI	Q54gm4 dictyosteli
405	6	25.0	268	Q557D6_DICDI	Q557d6 dictyosteli	478	6	25.0	290	Q5CKZ8_CRYHO	Q5ckz8 cryptospori
406	6	25.0	268	Q68LB6_9DIPT	Q68lb6 drosophila	479	6	25.0	291	Q25789_PLAFA	Q25789 plasmodium
407	6	25.0	268	Q86101_DICDI	Q86101 dictyosteli	480	6	25.0	292	Q54CX2_DICDI	Q54cx2 dictyosteli
408	6	25.0	268	Q4X934_PLACH	Q4x934 plasmodium	481	6	25.0	292	Q8YTY9_ANASP	Q8yty9 anabaena sp
409	6	25.0	268	Q95PK4_TRICA	Q95pk4 tribolium c	482	6	25.0	293	Q25785_PLAFA	Q25785 plasmodium
410	6	25.0	272	MSA2_PLAF7	P50498 plasmodium	483	6	25.0	295	Q8MR55_DROME	Q8mr55 drosophila
411	6	25.0	272	Q9TY97_PLAF7	Q9ty97 plasmodium	484	6	25.0	295	Q7K405_TRICA	Q7k405 tribolium c
412	6	25.0	274	MSA2_PLAF6	P50497 plasmodium	485	6	25.0	297	Q9FNN6_ARATH	Q9fnn6 arabidopsis
413	6	25.0	274	Q555M2_DICDI	Q555m2 dictyosteli	486	6	25.0	298	Q81T95_CAEBR	Q81t95 caenorhabdi
414	6	25.0	274	Q68LB4_9DIPT	Q68lb4 drosophila	487	6	25.0	299	Q81P99_DICDI	Q81p99 dictyosteli
415	6	25.0	274	P81395_ANTMA	P81395 antirrhinum	488	6	25.0	299	Q4Z4U6_PLABE	Q4z4u6 plasmodium
416	6	25.0	276	MSA2_PLAF8	Q99320 plasmodium	489	6	25.0	300	MSA2_PLAF1	Q03645 plasmodium
417	6	25.0	276	Q4SG06_TETNG	Q4sg06 tetraodon n	490	6	25.0	300	MSA2_PLAF2	Q03645 plasmodium
418	6	25.0	277	Q54E16_DICDI	Q54e16 dictyosteli	491	6	25.0	302	MSA2_PLAF9	Q03994 plasmodium
419	6	25.0	277	Q68L92_9DIPT	Q68l92 drosophila	492	6	25.0	302	Q4NZI7_9BELT	Q4nzi7 anaeronyxob
420	6	25.0	278	Q25862_PLAFA	Q25862 plasmodium	493	6	25.0	302	Q9PWL2_PSTMA	Q9pw12 petromyzon
421	6	25.0	279	Y170_BUCBP	Q89a82 buchnera ap	494	6	25.0	303	Q54C26_DICDI	Q54c26 dictyosteli
422	6	25.0	279	Q68L83_9DIPT	Q68l83 drosophila	495	6	25.0	305	Q4Y106_PLACH	Q4y106 plasmodium
423	6	25.0	279	Q68L68_9DIPT	Q68l68 drosophila	496	6	25.0	305	Q4Y106_PLACH	Q4y106 plasmodium
424	6	25.0	279	Q68L99_9DIPT	Q68l99 drosophila	497	6	25.0	307	Q4J809_SULAC	Q4j809 eulfolobus
425	6	25.0	280	Q5A893_CANAL	Q5a893 candida alb	498	6	25.0	308	Q54GM6_DICDI	Q54gm6 dictyosteli
426	6	25.0	280	Q68L89_9DIPT	Q68l89 drosophila	499	6	25.0	308	Q4YXZ2_PLABE	Q4yxz2 plasmodium
427	6	25.0	280	Q68L21_9DIPT	Q68l21 drosophila	500	6	25.0	310	Q54V44_DICDI	Q54v44 dictyosteli
428	6	25.0	280	Q68L85_9DIPT	Q68l85 drosophila	501	6	25.0	311	Q6B718_DROVI	Q6b718 drosophila
429	6	25.0	280	Q68LAI_9DIPT	Q68lai drosophila	502	6	25.0	311	Q4YEA7_PLABE	Q4yea7 plasmodium
430	6	25.0	280	Q93239_CABEL	Q93239 caenorhabdi	503	6	25.0	312	Q9BK04_TRICA	Q9bk04 tribolium c
431	6	25.0	280	Q8UVY9_BRARE	Q8uvy9 brachydanio	504	6	25.0	312	Q95UA8_TRICA	Q95ua8 tribolium c
432	6	25.0	280	Q6P612_BRARE	Q6p612 brachydanio	505	6	25.0	312	Q9NHBT_TRICA	Q9nhbt tribolium c
433	6	25.0	281	MSA2_PLAFH	Q99319 plasmodium	506	6	25.0	312	Q7RKQ6_PLAYO	Q7rkq6 plasmodium
434	6	25.0	281	Q68KZ6_9DIPT	Q68kz6 drosophila	507	6	25.0	312	Q86A98_DICDI	Q86a98 dictyosteli
435	6	25.0	281	Q68L43_9DIPT	Q68l43 drosophila	508	6	25.0	314	Q86A98_DICDI	Q86a98 dictyosteli
436	6	25.0	281	Q68L79_9DIPT	Q68l79 drosophila	509	6	25.0	315	Q6BSN7_DBBHA	Q6bsn7 debaryomyce
437	6	25.0	281	Q68L81_9DIPT	Q68l81 drosophila	510	6	25.0	315	Q54U06_DICDI	Q54u06 dictyosteli
438	6	25.0	281	Q54M55_DICDI	Q54m55 dictyosteli	511	6	25.0	316	Q55BJ7_DICDI	Q55bj7 dictyosteli
439	6	25.0	281	Q54ND8_DICDI	Q54nd8 dictyosteli	512	6	25.0	316	Q48607_9LACT	Q48607 lactococcus
440	6	25.0	282	Q68L07_9DIPT	Q68l07 drosophila	513	6	25.0	317	Q7REW9_PLAYO	Q7rew9 plasmodium
441	6	25.0	282	Q68L12_9DIPT	Q68l12 drosophila	514	6	25.0	317	Q4XEY8_PLACH	Q4xey8 plasmodium
442	6	25.0	282	Q68L84_9DIPT	Q68l84 drosophila	515	6	25.0	318	Q55B73_DICDI	Q55b73 dictyosteli
443	6	25.0	282	Q68L90_9DIPT	Q68l90 drosophila	516	6	25.0	321	Q54VG5_DICDI	Q54vg5 dictyosteli
444	6	25.0	282	Q68L91_9DIPT	Q68l91 drosophila	517	6	25.0	323	Q96835_DROME	Q96835 drosophila
445	6	25.0	282	Q68L94_9DIPT	Q68l94 drosophila	518	6	25.0	323	Q7RTG6_PLAYO	Q7rtg6 plasmodium
446	6	25.0	282	Q68L96_9DIPT	Q68l96 drosophila	519	6	25.0	324	HAM1_STRY1	Q5ml14 streptococc
447	6	25.0	282	Q68LA4_9DIPT	Q68la4 drosophila	520	6	25.0	324	HAM1_STRY2	Q5m626 streptococc
448	6	25.0	282	Q7RF40_PLAYO	Q7rf40 plasmodium	521	6	25.0	324	Q54BG2_DICDI	Q54bg2 dictyosteli
449	6	25.0	282	Q91K28_ARATH	Q91k28 arabidopsis	522	6	25.0	324	Q54NM1_DICDI	Q54nm1 dictyosteli
450	6	25.0	283	Q68L88_9DIPT	Q68l88 drosophila	523	6	25.0	324	Q9M4G1_SOLITU	Q9m4g1 solanum tub
451	6	25.0	283	Q68L02_9DIPT	Q68l02 drosophila	524	6	25.0	325	Q5C116_SCHJA	Q5c116 schistosoma
452	6	25.0	283	Q68L15_9DIPT	Q68l15 drosophila	525	6	25.0	328	Q5CYS1_CRYPV	Q5cys1 cryptospori
453	6	25.0	283	Q68L44_9DIPT	Q68l44 drosophila	526	6	25.0	328	Q5CKD9_CRYHO	Q5ckd9 cryptospori
454	6	25.0	283	Q68L72_9DIPT	Q68l72 drosophila	527	6	25.0	329	Q7RQG0_PLAYO	Q7rqg0 plasmodium
455	6	25.0	283	Q68L86_9DIPT	Q68l86 drosophila	528	6	25.0	330	Q585G1_9TRYP	Q585g1 trypanosoma
456	6	25.0	283	Q68LA2_9DIPT	Q68la2 drosophila	529	6	25.0	330	Q7RFJ2_PLAYO	Q7rfj2 plasmodium
457	6	25.0	284	Q68L11_9DIPT	Q68l11 drosophila	530	6	25.0	330	Q7ZW50_BRARE	Q7zw50 brachydanio
458	6	25.0	284	Q68L60_9DIPT	Q68l60 drosophila	531	6	25.0	331	Q54M88_DICDI	Q54m88 dictyosteli
459	6	25.0	284	Q68L93_9DIPT	Q68l93 drosophila	532	6	25.0	332	Q54DCM9_SCHJA	Q54dcm9 schistosoma
460	6	25.0	284	Q68L99_9DIPT	Q68l99 drosophila	533	6	25.0	332	Q6T4R0_9BILA	Q6t4r0 ptychodera
461	6	25.0	284	Q9V4R9_9DIPT	Q9v4r9 drosophila	534	6	25.0	334	Q55GI1_DICDI	Q55gi1 dictyosteli
462	6	25.0	284	Q9V4R9_DROME	Q9v4r9 drosophila	535	6	25.0	334	Q55KV26_GEOKA	Q55kv26 geobacillus
463	6	25.0	285	Q68L80_9DIPT	Q68l80 drosophila	536	6	25.0	336	Q59LJ8_CANAL	Q59lj8 candida alb
464	6	25.0	285	Q68L97_9DIPT	Q68l97 drosophila	537	6	25.0	336	Q6BFU4_PARTE	Q6bfu4 paramecium
465	6	25.0	286	MSA2_PLAF1	P50496 plasmodium	538	6	25.0	336	Q54D24_DICDI	Q54d24 dictyosteli
466	6	25.0	286	Q54TC8_DICDI	Q54tc8 dictyosteli	539	6	25.0	338	Q9GPT6_DICDI	Q9gpt6 dictyosteli
467	6	25.0	286	Q68L38_9DIPT	Q68l38 drosophila	540	6	25.0	338	Q7RNB8_PLAYO	Q7rnb8 plasmodium
468	6	25.0	286	Q68L42_9DIPT	Q68l42 drosophila	541	6	25.0	340	Q5AD61_CANAL	Q5ad61 candida alb
469	6	25.0	287	MSA2_PLAFG	P19260 plasmodium	542	6	25.0	340	Q5ADJ0_CANAL	Q5adj0 candida alb

543	6	25.0	341	2	Q81LN6_PLAF7	Q81ln6 plasmodium	616	6	25.0	388	2	Q8LFN5_ARATH	Q8lfn5 arabidopsis
544	6	25.0	342	2	Q61K72_CABBR	Q61k72 caenorhabdi	617	6	25.0	390	2	Q59YU0_CANAL	Q59yu0 candida alb
545	6	25.0	343	2	Q53EF5_9NEOB	Q53ef5 eleutheroda	618	6	25.0	390	2	Q54H17_DICDI	Q54h17 dictyosteli
546	6	25.0	344	2	Q8Q668_9BETA	Q8q668 pongine her	619	6	25.0	390	2	Q7MYC8_PHOLL	Q7myc8 photorhabdu
547	6	25.0	347	1	MSA2_PLAF2	Q03646 plasmodium	620	6	25.0	391	2	Q6CTE1_KUULA	Q6cte1 kluyveromyc
548	6	25.0	348	2	Q9GBZ9_BURPA	Q9gbz9 burramys pa	621	6	25.0	391	2	Q7SK08_DICDI	Q7sk08 dictyosteli
549	6	25.0	352	2	Q8XOP7_NEUCR	Q8xop7 neurospora	622	6	25.0	395	2	Q6FT46_CANGA	Q6ft46 candida gla
550	6	25.0	352	2	Q54DL2_DICDI	Q54dl2 dictyosteli	623	6	25.0	396	2	Q9FH24_ARATH	Q9fh24 arabidopsis
551	6	25.0	353	2	Q70W03_CIOIN	Q70w03 ciona intes	624	6	25.0	397	2	Q54UG1_DICDI	Q54ug1 dictyosteli
552	6	25.0	354	1	URE2_YEAST	P23202 saccharomyc	625	6	25.0	397	1	KNAT1_ARATH	P46639 arabidopsis
553	6	25.0	354	2	Q8NI6_YEAST	Q8nie6 saccharomyc	626	6	25.0	398	2	Q9W4Q1_DROME	Q9w4q1 drosophila
554	6	25.0	354	2	Q8NI17_YEAST	Q8ni17 saccharomyc	627	6	25.0	398	2	Q8EF23_SHEON	Q8ef23 shewanella
555	6	25.0	355	2	Q8NJQ9_YEAST	Q8njq9 saccharomyc	628	6	25.0	399	2	Q8HFS0_SACSE	Q8hfs0 saccharomyc
556	6	25.0	356	2	Q948W9_BRACM	Q948w9 brassica ca	629	6	25.0	399	2	Q4YN01_PLABE	Q4yn01 plasmodium
557	6	25.0	356	2	Q948X0_BRACM	Q948x0 brassica ca	630	6	25.0	400	2	Q7Y1H5_NEUCR	Q7y1h5 neurospora
558	6	25.0	357	2	Q4P797_USTMA	Q4p797 ustilago ma	631	6	25.0	400	2	Q95RV8_DROME	Q95rv8 drosophila
559	6	25.0	357	2	Q54E12_DICDI	Q54e12 dictyosteli	632	6	25.0	400	2	Q551X7_DICDI	Q551x7 dictyosteli
560	6	25.0	358	2	Q54KM1_DICDI	Q54km1 dictyosteli	633	6	25.0	400	2	Q8S3L9_ARATH	Q8s3l9 arabidopsis
561	6	25.0	359	1	URE2_SACPO	Q96x44 saccharomyc	634	6	25.0	400	2	Q8S3M0_ARATH	Q8s3m0 arabidopsis
562	6	25.0	359	1	URE2_SACPA	Q711z8 saccharomyc	635	6	25.0	401	2	Q54XJ5_DICDI	Q54xj5 dictyosteli
563	6	25.0	359	2	Q9AYO7_9RHOD	Q9ayq7 porphyra de	636	6	25.0	402	2	Q9W4N3_DROME	Q9w4n3 drosophila
564	6	25.0	360	2	Q59S54_CANAL	Q59s54 candida alb	637	6	25.0	402	2	Q9MB69_PORTE	Q9mb69 porphyra te
565	6	25.0	361	2	Q96424_9TRYP	Q96424 herpetonoma	638	6	25.0	402	2	Q9MB67_PORYE	Q9mb67 porphyra ye
566	6	25.0	362	2	Q9NG64_DROSI	Q9ng64 drosophila	639	6	25.0	402	2	Q9MB68_BANAT	Q9mb68 bangia atro
567	6	25.0	362	2	Q9NG83_DROSI	Q9ng83 drosophila	640	6	25.0	403	2	Q54PX6_DICDI	Q54px6 dictyosteli
568	6	25.0	362	2	Q9NG84_DROSI	Q9ng84 drosophila	641	6	25.0	404	2	Q4G199_HUMAN	Q4g199 homo sapien
569	6	25.0	362	2	Q9NG85_DROSI	Q9ng85 drosophila	642	6	25.0	406	2	Q5JHX4_PYRKO	Q5jhx4 pyrococcus
570	6	25.0	365	2	Q86156_DICDI	Q86156 dictyosteli	643	6	25.0	406	2	Q81T55_DROME	Q81t55 drosophila
571	6	25.0	365	2	Q9FNF6_ARATH	Q9fnf6 arabidopsis	644	6	25.0	406	2	Q4XNP7_PLACH	Q4xnp7 plasmodium
572	6	25.0	365	2	Q8EV30_MYCPE	Q8ev30 mycoplasma	645	6	25.0	407	2	Q7KMW0_DICDI	Q7kwm0 dictyosteli
573	6	25.0	367	2	Q8UGG6_ARATH	Q8ugg6 arabidopsis	646	6	25.0	408	2	Q5SG94_DICDI	Q5sg94 dictyosteli
574	6	25.0	368	1	YB11_YEAST	P38180 saccharomyc	647	6	25.0	408	2	Q4XSR6_PLACH	Q4xsr6 plasmodium
575	6	25.0	368	2	Q9UZV5_PVRAB	Q9uzv5 pyrococcus	648	6	25.0	409	2	Q86K12_DICDI	Q86k12 dictyosteli
576	6	25.0	368	2	Q54CX7_DICDI	Q54cx7 dictyosteli	649	6	25.0	410	1	MRAY_PARUW	Q6mb83 parachlamyd
577	6	25.0	368	2	Q54QL4_DICDI	Q54ql4 dictyosteli	650	6	25.0	410	2	Q6EBH8_9HEMI	Q6ebh8 darnis part
578	6	25.0	368	2	Q9VRB1_DROME	Q9vrbr1 drosophila	651	6	25.0	410	2	Q5WU57_LEGPL	Q5wu57 legionella
579	6	25.0	368	2	Q5JZR1_SOYBN	Q5jzr1 glycine max	652	6	25.0	410	2	Q5X2D6_LEGPA	Q5x2d6 legionella
580	6	25.0	369	1	D02P25_ARATH	Q92py0 arabidopsis	653	6	25.0	411	2	Q86HD7_DICDI	Q86hd7 dictyosteli
581	6	25.0	369	2	Q86175_DICDI	Q86175 dictyosteli	654	6	25.0	411	2	Q9SSA4_ARATH	Q9ssa4 arabidopsis
582	6	25.0	370	2	Q43458_SOYBN	Q43458 glycine max	655	6	25.0	412	2	Q54X20_DICDI	Q54x20 dictyosteli
583	6	25.0	371	2	Q82805_PEA	Q82805 pisum sativ	656	6	25.0	412	2	Q5ZSX6_LEGPH	Q5zsx6 legionella
584	6	25.0	372	1	COL9_ARATH	Q9sees5 arabidopsis	657	6	25.0	413	2	Q9GRY9_CABEL	Q9gry9 caenorhabdi
585	6	25.0	372	2	Q81JV8_PLAF7	Q81jv8 plasmodium	658	6	25.0	414	2	Q4H2S3_CIOIN	Q4h2s3 ciona intes
586	6	25.0	372	2	Q9LX18_ARATH	Q9lx18 arabidopsis	659	6	25.0	416	1	SO_DROME	Q27350 drosophila
587	6	25.0	372	2	Q65LU3_BACLD	Q65lu3 bacillus li	660	6	25.0	416	2	Q6ZG17_BURMA	Q6zg17 burkholderi
588	6	25.0	373	2	Q9U217_CABEL	Q9u217 caenorhabdi	661	6	25.0	418	2	Q6EJM2_9HIV1	Q6ejm2 human immun
589	6	25.0	374	2	Q54LM3_DICDI	Q54lw3 dictyosteli	662	6	25.0	419	2	Q6DBW2_BRARE	Q6dbw2 brachydanlo
590	6	25.0	374	2	Q54TA8_DICDI	Q54ta8 dictyosteli	663	6	25.0	420	2	Q54YH2_DICDI	Q54yh2 dictyosteli
591	6	25.0	374	2	Q54WE6_DICDI	Q54we6 dictyosteli	664	6	25.0	421	2	Q5AME8_CANAL	Q5ame8 candida alb
592	6	25.0	374	2	Q72YN0_XENLA	Q72yn0 xenopus lae	665	6	25.0	421	2	Q54J70_DICDI	Q54j70 dictyosteli
593	6	25.0	375	2	Q59VK5_CANAL	Q59vk5 candida alb	666	6	25.0	421	2	Q8MTX3_9ANNE	Q8mtx3 theromyzon
594	6	25.0	375	2	Q85154_9TREM	Q85154 orientobilh	667	6	25.0	421	2	Q9LGX8_ORYSA	Q9lgx8 oryza sativ
595	6	25.0	375	2	Q85L57_9TREM	Q85157 schistosoma	668	6	25.0	422	2	Q9Y1V4_HALRO	Q9y1v4 halocynthia
596	6	25.0	375	2	Q85L66_9TREM	Q85166 gigantobilh	669	6	25.0	422	2	Q54LT6_DICDI	Q54lt6 dictyosteli
597	6	25.0	376	2	Q85L67_9TREM	Q85167 dendritobil	670	6	25.0	423	2	Q967M5_DICDI	Q967m5 dictyosteli
598	6	25.0	378	2	Q514K4_DROAE	Q514k4 drosophila	671	6	25.0	423	2	Q8T1C6_DICDI	Q8t1c6 dictyosteli
599	6	25.0	378	2	Q54DL0_DICDI	Q54dl0 dictyosteli	672	6	25.0	423	2	Q4XYN4_PLACH	Q4xyn4 plasmodium
600	6	25.0	378	2	Q86188_DICDI	Q86188 dictyosteli	673	6	25.0	423	2	Q95TK1_DROME	Q95tk1 drosophila
601	6	25.0	379	2	Q59W09_CANAL	Q59w09 candida alb	674	6	25.0	423	2	Q6EJMS_9HIV1	Q6ejms human immun
602	6	25.0	380	2	Q55C29_DICDI	Q55c29 dictyosteli	675	6	25.0	423	2	Q6EJMJ_9HIV1	Q6ejmj human immun
603	6	25.0	380	2	Q7S7N8_NEUCR	Q7s7n8 neurospora	676	6	25.0	424	2	Q6EJMJ_9HIV1	Q6ejmj human immun
604	6	25.0	381	2	Q514K0_DROAE	Q514k0 drosophila	677	6	25.0	424	2	Q4XZJ4_9HIV1	Q4xzj4 plasmodium
605	6	25.0	381	2	Q55FX1_DICDI	Q55fx1 dictyosteli	678	6	25.0	425	2	Q4XZJ9_PLACH	Q4xzj9 plasmodium
606	6	25.0	382	2	Q968T5_SCHJA	Q968t5 schistosoma	679	6	25.0	426	2	Q5APN2_CANAL	Q5apn2 candida alb
607	6	25.0	382	2	Q9FRV6_9RHOD	Q9frv6 porphyra on	680	6	25.0	426	2	Q4YIR5_PLABE	Q4yir5 plasmodium
608	6	25.0	382	2	Q9FRV7_PORCA	Q9frv7 porphyra ca	681	6	25.0	427	1	BSH_DROME	Q04787 drosophila
609	6	25.0	382	2	Q9FRV5_PORTE	Q9frv5 porphyra te	682	6	25.0	428	2	Q9Y1V5_HALRO	Q9y1v5 halocynthia
610	6	25.0	384	1	ERD1_KUULA	P41771 kluyveromyc	683	6	25.0	429	2	Q86J11_DICDI	Q86j11 dictyosteli
611	6	25.0	385	2	Q54DV6_DICDI	Q54dv6 dictyosteli	684	6	25.0	429	2	Q618V6_CABBR	Q618v6 caenorhabdi
612	6	25.0	386	2	Q9VRA9_DROME	Q9vra9 drosophila	685	6	25.0	429	2	Q4V6V3_DROME	Q4v6v3 drosophila
613	6	25.0	388	2	Q54T14_DICDI	Q54t14 dictyosteli	686	6	25.0	431	2	Q12124_YEAST	Q12124 saccharomyc
614	6	25.0	388	2	Q81ZV5_PLAF7	Q81zv5 plasmodium	687	6	25.0	431	2	Q55SU7_DICDI	Q55su7 dictyosteli
615	6	25.0	388	2	Q54E41_DICDI	Q54e41 dictyosteli	688	6	25.0	434	2	Q63PS6_BURPS	Q63ps6 burkholderi

689	6	25.0	436	2	Q6PBC6_ACTAD	Q6fec6 acinetobact	762	6	25.0	482	2	Q40491_TOBAC	Q40491 nicotiana t
690	6	25.0	437	2	Q9VMQ7_DROME	Q9vmq7 drosophila	763	6	25.0	483	2	Q40490_TOBAC	Q40490 nicotiana t
691	6	25.0	438	2	Q54SX2_DICDI	Q54sx2 dictyosteli	764	6	25.0	484	2	Q40514_TOBAC	Q40514 nicotiana t
692	6	25.0	439	2	Q5V6W5_HALWA	Q5v6w5 haloarcula	765	6	25.0	485	2	Q54JG7_DICDI	Q54jg7 dictyosteli
693	6	25.0	439	2	Q5UTZ4_ANOGA	Q5utz4 anopheles g	766	6	25.0	486	2	Q875P0_SACKL	Q875p0 saccharomyc
694	6	25.0	439	2	Q4Z6M7_PLABE	Q4z6m7 plasmodium	767	6	25.0	488	2	Q54KL8_DICDI	Q54kl8 dictyosteli
695	6	25.0	439	2	Q6PG25_XENLA	Q6pg25 xenopus lae	768	6	25.0	489	2	Q4XXF6_PLACH	Q4xxf6 plasmodium
696	6	25.0	440	2	Q5B1X9_EMENI	Q5b1x9 aspergillus	769	6	25.0	490	2	Q9XG15_LYCES	Q9xg15 lycopersico
697	6	25.0	440	2	Q96110_PLAF7	Q96110 plasmodium	770	6	25.0	491	2	Q8IAZ2_PLAF7	Q8iaz2 plasmodium
698	6	25.0	440	2	Q9VJ02_DROME	Q9vj02 drosophila	771	6	25.0	491	2	Q8IAZ2_PLAF7	Q8iaz2 plasmodium
699	6	25.0	440	2	Q96686_DROME	Q96686 drosophila	772	6	25.0	492	2	Q85YH5_9ROSI	Q85yh5 euphorbia a
700	6	25.0	442	2	Q54EK9_DICDI	Q54ek9 dictyosteli	773	6	25.0	493	1	Q85YH4_9ROSI	Q85yh4 euphorbia l
701	6	25.0	442	2	Q54U82_DICDI	Q54u82 dictyosteli	774	6	25.0	493	1	ABDB_DROME	P09087 drosophila
702	6	25.0	443	2	Q555Q0_DICDI	Q555q0 dictyosteli	775	6	25.0	495	2	Q54EN1_DICDI	Q54en1 dictyosteli
703	6	25.0	444	2	Q7KVX1_DROME	Q7kvx1 drosophila	776	6	25.0	497	2	Q7RGQ7_PLAYO	Q7rgq7 plasmodium
704	6	25.0	444	2	Q4UJH6_THEAN	Q4uhj6 theileria a	777	6	25.0	500	2	Q54K78_DICDI	Q54k78 dictyosteli
705	6	25.0	445	2	Q54U04_DICDI	Q54u04 dictyosteli	778	6	25.0	500	2	Q6R8D8_SODGL	Q6r8d8 sodalis glo
706	6	25.0	445	2	Q92B15_LISIN	Q92b15 listeria in	779	6	25.0	501	2	Q54DN6_DICDI	Q54dn6 dictyosteli
707	6	25.0	446	2	Q7QVW4_GIALA	Q7qvn4 giardia lam	780	6	25.0	502	2	Q54CJ6_DICDI	Q54cj6 dictyosteli
708	6	25.0	446	2	Q54QY7_DICDI	Q54qy7 dictyosteli	781	6	25.0	502	2	Q4YWB5_PLABE	Q4ywb5 plasmodium
709	6	25.0	447	1	SLFI_YEAST	Q12034 saccharomyc	782	6	25.0	502	2	Q15698_DICDI	Q15698 dictyosteli
710	6	25.0	447	2	Q6B1Z1_YEAST	Q6b1z1 saccharomyc	783	6	25.0	503	2	Q96563_PLAFA	Q96563 plasmodium
711	6	25.0	448	1	AAC2_DICDI	P14196 dictyosteli	784	6	25.0	503	2	Q7RD97_PLAYO	Q7rd97 plasmodium
712	6	25.0	449	2	Q8PX08_METWA	Q8px08 methanosarc	785	6	25.0	505	2	Q5SCB0_OSTTA	Q5scb0 ostreococcu
713	6	25.0	449	2	Q54P66_DICDI	Q54p66 dictyosteli	786	6	25.0	507	2	Q70MC5_CUPSA	Q70mc5 cupeniuss
714	6	25.0	449	2	Q86KK1_DICDI	Q86kk1 dictyosteli	787	6	25.0	507	2	Q8BRY5_MOUSE	Q8bry5 mus musculu
715	6	25.0	449	2	Q4UMG4_THEAN	Q4umg4 theileria a	788	6	25.0	508	1	CPI17A_CAVPO	Q64410 cavia porce
716	6	25.0	451	2	Q61L68_CABER	Q61l68 caenorhabdi	789	6	25.0	508	1	CROC_DROME	P32027 drosophila
717	6	25.0	451	2	Q4YXR7_PLABE	Q4yxr7 plasmodium	790	6	25.0	508	2	Q55E40_DICDI	Q55e40 dictyosteli
718	6	25.0	451	2	Q82690_LEPBU	Q82690 lepicincliis	791	6	25.0	508	2	Q4YQ62_PLABE	Q4yq62 drosophila
719	6	25.0	455	2	Q86A18_DICDI	Q86a18 dictyosteli	792	6	25.0	509	2	Q53YH1_DROME	Q53yh1 drosophila
720	6	25.0	455	2	Q86HL1_DICDI	Q86hl1 dictyosteli	793	6	25.0	509	2	Q86AF3_DICDI	Q86af3 dictyosteli
721	6	25.0	456	2	Q8TIV8_METAC	Q8t1v8 methanosarc	794	6	25.0	512	2	Q7VLL1_HELHP	Q7vj11 helicobacte
722	6	25.0	456	2	Q9V8V7_DROME	Q9v8v7 drosophila	795	6	25.0	512	2	Q8DY11_STRAS	Q8dy11 streptococ
723	6	25.0	457	2	Q7SGR7_NEUCR	Q7sgr7 neurospora	796	6	25.0	513	2	Q9NHP8_DROME	Q9nhp8 drosophila
724	6	25.0	457	2	Q54E72_DICDI	Q54e72 dictyosteli	797	6	25.0	514	2	Q559E8_DICDI	Q559e8 dictyosteli
725	6	25.0	458	2	Q4N2N8_THRPA	Q4n2n8 theileria p	798	6	25.0	514	2	Q86A26_DICDI	Q86a26 dictyosteli
726	6	25.0	458	2	Q5WYB1_LEGPL	Q5wyb1 legionella	799	6	25.0	514	2	Q8ILZ7_PLAF7	Q8ilz7 plasmodium
727	6	25.0	459	1	STB1_YEAST	P42845 saccharomyc	800	6	25.0	514	2	Q9GZ33_TRYCR	Q9gz33 trypanosoma
728	6	25.0	461	2	Q4YDB8_PLABE	Q4ydb8 plasmodium	801	6	25.0	516	2	Q7PMQ4_ANOGA	Q7pmq4 anopheles g
729	6	25.0	462	2	Q4QUH5_9HIV1	Q4quh5 human immun	802	6	25.0	517	2	Q54S29_DICDI	Q54s29 dictyosteli
730	6	25.0	463	2	Q6BR67_DEBHA	Q6br67 debaryomyce	803	6	25.0	518	2	Q9NJZ1_DROSL	Q9njz1 drosophila
731	6	25.0	463	2	Q61ZEB_CABER	Q61ze8 caenorhabdi	804	6	25.0	518	2	Q9NJZ5_DROME	Q9njz5 drosophila
732	6	25.0	463	2	Q54U71_DICDI	Q54u71 dictyosteli	805	6	25.0	519	2	Q54LH2_DICDI	Q54lh2 dictyosteli
733	6	25.0	463	2	Q7RM05_PLAYO	Q7rm05 plasmodium	806	6	25.0	520	2	Q9VJ00_DROME	Q9vj00 drosophila
734	6	25.0	464	2	Q54NT7_DICDI	Q54nt7 dictyosteli	807	6	25.0	521	2	Q54Q09_DICDI	Q54q09 dictyosteli
735	6	25.0	465	2	Q5UR38_MIMIV	Q5ur38 mimivirus.	808	6	25.0	521	2	Q54R09_DICDI	Q54r09 dictyosteli
736	6	25.0	467	2	Q54RY6_DICDI	Q54ry6 dictyosteli	809	6	25.0	523	2	Q86P58_DROME	Q86p58 drosophila
737	6	25.0	467	2	Q80010_CHICK	Q80010 gallus gall	810	6	25.0	525	1	ESR1_MTCUN	P57753 microgoni
738	6	25.0	468	2	Q7RP17_PLAYO	Q7rf17 plasmodium	811	6	25.0	525	2	Q5TQB4_ANOGA	Q5tqb4 anopheles g
739	6	25.0	470	2	Q5AZL1_CANAL	Q5azl1 candida alb	812	6	25.0	527	2	Q54V97_DICDI	Q54v97 dictyosteli
740	6	25.0	471	2	Q81KA4_PLAF7	Q81ka4 plasmodium	813	6	25.0	531	2	Q57VM1_9TRYP	Q57vm1 trypanosoma
741	6	25.0	472	1	SOX14_DROME	P40656 drosophila	814	6	25.0	531	2	Q7R9R0_PLAYO	Q7r9r0 plasmodium
742	6	25.0	472	2	Q16804_DROME	P16804 drosophila	815	6	25.0	532	2	Q5AJI6_CANAL	Q5aji6 candida alb
743	6	25.0	473	2	Q7PNH3_ANOGA	Q7pnh3 anopheles g	816	6	25.0	533	1	YD3D_SCHPO	Q10277 schizosacch
744	6	25.0	473	2	Q818X1_ENTHI	Q818x1 entamoeba n	817	6	25.0	533	2	Q9CGU2_LACLA	Q9cgu2 lactococcus
745	6	25.0	473	2	Q869M2_DICDI	Q869m2 dictyosteli	818	6	25.0	534	2	Q5A479_CANAL	Q5a479 candida alb
746	6	25.0	474	2	Q73V86_MYCPA	Q73v86 mycobacteri	819	6	25.0	534	2	Q54L39_DICDI	Q54l39 candida alb
747	6	25.0	474	2	Q54LK7_DICDI	Q54lk7 dictyosteli	820	6	25.0	534	2	Q54Y77_DICDI	Q54y77 dictyosteli
748	6	25.0	475	2	Q54XW6_DICDI	Q54xw6 dictyosteli	821	6	25.0	535	2	Q9VZM2_DROME	Q9vzm2 drosophila
749	6	25.0	475	2	Q9VEA3_DROME	Q9vea3 drosophila	822	6	25.0	537	2	Q54MJ3_DICDI	Q54mj3 dictyosteli
750	6	25.0	478	2	Q9UEM8_HUMAN	Q9uem8 homo sapien	823	6	25.0	538	1	YAJ8_SCHPO	Q09908 schizosacch
751	6	25.0	478	2	Q9UIU5_HUMAN	Q9uiu5 homo sapien	824	6	25.0	538	2	Q75JS0_DICDI	Q75js0 dictyosteli
752	6	25.0	478	2	Q553R0_DICDI	Q553r0 dictyosteli	825	6	25.0	539	2	Q54VF0_DICDI	Q54vf0 dictyosteli
753	6	25.0	478	2	Q6ITT3_PIG	Q6itt3 sus scrofa	826	6	25.0	541	2	Q5AJM4_CANAL	Q5ajm4 candida alb
754	6	25.0	478	2	Q4R4A8_MACFA	Q4r4a8 macaca fasc	827	6	25.0	542	2	Q59LD1_CANAL	Q59ld1 candida alb
755	6	25.0	478	2	Q9D2X2_MOUSE	Q9d2x2 mus musculu	828	6	25.0	543	2	Q5TNB0_ANOGA	Q5tnb0 anopheles g
756	6	25.0	478	2	Q9D306_MOUSE	Q9d306 m mus musculu	829	6	25.0	546	2	Q7RNT2_PLAYO	Q7rnt2 plasmodium
757	6	25.0	479	1	YP66_YEAST	Q12194 saccharomyc	830	6	25.0	546	2	Q5E7Z2_VIBF1	Q5e7z2 vibrio fisc
758	6	25.0	479	2	Q8L459_ORYSA	Q8l459 oryza sativ	831	6	25.0	547	2	Q9B8Z3_SCHJA	Q9b8z3 schistosoma
759	6	25.0	480	2	Q9VWD5_DROME	Q9vwd5 drosophila	832	6	25.0	549	2	Q6FV05_CANGA	Q6fv05 candida gla
760	6	25.0	480	2	Q9N572_CABEL	Q9n572 caenorhabdi	833	6	25.0	550	2	Q54DAL_DICDI	Q54dal dictyosteli
761	6	25.0	480	2	Q8SXX1_DROME	Q8sxx1 drosophila	834	6	25.0	550	2	Q24709_DROVI	Q24709 drosophila

835	6	25.0	552	2	045117_CHITE	045117 chironomus	908	6	25.0	601	2	Q5DEC2_SCHJA	Q5dec2 schistosoma
836	6	25.0	552	2	Q4Y7Q4_PLACH	Q4y7q4 plasmidium	909	6	25.0	601	2	Q55C15_DICDI	Q55c15 dictyosteli
837	6	25.0	554	2	Q4Y761_PLACH	Q4y761 plasmidium	910	6	25.0	601	2	Q8S853_ORYSA	Q8s853 oryza sativ
838	6	25.0	555	2	Q76770_DICDI	Q76770 dictyosteli	911	6	25.0	603	2	Q6B223_DBBHA	Q6b223 debaryomyce
839	6	25.0	555	2	Q61UB8_CABER	Q61ub8 caenorhabdi	912	6	25.0	603	2	Q9C6K3_ARATH	Q9c6k3 arabidopsis
840	6	25.0	556	2	Q817Q3_BACCR	Q817q3 bacillus ce	913	6	25.0	605	1	WSC4_YEAST	P38739 saccharomyc
841	6	25.0	557	2	Q541T7_DICDI	Q541t7 dictyosteli	914	6	25.0	605	2	Q7S971_NEUCR	Q7s971 neurospora
842	6	25.0	557	2	Q4MS76_BACCE	Q4ms76 bacillus ce	915	6	25.0	606	2	Q4Y219_PLABE	Q4y219 plasmidium
843	6	25.0	557	2	Q6HD55_BACHK	Q6hd55 bacillus th	916	6	25.0	608	2	Q7RTD1_PLAYO	Q7rtd1 plasmidium
844	6	25.0	557	2	Q722V5_BACC1	Q722v5 bacillus ce	917	6	25.0	609	2	Q54BH1_DICDI	Q54bh1 dictyosteli
845	6	25.0	557	2	Q633X3_BACCC	Q633x3 bacillus ce	918	6	25.0	613	2	Q55BD4_DICDI	Q55bd4 dictyosteli
846	6	25.0	557	2	Q81LC0_BACAN	Q81lc0 bacillus an	919	6	25.0	613	2	Q9XZS8_DROME	Q9xzs8 drosophila
847	6	25.0	560	2	Q81516_PLAF7	Q81516 plasmidium	920	6	25.0	613	2	Q9S5V5_DROME	Q9s5v5 drosophila
848	6	25.0	561	2	Q54WV9_DICDI	Q54wv9 dictyosteli	921	6	25.0	616	2	Q875Y0_SACCA	Q875y0 saccharomyc
849	6	25.0	561	2	Q81J78_PLAF7	Q81j78 plasmidium	922	6	25.0	617	2	Q97240_PLAF7	Q97240 plasmidium
850	6	25.0	562	2	Q7RLP5_PLAYO	Q7rlp5 plasmidium	923	6	25.0	617	2	Q4X364_PLACH	Q4x364 plasmidium
851	6	25.0	562	2	Q23220_CABEL	Q23220 caenorhabdi	924	6	25.0	619	2	Q81JL5_PLAF7	Q81jl5 plasmidium
852	6	25.0	563	2	Q54J98_DICDI	Q54j98 dictyosteli	925	6	25.0	620	2	Q62004_BRAFL	Q62004 branchiosto
853	6	25.0	564	2	Q54YB7_DICDI	Q54yb7 dictyosteli	926	6	25.0	620	2	Q62007_BRALA	Q62007 branchiosto
854	6	25.0	564	2	Q54Y70_DICDI	Q54y70 dictyosteli	927	6	25.0	620	2	Q8LLE0_SOLTU	Q8lle0 solanum tub
855	6	25.0	565	2	Q815X8_PLAF7	Q815x8 plasmidium	928	6	25.0	620	2	Q5M7Y0_BRARE	Q5m7y0 brachydanio
856	6	25.0	566	2	Q9U0J5_PLAF7	Q9u0j5 plasmidium	929	6	25.0	622	2	Q5SEJ7_DICDI	Q5sej7 dictyosteli
857	6	25.0	567	2	Q59LK6_CANAL	Q59lk6 candida alb	930	6	25.0	624	2	Q55BE5_DICDI	Q55be5 dictyosteli
858	6	25.0	567	2	Q54RV4_DICDI	Q54rv4 dictyosteli	931	6	25.0	627	2	Q54L13_DICDI	Q54l13 dictyosteli
859	6	25.0	567	2	Q54X11_DICDI	Q54x11 dictyosteli	932	6	25.0	627	2	Q81LG2_PLAF7	Q81lg2 plasmidium
860	6	25.0	568	2	Q54PT1_DICDI	Q54pt1 dictyosteli	933	6	25.0	628	1	8IN3_ARATH	Q24606 arabidopsis
861	6	25.0	569	1	MANC_PIRSP	P55298 pitomyces s	934	6	25.0	628	2	Q81LB8_PLAF7	Q81lb8 plasmidium
862	6	25.0	569	1	P2B2_DROME	Q5xxr5 anopheles g	935	6	25.0	628	2	Q5SDN7_DROME	Q5sdn7 drosophila
863	6	25.0	570	1	MANE_PIRSP	Q27889 drosophila	936	6	25.0	630	2	Q5SD16_DICDI	Q5sd16 dictyosteli
864	6	25.0	571	1	MANE_PIRSP	P55297 pitomyces s	937	6	25.0	630	2	Q56C43_9CAUD	Q56c43 enterobacte
865	6	25.0	572	2	Q54H16_DICDI	Q54h16 dictyosteli	938	6	25.0	631	2	Q54WN7_DICDI	Q54wn7 dictyosteli
866	6	25.0	572	2	Q559A6_DICDI	Q559a6 dictyosteli	939	6	25.0	632	2	Q5CIY5_CRYHO	Q5ciy5 cryptospori
867	6	25.0	575	2	Q81GJ2_ARATH	Q81gj2 arabidopsis	940	6	25.0	633	2	Q9VD13_DROME	Q9vd13 drosophila
868	6	25.0	575	2	Q9LZM8_ARATH	Q9lzm8 arabidopsis	941	6	25.0	633	2	Q86AP6_DICDI	Q86ap6 dictyosteli
869	6	25.0	575	2	Q8H147_ARATH	Q8h147 arabidopsis	942	6	25.0	633	2	Q54ZV8_DICDI	Q54zv8 dictyosteli
870	6	25.0	575	2	Q6NT95_BRARE	Q6ny95 brachydanio	943	6	25.0	634	2	Q95R62_DICDI	Q95r62 drosophila
871	6	25.0	578	1	PSP2_YEAST	P50109 saccharomyc	944	6	25.0	637	2	Q86B13_DICDI	Q86b13 dictyosteli
872	6	25.0	578	2	Q25419_HELPF	Q25419 helicobacte	945	6	25.0	637	2	Q81I24_PLAF7	Q81i24 plasmidium
873	6	25.0	578	2	Q80H10_PAROL	Q80h10 paralichthy	946	6	25.0	637	2	Q81I14_PLAF7	Q81i14 plasmidium
874	6	25.0	579	2	Q580V0_9TRYP	Q580v0 trypanosoma	947	6	25.0	638	2	Q5CQ13_CRYPV	Q5cq13 cryptospori
875	6	25.0	579	2	Q54DK8_DICDI	Q54dk8 dictyosteli	948	6	25.0	638	2	Q8T2T4_DICDI	Q8t2t4 dictyosteli
876	6	25.0	579	2	Q54PG2_DICDI	Q54pg2 dictyosteli	949	6	25.0	640	2	Q5CFA2_CRYHO	Q5cpa2 cryptospori
877	6	25.0	580	2	Q54VL8_DICDI	Q54vl8 dictyosteli	950	6	25.0	641	2	Q54Y11_DICDI	Q54y11 dictyosteli
878	6	25.0	580	2	Q86JP4_DICDI	Q86jp4 dictyosteli	951	6	25.0	641	2	Q54I00_DICDI	Q54iq0 dictyosteli
879	6	25.0	580	2	Q55AB2_DICDI	Q55ab2 dictyosteli	952	6	25.0	642	2	Q9NH51_DROME	Q9nh51 drosophila
880	6	25.0	581	2	Q54UG5_DICDI	Q54ug5 dictyosteli	953	6	25.0	642	2	Q6RW12_ARATH	Q6rw12 arabidopsis
881	6	25.0	582	2	Q8SY46_DROME	Q8sy46 drosophila	954	6	25.0	643	2	Q9VZY3_DROME	Q9vzy3 drosophila
882	6	25.0	582	2	Q9ZLC5_HELPF	Q9zlc5 helicobacte	955	6	25.0	643	2	Q54Y78_DICDI	Q54y78 dictyosteli
883	6	25.0	583	2	Q6CM16_KJULA	Q6cm16 kluveromyc	956	6	25.0	645	1	BARH2_DROME	Q24256 drosophila
884	6	25.0	584	2	Q81D54_PLAF7	Q81d54 plasmidium	957	6	25.0	647	2	Q55AW1_DICDI	Q55aw1 dictyosteli
885	6	25.0	584	2	Q4XV15_PLACH	Q4xv15 plasmidium	958	6	25.0	647	2	Q8SZT1_DROME	Q8sztl drosophila
886	6	25.0	586	2	Q54Z94_DICDI	Q54z94 dictyosteli	959	6	25.0	647	2	Q8IM96_DROME	Q8im96 drosophila
887	6	25.0	586	2	Q8MND9_DICDI	Q8mnd9 dictyosteli	960	6	25.0	648	1	KAPC_DICDI	P34099 plasmidium
888	6	25.0	587	2	Q55G76_DICDI	Q55g76 dictyosteli	961	6	25.0	648	2	Q6T7E7_PLAFA	Q6t7e7 dictyosteli
889	6	25.0	588	2	Q54VF4_DICDI	Q54vf4 dictyosteli	962	6	25.0	648	2	Q81IK0_DROVI	Q81ik0 drosophila
890	6	25.0	588	2	Q511G7_ENTHI	Q511g7 entamoeba h	963	6	25.0	648	2	Q5CUP3_CRYPV	Q5cup3 cryptospori
891	6	25.0	588	2	Q4YUJ3_PLABE	Q4yuj3 plasmidium	964	6	25.0	648	2	Q54QA3_DICDI	Q54qa3 dictyosteli
892	6	25.0	590	2	Q54D91_DICDI	Q54d91 dictyosteli	965	6	25.0	648	2	Q9TXB8_9MICE	Q9txb8 dictyosteli
893	6	25.0	591	2	Q4XUP3_PLACH	Q4xup3 plasmidium	966	6	25.0	649	2	Q9VW88_DROME	Q9vw88 drosophila
894	6	25.0	591	2	Q4YVL6_PLABE	Q4yvl6 plasmidium	967	6	25.0	649	2	Q95SS7_DROME	Q95ss7 drosophila
895	6	25.0	592	1	HMDH1_ARATH	P14891 arabidopsis	968	6	25.0	650	2	Q9GZ01_PLAFA	Q9gz01 plasmidium
896	6	25.0	593	2	Q5XXR4_ANOGA	Q5xxr4 anopheles g	969	6	25.0	650	2	Q54DL3_DICDI	Q54dl3 dictyosteli
897	6	25.0	594	2	Q86JK0_DICDI	Q86jk0 dictyosteli	970	6	25.0	652	2	Q4WXU4_ASPPU	Q4wxu4 aspergillus
898	6	25.0	595	2	Q7SPY1_NEUCR	Q7spy1 neurospora	971	6	25.0	652	2	Q8X018_NEUCR	Q8x018 neurospora
899	6	25.0	595	2	Q54K19_DICDI	Q54k19 dictyosteli	972	6	25.0	652	2	Q54RJ3_DICDI	Q54rj3 dictyosteli
900	6	25.0	597	2	Q6WIA6_BPKVA	Q6wia6 bacterioph	973	6	25.0	652	2	Q81427_PLAF7	Q81427 plasmidium
901	6	25.0	597	2	Q81103_PRRAR	Q81103 prunus arme	974	6	25.0	652	2	Q5CFV3_CRYHO	Q5cfv3 cryptospori
902	6	25.0	598	2	Q58774_PRRHO	Q58774 pyrococcus	975	6	25.0	654	2	Q62199_CABEL	Q62199 caenorhabdi
903	6	25.0	598	2	Q8SSN1_DICDI	Q8ssn1 dictyosteli	976	6	25.0	655	2	Q55IA2_DICDI	Q55ia2 dictyosteli
904	6	25.0	599	2	Q5A4L6_CANAL	Q5a4l6 candida alb	977	6	25.0	655	2	Q815P8_PLAF7	Q815p8 plasmidium
905	6	25.0	600	2	Q4PHL9_USTMA	Q4phl9 ustilago ma	978	6	25.0	656	2	Q6YYW2_ORYSA	Q6yyw2 oryza sativ
906	6	25.0	600	2	Q54K20_DICDI	Q54k20 dictyosteli	979	6	25.0	657	2	Q558W6_DICDI	Q558w6 dictyosteli
907	6	25.0	601	1	KEN_DROME	Q77459 drosophila	980	6	25.0	658	2	Q59779_SCHPO	Q59779 schizosacch

981 6 25.0 658 2 Q5ALR8 CANAL
 982 6 25.0 658 2 Q18703_CAEEL
 983 6 25.0 659 2 Q9VY77 DROSOPHILA
 984 6 25.0 660 2 Q94485 DICTYOESTELI
 985 6 25.0 662 2 Q55FD2 DICTDI
 986 6 25.0 662 2 Q4VPM5 PLABE
 987 6 25.0 662 2 Q5WBH7_BACSK
 988 6 25.0 662 2 Q5XIZ8_BRARE
 989 6 25.0 665 2 Q86HZ3_DICDI
 990 6 25.0 666 2 Q8IM66_PLAF7
 991 6 25.0 667 2 Q54QEB8_DICDI
 992 6 25.0 667 2 Q54QEB8_DICDI
 993 6 25.0 668 2 Q4UFQ5_THEAN
 994 6 25.0 668 2 Q86HC6_DICDI
 995 6 25.0 668 2 Q5SGI4_DICDI
 996 6 25.0 669 2 Q6C5E9_YARLI
 997 6 25.0 671 2 Q5IGF3_ENTHI
 998 6 25.0 672 2 Q9UOK1_PLAFA
 999 6 25.0 672 2 Q7K734_PLAF7
 1000 6 25.0 673 2 Q55A01_DICDI

ALIGNMENTS

RESULT 1
 Q56CY1 HUMAN
 ID Q56CY1 HUMAN PRELIMINARY; PRT; 182 AA.
 AC Q56CY1;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Bladder cancer related CD9 variant.
 GN Name=BTC-1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC TISSUE=Bladder;
 RA Ma F., Wang H., Wang X., Chang J.
 RT "The full-length cloning of a differentially expressed EST sequence in
 a bladder cancer subtractive cDNA library."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY966455; AAX78197.1; -; mRNA.
 SQ SEQUENCE 182 AA; 20750 MW; C26F856F584AADEE CRC64;

Query Match 100.0%; Score 24; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 7.5e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTQKSIPEQETNNNSFFYT 24
 |||||
 Db 35 LRFDSTQKSIPEQETNNNSFFYT 58

RESULT 2
 ID CD9_CERAE
 AC P30409; STANDARD; PRT; 227 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein)
 DE (DRAP27).
 GN Name=CD9;
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopitheciinae; Cercopithecus.
 OX NCBI_TaxID=9534;

RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;
 RA Mitamura T., Iwamoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,
 RA Mekada E.;
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from
 vero cells is the monkey homologue of human CD9 antigen: expression of
 DRAP27 elevates the number of diphtheria toxin receptors on toxin-
 sensitive cells.";
 RL J. Cell Biol. 118:1389-1399(1992).
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 fusion. Involved in cell adhesion, cell motility and tumor
 metastasis (By similarity).
 CC -!- FUNCTION: Expression of DRAP27 elevates the number of diphtheria
 CC toxin receptors on toxin-sensitive cells.
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC tetraoligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; D10726; BAA01569.1; -; mRNA.
 DR PIR; A42929; A42929.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005515; P:protein binding; ISS.
 DR GO; GO:0007155; P:cell adhesion; ISS.
 DR GO; GO:0006928; P:cell motility; ISS.
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
 DR GO; GO:0030913; P:paranodal junction formation; ISS.
 DR GO; GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspannin; 1.
 DR PRINTS; PR00359; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
 KW Palmitate; Phosphorylation; Transmembrane.
 FT INIT MET 0
 FT TOPO DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO DOM 33 54 Extracellular (Potential).
 FT TRANSMEM 55 75 Potential.
 FT TOPO DOM 76 86 Cytoplasmic (Potential).
 FT TRANSMEM 87 110 Potential.
 FT TOPO DOM 111 194 Extracellular (Potential).
 FT TRANSMEM 195 220 Potential.
 FT TOPO DOM 221 227 Cytoplasmic (Potential).
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
 FT LIPID 77 77 S-palmitoyl cysteine (By similarity).
 FT LIPID 78 78 S-palmitoyl cysteine (By similarity).
 FT LIPID 86 86 S-palmitoyl cysteine (By similarity).
 FT LIPID 217 217 S-palmitoyl cysteine (By similarity).
 FT LIPID 218 218 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 51 51 N-linked (GLCNAc...) (Potential).
 FT CARBOHYD 52 52 N-linked (GLCNAc...) (Potential).
 SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 9.1e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSTQKSIPEQETNNNSFFYT 24
 |||||
 Db 34 LRFDSTQKSIPEQETNNNSFFYT 57

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).
RL [7]
RN PROTEIN SEQUENCE OF 1-20.
RP TISSUE=Placenta;
RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;
RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;
RT "Purification and partial characterization of CD9 antigen of human
RT platelets."; *FEBS Lett.* 264:270-274(1990).
RL [8]
RN ROLE IN CELL MOTILITY AND METASTASIS.
RP PubMed=8478605; DOI=10.1084/jem.177.5.1231;
RX Ikegami S., Koyama M., Yamaoka M., Sasada R., Miyake M.;
RA "Suppression of cell motility and metastasis by transfection with
RT human motility-related protein (MRP-1/CD9) DNA."; *J. Exp. Med.* 177:1231-1237(1993).
RN [9]
RP ROLE IN CELL ADHESION.
RX PubMed=7511626;
RA Masellis-Smith A., Shaw A.R.;
RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B
RT cell adhesion to bone marrow fibroblasts through de novo recognition
RT of fibronectin."; *J. Immunol.* 152:2768-2777(1994).
RN [10]
RP ROLE IN GAMETE FUSION.
RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;
RA Higginbottom A., Takahashi Y., Bolling L., Connor S.A., White J.M.,
RA Partridge I.J., Monk P.N.;
RT "Structural requirements for the inhibitory action of the CD9 large
RT extracellular domain in sperm/oocyte binding and fusion."; *Biochem. Biophys. Res. Commun.* 311:208-214(2003).
RL [11]
RP SUBUNIT.
RX PubMed=14556650; DOI=10.1042/BJ20031037;
RA Kovalenko O.V., Yang X., Kolesnikova T.V., Hemler M.E.;
RT "Evidence for specific tetraspanin homodimers: inhibition of
RT palmitoylation makes cysteine residues available for cross-linking."; *Biochem. J.* 377:407-417(2004).
RN [12]
RP PHOSPHORYLATION.
RX MEDLINE=93327758; PubMed=7687539;
RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,
RA Aruffo A., Ledbetter J.A.;
RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells."; *EMBO J.* 12:2691-2696(1993).
RN [13]
RP PALMITOYLATION, AND MUTAGENESIS OF CYS-8; CYS-77; CYS-86;
RX CYS-217 AND CYS-218.
RA PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;
RX Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,
RA Rubinstein E.;
RT "Differential stability of tetraspanin/tetraspanin interactions: role
RT of palmitoylation."; *FEBS Lett.* 516:139-144(2002).
RN [14]
RP INTERACTION WITH PTGFRN.
RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;
RA Charrin S., Le Naour F., Oualid M., Billard M., Faure G., Hanash S.M.,
RA Boucheix C., Rubinstein E.;
RT "The major CD9 and CD81 molecular partner. Identification and
RT characterization of the complexes."; *J. Biol. Chem.* 276:14329-14337(2001).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paracellular junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis.
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher

RA CD9 HUMAN
ID CD9_HUMAN STANDARD; PRT; 227 AA.
AC P21926; Q9SES4;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)
DE (MRP-1) (Tetraspanin-29) (Tspan-29).
GN Name=CD9; Synonyms=MIC3, TSPAN29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.
RX MEDLINE=91093112; PubMed=1840589;
RA Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E.,
RA Gagnon J., Uzan G.;
RT "Molecular cloning of the CD9 antigen. A new family of cell surface
RT proteins."; *J. Biol. Chem.* 266:117-122(1991).
RL [2]
RN NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=91244846; PubMed=2037603;
RA Lanza F., Wolf D., Fox C.P., Kieffer N., Seyer J.M., Fried V.A.,
RA Coughlin S.R., Phillips D.R., Jennings L.K.;
RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new
RT family of multiple membrane-spanning proteins."; *J. Biol. Chem.* 266:10638-10645(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;
RA Miyake M., Koyama M., Seno M., Ikegami S.;
RT "Identification of the motility-related protein (MRP-1), recognized by
RT monoclonal antibody M31-15, which inhibits cell motility."; *J. Exp. Med.* 174:1347-1354(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX TISSUE=Leukocyte;
RT MEDLINE=93252369; PubMed=8486348;
RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,
RA Uzan G., Boucheix C.;
RT "Organization of the human CD9 gene."; *Genomics* 16:132-138(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahern M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rasmussen M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murthy N.B., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,


```

DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0006928; P:cell motility; ISS.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0
FT TOPO_DOM 1 11
FT TRANSMEM 12 32
FT TOPO_DOM 33 52
FT TRANSMEM 53 73
FT TOPO_DOM 74 84
FT TRANSMEM 85 108
FT TOPO_DOM 109 192
FT TRANSMEM 193 218
FT TOPO_DOM 219 225
FT LIPID 8
FT LIPID 75
FT LIPID 76
FT LIPID 84
FT LIPID 85
FT LIPID 215
FT LIPID 216
FT CARBOHYD 49
SQ SEQUENCE 225 AA; 25084 MW; 7889619F99A59C9D CRC64;

Query Match 66.7%; Score 16; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTKSIFQETN 16
DB 34 LRPDSQTKSIFQETN 49
|||||
|||||

RESULT 6
CD9_BOVIN
ID CD9_BOVIN STANDARD; PRT; 225 AA.
AC P30932;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ocular ciliary epithelium;
RX MEDLINE=93054422; PubMed=1339429;
RA Martin-Alonso J.M., Hernando N., Ghosh S., Coca-Prados M.;
RT "Molecular cloning of the bovine CD9 antigen from ocular ciliary
RT epithelial cells."
RL J. Biochem. 112:63-67(1992).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).

```

```

CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M81720; AAA30439.1; -, mRNA.
DR PIR; JX0221; JX0221.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0006928; P:cell motility; ISS.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0
FT TOPO_DOM 1 11
FT TRANSMEM 12 32
FT TOPO_DOM 33 52
FT TRANSMEM 53 73
FT TOPO_DOM 74 84
FT TRANSMEM 85 108
FT TOPO_DOM 109 192
FT TRANSMEM 193 218
FT TOPO_DOM 219 225
FT LIPID 8
FT LIPID 75
FT LIPID 76
FT LIPID 84
FT LIPID 215
FT LIPID 216
FT CARBOHYD 49
SQ SEQUENCE 225 AA; 25127 MW; EC867DB91A0898E7 CRC64;

Query Match 58.3%; Score 14; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTKSIFQEQ 14
DB 34 LRPDSQTKSIFQEQ 47
|||||
|||||

RESULT 7
CD9_MOUSE
ID CD9_MOUSE STANDARD; PRT; 225 AA.
AC P40240;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=BALE/c; TISSUE=Kidney;
RX MEDLINE=94054345; PubMed=82316164; DOI=10.1016/0049-3848(93)90162-H;
RA Rubinstein E., Billard M., Plaisance S., Prenant M., Bouchec C.;
RT "Molecular cloning of the mouse equivalent of CD9 antigen."
RT Thromb. Res. 71:377-383(1993).
RN [2]

```


RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	RP	FUNCTION AS RECEPTOR FOR PSG17.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;	RX	PubMed=11805154; DOI=10.1084/jem.20011741;
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;	RA	Waterhouse R., Ha C., Dvekle G.S.;
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,	RT	"Murine CD9 is the receptor for pregnancy-specific glycoprotein 17.";
RA	Nakada I., Oatono N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,	RL	J. Exp. Med. 195:277-282(2002).
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,	CC	-!- FUNCTION: Involved in platelet activation and aggregation.
RA	Baldarrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,	CC	Regulates paranodal junction formation. Required for gamete
RA	Schriml L.M., Kanapin A., Matsuda H., Baralov S., Beisel K.W.,	CC	fusion. Involved in cell adhesion, cell motility and tumor
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,	CC	metastasis. Acts as a receptor for PSG17.
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,	CC	-!- SUBUNIT: Forms both disulfide-linked homodimers and higher
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,	CC	homooligomers as well as heterooligomers with other members of the
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,	CC	tetraspanin family. Associates with CR2/CD21 and with PTGFRM/CD9P1
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,	CC	(By similarity).
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,	CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
RA	Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,	CC	-!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,	CC	nervous system.
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,	CC	-!- PTM: Phosphorylated on tyrosine following B-cell activation (By
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,	CC	similarity).
RA	Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,	CC	-!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	CC	-----
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	CC	the European Bioinformatics Institute. There are no restrictions on its
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	CC	use as long as its content is in no way modified and this statement is not
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,	CC	removed.
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,	CC	-----
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,	DR	EMBL; L08115; AAA37405.1; -; mRNA.
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,	DR	EMBL; AK002251; BAB21965.1; -; mRNA.
RA	Birney E., Hayashizaki Y.;	DR	EMBL; AK012793; BAB28473.1; -; mRNA.
RT	"Analysis of the mouse transcriptome based on functional annotation of	DR	EMBL; BC070474; AAH70474.1; -; mRNA.
RT	60,770 full-length cDNAs.";	DR	PIR; I49589; I49589.
RL	Nature 420:563-573 (2002).	DR	Ensembl; ENSMUSG00000030342; Mus musculus.
RN	[3]	DR	MGI; MGI:88348; Cd9.
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	DR	GO; GO:0005887; C:integral to plasma membrane; ISS.
RC	STRAIN=C57BL/6J; TISSUE=Brain;	DR	GO; GO:0005886; C:plasma membrane; TAS.
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	DR	GO; GO:0005515; P:protein binding; IPI.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	DR	GO; GO:0007155; P:cell adhesion; ISS.
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	DR	GO; GO:0006928; P:cell motility; ISS.
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	DR	GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	DR	GO; GO:0030913; P:paranodal junction formation; IDA.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	DR	GO; GO:0030168; P:platelet activation; ISS.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	DR	InterPro; IPR00301; Transmem 4.
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	DR	Pfam; PF00335; Tetraspanin; I.
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	DR	PRINTS; PR00259; TMFOUR.
RA	Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	DR	PROSITE; PS00421; TM4.1.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	KW	Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	KW	Palmitate; Phosphorylation; Transmembrane.
RA	Fahy J., Helton E., Yettem A.C., Shevchenko Y., Bouffard G.G.,	FT	INIT MET 0
RA	Whiting M., Madan A., Keenan A.C., Shevchenko Y., Bouffard G.G.,	FT	TOPO_DOM 1 11
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	FT	TRANSMEM 12 32
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	FT	TOPO_DOM 33 52
RA	Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,	FT	TRANSMEM 53 73
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;	FT	TOPO_DOM 74 84
RT	"Generation and initial analysis of more than 15,000 full-length human	FT	TRANSMEM 85 108
RT	and mouse cDNA sequences.";	FT	TOPO_DOM 109 192
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	FT	TRANSMEM 193 218
RN	[4]	FT	TOPO_DOM 219 225
RP	ROLE IN GAMETE FUSION.	FT	LIPID 8 8
RX	PubMed=10700183; DOI=10.1038/73502;	FT	LIPID 75 75
RA	Kaji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,	FT	LIPID 76 76
RA	Tada N., Miyazaki S., Kudo A.;	FT	LIPID 84 84
RT	"The gamete fusion process is defective in eggs of Cd9-deficient	FT	LIPID 215 215
RT	mic.";	FT	LIPID 216 216
RL	Nat. Genet. 24:279-282(2000).	FT	CARBOHYD 49 49
RN	[5]	SQ	SEQUENCE 225 AA; 25127 MW; 2BBE40B8D7C31BC0 CRC64;
RP	ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.		
RX	PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;	Query Match	58.3%; Score 14; DB 1; Length 225;
RA	Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,	Best Local Similarity	100.0%; Pred. No. 1.7e-06;
RA	Baba H.;	Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
RT	"Tetraspanin protein CD9 is a novel paranodal component regulating		
RT	paranodal junctional formation.";	Oy	1 LRFDSQTKSIFEQE 14
RL	J. Neurosci. 24:96-102(2004).	Db	34 LRFDSQTKSIFEQE 47
RN	[6]		


```

RESULT 8
CD9_PIG
ID CD9_PIG STANDARD; PRT; 225 AA.
AC Q8MJ48_PIG PRELIMINARY; PRT; 226 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=Smooth muscle;
RX PubMed=14610355; DOI=10.1159/000074170;
RA Yubero N., Jimenez-Marín A., Yerle M., Morera L., Barbancho M.J.,
RA Lilanes D., Garrido J.J.;
RT "Molecular cloning, expression pattern and chromosomal mapping of pig
CD9 antigen.";
RL Cytogenet. Genome Res. 101:143-146(2003).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC -!- FUNCTION: Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY072785; AAL69666.1; -; mRNA.
DR GO; GO:005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0006928; P:cell motility; ISS.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR GO; GO:0030913; P:paxanodal junction formation; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR Palmitate; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT_MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).

Query Match 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 25070 MW; FF280PE39BCL1545 CRC64;

Query Match 58.3%; Score 14; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTSIFEQE 14
DB 34 LRPDSQTSIFEQE 47

RESULT 9
Q8MJ48_PIG PRELIMINARY; PRT; 226 AA.
AC Q8MJ48;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane protein CD9.
GN Name=CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,
RA Kurilla-Mahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,
RA Down J.D., Sachs D.H., Goodell M.A.;
RT "Use of CD9 Expression to Enrich for Porcine Hematopoietic
RT Progenitors.";
RL Exp. Hematol. 0:0-0(2002).
DR EMBL; AF525029; AAM81376.1; -; mRNA.
DR HSP; P60033; IG80.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR Transmembrane.
SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;

Query Match 58.3%; Score 14; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRPDSQTSIFEQE 14
DB 35 LRPDSQTSIFEQE 48

RESULT 10
CD9_FELCA
ID CD9_FELCA STANDARD; PRT; 225 AA.
AC P40239;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;
RA Willett B.J., Neil J.C.;
```

RT "cDNA cloning and eukaryotic expression of feline CD9.";
RL Mol. Immunol. 32:417-423(1995).
RN [2].
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Morikawa S.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L35275; AAA92867.1; -; mRNA.
CC EMBL; D30786; BAA06452.1; -; mRNA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; F:protein binding; ISS.
CC DR GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC InterPro; IPR000301; Transmem_4.
CC Pfam; PF00335; Tetraspanin; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4_1, 1.
CC Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
KW Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CONFLICT 82 82 S -> Y (in Ref. 2).
SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 54.2%; Score 13; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTKSIFPQ 13
Db 34 LRFDSQTKSIFPQ 46
|||||
|||||

RESULT 11
Q8AV92 PETMA
ID Q8AV92 PETMA PRELIMINARY; PRT; 228 AA.
AC Q8AV92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD9-like protein.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Heteroartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Typhlosolole;
RX MEDLINE=23295056; PubMed=12391333; DOI=10.1073/pnas.212527699;
RA Uinuk-Ool T., Mayer W.E., Sato A., Dongak R., Cooper M.D., Klein J.;
RT "Lamprey lymphocyte-like cells express homologs of genes involved in
RT immunologically relevant activities of mammalian lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14356-14361(2002).
DR EMBL; AY152677; AAG64299.1; -; mRNA.
DR HSSP; P60033; 1G8Q.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
SQ SEQUENCE 228 AA; 25331 MW; DDE0EAA31E988935 CRC64;

Query Match 33.3%; Score 8; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTK 8
Db 35 LRFDSQTK 42
|||||
|||||

RESULT 12
Q6GOE5 XENLA
ID Q6GOE5 XENLA PRELIMINARY; PRT; 228 AA.
AC Q6GOE5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC80123 protein.
GN Name=MGC80123;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;

```

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072800; AAH72800.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; I.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM_1; 1.
SQ SEQUENCE 228 AA; 25155 MW; 9A826DEC2D9980A2 CRC64;

Query Match 33.3%; Score 8; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTK 8
Db 35 LRFDSQTK 42

RESULT 13
Q56F04_9CAUD
ID Q56F04_9CAUD PRELIMINARY; PRT; 607 AA.
AC Q56F04;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Gp60plus39.
GN Name=60plus39; ORFNames=PHG31p7;
OS Aeromonas phage 31.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=321023;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nolan J.M., Petrov V., Bertrand C., Krisch H.M., Karam J.D.;
RT "Comparative analysis of the Aeromonas bacteriophage 31 genome.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY962392; AAX63496.1; -; Genomic DNA.
SQ SEQUENCE 607 AA; 68086 MW; E772C3DD1FA916D7 CRC64;

Query Match 33.3%; Score 8; DB 2; Length 607;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTK 8
Db 323 LRFDSQTK 330

RESULT 14
Q6U9U5_9CAUD
ID Q6U9U5_9CAUD PRELIMINARY; PRT; 607 AA.
AC Q6U9U5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Topoisomerase II large subunit.
GN Name=60plus39;
OS Bacteriophage 44RR2.8t.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=115987;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nolan J.M., Petrov V., Bertrand C., Krisch H.M., Karam J.D.;

```

```

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY375531; AAQ81326.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; F:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA gyrase B.
DR InterPro; IPR011241; DNA topoisom.
DR Pfam; PF00204; DNA gyraseB; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
SQ SEQUENCE 607 AA; 68074 MW; AFDACD841EA8ADD1 CRC64;

Query Match 33.3%; Score 8; DB 2; Length 607;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDSQTK 8
Db 323 LRFDSQTK 330

RESULT 15
Q76XL0_9CAUD
ID Q76XL0_9CAUD PRELIMINARY; PRT; 607 AA.
AC Q76XL0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Topoisomerase II large subunit.
OS Enterobacteria phage RB49.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=50948;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97250366; PubMed=9096222; DOI=10.1006/jmbi.1996.0867;
RA Monod C., Repoila F., Kutateladze M., Tetart F., Krisch H.M.;
RT "The genome of the pseudo T-even bacteriophages, a diverse group that
RT resembles T4.";
RL J. Mol. Biol. 267:237-249(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21062343; PubMed=11092834; DOI=10.1146/annurev.genet.34.1.439;
RA Ang D., Keppel F., Klein G., Richardson A., Georgopoulos C.;
RT "Genetic analysis of bacteriophage-encoded co-chaperonins.";
RL Annu. Rev. Genet. 34:439-456(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21972795; PubMed=11976309;
DOI=10.1128/JB.184.10.2789-2804.2002;
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RT "Snapshot of the genome of the pseudo-T-even bacteriophage RB49.";
RL J. Bacteriol. 184:2789-2804(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Ang D., Richardson A., Mayer M.P., Keppel F., Krisch H.,
RA Georgopoulos C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Tetart F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,

```

```

RA Krisch H.M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE.
RA Krisch H.M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RA Zhao L., Tetart F., Krisch H.M., Arisaka F.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RA Thiemer C.A., Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE.
RA Krisch H.M.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP NUCLEOTIDE SEQUENCE.
RA Desplats C., Krisch H.M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [13]
RP NUCLEOTIDE SEQUENCE.
RA Letarov A.V., Krisch H.M., Tetart P.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP NUCLEOTIDE SEQUENCE.
RA Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,
RA Karam J.D., Krisch H.M.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY343333; AAL15132.2; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00418; TPI2FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00433; TOP2c; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
SQ SEQUENCE 607 AA; 68461 MW; 3A6C4B35C7E66AFF CRC64;

```

```

Query Match          33.3%; Score 8; DB 2; Length 607;
Best Local Similarity 100.0%; Pred.No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LRFDSTQTK 8
Db 323 LRFDSTQTK 330

```

```

Search completed: January 20, 2006, 17:44:14
Job time : 57.2308 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:03:51 ; Search time 133.704 Seconds
(without alignments)
124.876 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDFPQRETLKAIHYALNCCGLAGVQVFISDICPKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	38	ADJ57561	Adj57561 Human CD9
2	207	100.0	227	AAR86834	Aar86834 Human CD9
3	207	100.0	227	ABB78366	Abb78366 Amino aci
4	207	100.0	227	AAE14636	Aae14636 Human CD9
5	207	100.0	227	ABU05057	Abu05057 Human exp
6	207	100.0	227	ABU05060	Abu05060 Human exp
7	207	100.0	227	ABW00436	Abw00436 Human CD9
8	207	100.0	227	ADK69862	Adk69862 Human CD9
9	207	100.0	227	ADI19366	Adi19366 Human CD9
10	207	100.0	227	AEA99005	Aea99005 Human CD9
11	207	100.0	228	AAR27525	Aar27525 Metastasi
12	207	100.0	228	ABBA4581	Abba4581 Human wou
13	207	100.0	228	ABU05059	Abu05059 Human exp
14	207	100.0	228	ABU05052	Abu05052 Human exp
15	207	100.0	228	ABU05048	Abu05048 Human exp
16	207	100.0	228	ABU05056	Abu05056 Human exp
17	207	100.0	228	ABU05049	Abu05049 Human exp
18	207	100.0	228	ABU05050	Abu05050 Human exp
19	207	100.0	228	ABU05053	Abu05053 Human exp
20	207	100.0	228	ABW01519	Abw01519 Protein #
21	207	100.0	228	ADD89037	Add89037 TAI278. 1
22	207	100.0	228	ADG32002	Adg32002 Human hom
23	207	100.0	228	ADJ57558	Adj57558 Human CD9
24	207	100.0	228	ADL26782	Adl26782 Human CD9

25	207	100.0	228	8	ADL82853	Adl82853 Human PRO
26	207	100.0	228	8	ADP23088	Adp23088 PRO polyp
27	207	100.0	228	8	ADR73450	Adr73450 Human CD9
28	207	100.0	228	9	ADV70263	Adv70263 Tumor-as8
29	207	100.0	228	9	ADY97163	Ady97163 Human CD9
30	207	100.0	228	9	ADY19604	Ady19604 PRO polyp
31	207	100.0	228	9	ADY14362	Ady14362 PRO polyp
32	207	100.0	228	9	AE898450	Aeb98450 Human CD9
33	207	100.0	275	3	ABA43936	Aab43936 Human can
34	207	100.0	275	4	AA675156	Aag75156 Human col
35	207	100.0	275	6	ABU05055	Abu05055 Human exp
36	207	100.0	275	6	ABU05054	Abu05054 Human exp
37	201	97.1	79	2	AAW35851	Aaw35851 Human CD9
38	201	97.1	79	6	ABU05058	Abu05058 Human exp
39	191	92.3	226	7	ADB85281	Adb85281 Rat G9 su
40	187	90.3	454	4	ABG14067	Abg14067 Novel hum
41	167	80.7	226	4	ABB44580	Abb44580 Mouse wou
42	167	80.7	226	5	ABB57234	Abb57234 Mouse isc
43	167	80.7	226	9	ADV25799	Adv25799 Mouse CD9
44	167	80.7	226	9	AEA55045	Aea55045 Mouse CD9
45	128	61.8	30	6	ABU05051	Abu05051 Human exp

ALIGNMENTS

RESULT 1

ADJ57561

ID ADJ57561 standard; protein; 38 AA.

AC ADJ57561;

DT 06-MAY-2004 (first entry)

DE Human CD9 fibronectin-binding domain polypeptide fragment.

KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;

KW haemostatic; angiogenic; cytostatic.

OS Homo sapiens.

XX WO2004007685-A2.

XX 22-JAN-2004.

PF 14-JUL-2003; 2003WO-US022050.

PR 12-JUL-2002; 2002US-0395964P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;

PI Crosseno JT, Lu Y;

DR WPI; 2004-122924/12.

PT Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

PS Claim 7; SEQ ID NO 4; 126pp; English.

XX The present sequence is that of a polypeptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion; inhibiting or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of CD9-expressing cells; modifying pericellular fibronectin matrix assembly; modifying invasiveness of a cell through a collagen and/or laminin matrix; and modifying cell-to-cell interaction. The methods are based on the finding that increased CD9 expression is implicated in (i) decreased adhesiveness of cells to extracellular matrix

CC (via alpha5-beta-1 integrin) and/or decreased cell invasiveness and/or
 CC decreased pericellular fibronectin matrix assembly, and/or (ii) increased
 CC cell motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX Sequence 38 AA;

Query Match 100.0%; Score 207; DB 8; Length 38;
 Best Local Similarity 100.0%; Pred. No. 5.1e-22;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
 |||||
 Db 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38

RESULT 2
 AAR86834
 ID AAR86834 standard; protein; 227 AA.
 AC AAR86834;

DT 12-JUL-1996 (first entry)

DE Human CD9 sequence.

XX CD9 antigen; stimulated T cell; antibody; ligand; proliferation;
 KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;
 KW immune response; cancer; infectious disease; growth factor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 51 /note= "Potential N-linked glycosylation site"
 FT Modified-site 52 /note= "Potential N-linked glycosylation site"
 FT Domain 111..194 /note= "Extracellular domain"
 FT Domain 195..220 /note= "Transmembrane domain"
 FT Domain 221..227 /note= "Cytoplasmic domain"

XX WO9533823-A1.

XX 14-DEC-1995.

XX 01-DEC-1994; 94WO-US013782.

XX 03-JUN-1994; 94US-00253751.

XX 03-JUN-1994; 94US-00253964.

XX (USNA) US SEC OF NAVY.

XX (UNMI) UNIV MICHIGAN.

XX (REPK) REPLIGEN CORP.

XX (DAND) DANA FARBER CANCER INST INC.

XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;

XX WPI; 1996-040230/04.

XX Selectively inducing CD8 positive T cell proliferation - by activating
 PT the T cells and stimulating CD9 cell surface ligand, useful for
 PT immuno:therapy of, e.g. cancer.

XX Example 10; Page 38-39; 79pp; English.

CC This sequence represents CD9 from the surface of stimulated T cells. The
 CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an
 CC antibody or other ligand to stimulate the T cell population to
 CC proliferate and expand leading to a 100- to 10000-fold increase in cell
 CC number compared to the original population. The antigenic sequence fits
 CC the generic sequence given in AAR86827. This epitope is recognised by the
 CC monoclonal antibody (WAB) ES5.2D8. CD9 is a 27 kD accessory protein found
 CC on activated T cells. The epitope was recognised by screening a phage
 CC display library. Selective proliferation of an antigen-specific T cell
 CC population is useful in cases where the immune response is to be up
 CC regulated, e.g. in the treatment of cancer or infectious diseases. By
 CC causing proliferation of the T cell population by stimulating T cell
 CC epitope removes the need for exogenous growth factors or accessory cells
 XX Sequence 227 AA;

Query Match 100.0%; Score 207; DB 2; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.8e-21;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
 |||||
 Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 171

RESULT 3

ABE78366

ID ABB78366 standard; protein; 227 AA.

AC ABB78366;

DT 16-DEC-2002 (first entry)

DE Amino acid sequence of CD9.

XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;
 KW immunotherapy; CD9.

XX Homo sapiens.

XX US2002115214-A1.

XX 22-AUG-2002.

XX 26-JAN-1996; 96US-00592711.

XX 23-NOV-1988; 88US-00275433.

XX 07-APR-1992; 92US-00864805.

XX 07-APR-1992; 92US-00864807.

XX 07-APR-1992; 92US-00864866.

XX 04-JUN-1993; 93US-00073223.

XX 03-JUN-1994; 94US-00253964.

XX 10-MAR-1995; 95US-00403253.

XX 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABEL/) NABEL G J.

XX (GRAY/) GRAY G S.

XX (RENN/) RENNERT P D.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-712476/77.

XX Inducing a population of T cells to proliferate, by activating population
 PT of T cells and stimulating an accessory molecule on the surface of the T
 PT cells with a ligand which binds the accessory molecule.

XX Example 10; Page 25; 88pp; English.

XX The specification describes method for inducing a population of T cells
 CC to proliferate. The method involves activating population of T cells,

CC stimulating an accessory molecule on T cell surface with a ligand
 CC protein) which binds the molecule, to induce proliferation of T cells,
 CC monitoring proliferation of T cells in response to continuing exposure to
 CC the ligand, and reactivating and restimulating T cells when rate of
 CC proliferation has decreased to induce further proliferation of the cells.
 CC The method is useful for inducing proliferation of T cells, for use in
 CC treatment of infectious disease, cancer and immunotherapy. The method
 CC allows for the expansion of a population of T cells in numbers sufficient
 CC to reconstitute an individual's total CD4+ or CD8+ T cell population.
 CC The resulting T cell population can be genetically transduced and used
 CC for immunotherapy or can be used in methods of in vitro analyses of
 CC infectious agents. A population of tumour-infiltrating lymphocytes can be
 CC obtained from an individual afflicted with cancer and the T cells
 CC stimulated to proliferate to sufficient numbers. The resulting T cell
 CC population can be genetically transduced to express tumour necrosis
 CC factor (TNF) or other factor and restored to the individual. CD4+ T cells
 CC expanded by this method are useful in the treatment of HIV infection in
 CC an individual. The present sequence represents CD9, an antigen present on
 CC the surface of activated T cells
 XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 207; DB 5; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDBPQRETLKAIHYALNCCGLAGGVQFISDICKPKDV 38
 |||||
 Db 134 KDBPQRETLKAIHYALNCCGLAGGVQFISDICKPKDV 171

RESULT 4

AAE14636
 ID AAE14636 standard; protein; 227 AA.

AC AAE14636;

XX 16-JUL-2002 (first entry)

XX Human CD9 antigen.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;
 KW human; CD9 antigen.

XX Homo sapiens.

XX US6352694-B1.

XX 05-MAR-2002.

XX 10-MAR-1995; 95US-00403253.

XX 03-JUN-1994; 94US-00253964.

XX (GEM) GENETICS INST INC.

XX (UNMI) UNIV MICHIGAN.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,
 PT comprises activating T cells by contacting T cells in vitro with
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T
 PT cell surface.

XX Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to
 CC proliferate for use in therapy comprising activating T cells by
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
 CC on solid phase surface, and stimulating accessory molecule on T cell

CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a
 CC population of T cells to proliferate in sufficient numbers for use in
 CC therapy e.g., for treating cancer or an infectious disease. The method
 CC can be used to selectively expand the population of CD28⁺, CD4⁺, CD8⁺,
 CC CD28RA⁺ or CD28RO⁺ T cells for immunotherapy. The T cell population
 CC resulting by the method can be genetically transduced and used for
 CC immunotherapy or can be used for in vitro analysis of infectious agents
 CC such as human immunodeficiency virus (HIV). Proliferation of a population
 CC of CD4⁺ T cells obtained from an individual infected with HIV can be
 CC achieved and the cells rendered resistant to HIV infection. Following the
 CC expansion of the T cells to sufficient numbers, the expanded T cells are
 CC restored to the individual. Also CD4⁺ T cells expanded by the above
 CC mentioned is useful for treating HIV infection in an individual. A
 CC population of tumour-infiltrating lymphocytes can be obtained from an
 CC individual afflicted with cancer and the T cells stimulated to
 CC proliferate to sufficient numbers and restored to the individual. The
 CC supernatants from cultures of T cells expanded from above mentioned
 CC method are useful as a rich source of cytokines and can be used to
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a
 CC population of antigen specific T cells are useful in therapeutic
 CC conditions where it is desirable to upregulate an immune response. The T
 CC cell proliferation occurs in the absence of exogenous growth factors or
 CC accessory cells. The present sequence is human CD9 antigen which is
 CC expressed on surface of activated T cells
 XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 207; DB 5; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDBPQRETLKAIHYALNCCGLAGGVQFISDICKPKDV 38
 |||||
 Db 134 KDBPQRETLKAIHYALNCCGLAGGVQFISDICKPKDV 171

RESULT 5

ABU05057

ID ABU05057 standard; protein; 227 AA.

XX ABU05057;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1723.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chiciz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

```

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1723; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 207; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKIHYALNCCGLAGGVEQFISDICPKDV 38
Db 134 KDEPQRETAKIHYALNCCGLAGGVEQFISDICPKDV 171

RESULT 6
ABU05060
ID ABU05060 standard; protein; 227 AA.
AC ABU05060;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1726.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX

```

```

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1726; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 207; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKIHYALNCCGLAGGVEQFISDICPKDV 38
Db 134 KDEPQRETAKIHYALNCCGLAGGVEQFISDICPKDV 171

RESULT 7
ABW00436
ID ABW00436 standard; protein; 227 AA.
AC ABW00436;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human CD9 antigenic protein.
XX
XX HIV infection; human immunodeficiency virus; therapy; antigen; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 111..194
FT /note= "Extracellular domain"
FT Domain 195..220
FT /note= "Transmembrane domain"
FT Domain 221..227
FT /note= "Cytoplasmic domain"
XX
XX US2003099643-A1.
XX
XX 29-MAY-2003.
XX
XX 08-JUL-1999; 99US-00350202.
XX
XX 23-NOV-1988; 88US-00275433.
PR 22-NOV-1989; 89WO-US005304.
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253694.
PR 10-MAR-1995; 95US-00403253.

```


XX (JUNE/) JUNE C H.
 PA (THOM/) THOMPSON C B.
 PA (NABEL/) NABEL G J.
 PA (GRAY/) GRAY G S.
 PA (RENN/) RENNERT P D.
 XX

June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
 WPI; 2003-801206/75.

Treating HIV infection in individual by isolating T cells from
 leukocytes, contacting T cells with anti-CD3 antibody for T cell
 proliferation, separating antibody from T cells, monitoring proliferation
 of T cells.

XX Example 10; Page 23; Opp; English.

XX The present invention relates to a novel method of treating human
 CC immunodeficiency virus (HIV) infection in an individual. The method
 CC involves isolating population of CD4 T cells from leukocytes, contacting
 CC population of CD4+ T cells with an anti-CD3 antibody for stimulating T
 CC cell proliferation, separating antibody from T cells, monitoring
 CC proliferation of T cells, restimulating T cells with antibody and
 CC restoring T cells to individual. The present sequence is human CD9
 CC antigenic protein. This sequence is used to illustrate the method of the
 CC invention

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 207; DB 7; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
 DB 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 171
 |||||

RESULT 8
 ADK69862
 ID ADK69862 standard; protein; 227 AA.
 XX
 AC ADK69862;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human CD9 protein.
 XX
 KW CD28-associated signal; immunotherapy; infectious disease; cancer;
 KW Leukopenia; human.
 XX
 OS Homo sapiens.
 XX
 PN US6534055-B1.
 XX
 PD 18-MAR-2003.
 XX
 PF 04-MAY-1995; 95US-00435816.
 XX
 PR 07-APR-1992; 92US-00864805.
 PR 07-APR-1992; 92US-00864807.
 PR 07-APR-1992; 92US-00864866.
 PR 04-JUN-1993; 93US-00073223.
 PR 03-JUN-1994; 94US-00253964.
 PR 10-MAR-1995; 95US-00403253.
 XX
 PA (GEM) GENETICS INST INC.
 XX
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
 XX WPI; 2003-531074/50.
 XX

PT Expanding T cell populations, useful for preparing renewable sources of T
 PT cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28
 PT -associated signal on the surface of the cells with an anti-CD28
 PT antibody, B7-1 or B7-2.
 XX
 PS Example 10; SEQ ID NO 6; 82pp; English.

XX The invention relates to a method for expanding a population of T cells
 CC to about 100-100000-fold over the original T cell population, or to about
 CC 10 log 1 to 12 log 1.2. The method comprises stimulating a CD28-
 CC associated signal on the surface of the T cells with agent comprising an
 CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a
 CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T
 CC cells) to proliferate. The method is particularly useful for preparing a
 CC renewable source of CD4+ T cells. The expanded T cell population can be
 CC genetically transduced, and used for immunotherapy to treat a variety of
 CC human diseases (e.g. infectious diseases or cancer), or used in
 CC diagnostic protocols. T cells were obtained from leukopheresis of a
 CC normal donor, and purified with FICOLL density gradient centrifugation,
 CC followed by magnetic immunobead sorting. The present sequence is CD9 used
 CC in the exemplification of the invention.

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 207; DB 7; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
 DB 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 171
 |||||

RESULT 9
 ADI19366
 ID ADI19366 standard; protein; 227 AA.
 XX
 AC ADI19366;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human CD9 protein.
 XX
 KW T cell; immunotherapy; therapy; HIV infection; cancer;
 KW infectious disease; cytostatic; antimicrobial; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004001829-A1.
 XX
 PD 01-JAN-2004.
 XX
 PF 17-MAR-2003; 2003US-00390330.
 XX
 PR 23-NOV-1988; 88US-00275433.
 PR 22-NOV-1989; 89WO-US005304.
 PR 07-APR-1992; 92US-00864805.
 PR 07-APR-1992; 92US-00864807.
 PR 07-APR-1992; 92US-00864866.
 PR 04-JUN-1993; 93US-00073223.
 PR 03-JUN-1994; 94US-00253964.
 PR 10-MAR-1995; 95US-00403253.
 PR 04-MAY-1995; 95US-00435816.
 XX
 PA (JUNE/) JUNE C H.
 PA (THOM/) THOMPSON C B.
 PA (NABEL/) NABEL G J.
 PA (GRAY/) GRAY G S.
 PA (RENN/) RENNERT P D.
 XX
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
 XX WPI; 2004-061648/06.
 XX

XX Inducing a population of T cells to proliferate, for immunotherapy or
 PT treating HIV infection, cancer or infectious disease, comprises
 PT activating a population of T cells and stimulating an accessory molecule
 PT on the surface of the T cells.

XX Example 10; SEQ ID NO 6; 80pp; English.

XX The invention relates to a method for inducing a population of T cells to
 CC proliferate. The method comprising activating a population of T cells,
 CC and stimulating an accessory molecule on the surface of the T cells with
 CC a ligand that binds the accessory molecule. The invention is useful for
 CC immunotherapy, for treating HIV infection, cancer or infectious disease,
 CC or in diagnostic applications. The present sequence is human CD9 protein.

XX Sequence 227 AA;

Query Match 100.0%; Score 207; DB 8; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDLCPPKDV 38
 |||||
 Db 134 KDEPQRETLLKAIHYALNCCGLAGGVQFISDLCPPKDV 171

RESULT 10

AEA89005
 ID AEA89005 standard; protein; 227 AA.

AC AEA89005;

DT 25-AUG-2005 (first entry)

DE Human CD9 antigenic protein, SEQ ID NO: 6.

KW Cell therapy; immune stimulation; immunotherapy; diagnosis;
 KW infectious disease; antimicrobial; infection; cancer; cytostatic;
 KW neoplasm; CD9; antigen.

OS Homo sapiens.

PN US6905681-B1.

PD 14-JUN-2005.

PF 08-JUL-1999; 99US-00349915.

PR 03-JUN-1994; 94US-00253964.

PR 10-MAR-1995; 95US-00403253.

XX (GEMY) GENETICS INST INC.

PA (UNMI) UNIV MICHIGAN.

PA (USNA) US SEC OF NAVY.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2005-464777/47.

XX Ex vivo proliferation of T cell population for use in therapy, involves
 PT contacting population of T cells with surface having anti-CD3 antibody
 PT and anti-CD28 antibody for activating T cells and stimulating activated T
 PT cells, respectively.

XX Example 10; SEQ ID NO 6; 76pp; English.

XX The present invention relates to a method of including ex vivo
 CC proliferation of a population of T cells to sufficient numbers for use in
 CC therapy. The method involves contacting population of T cells with
 CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T
 CC cells and stimulating activated T cells, respectively. The invention is
 CC useful for treating cancer and infectious disease and also useful in cell
 CC therapy. The present sequence is the human CD9 antigenic protein. This

CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used
 CC to stimulate a CD8+ T cell population.

XX Sequence 227 AA;

Query Match 100.0%; Score 207; DB 9; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDLCPPKDV 38
 |||||

Db 134 KDEPQRETLLKAIHYALNCCGLAGGVQFISDLCPPKDV 171

RESULT 11

AAR27525

ID AAR27525 standard; protein; 228 AA.

AC AAR27525;

DT 25-MAR-2003 (revised)

DT 05-MAR-1993 (first entry)

DE Metastasis controlling peptide.

KW M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;
 KW lung; glioblastoma.

OS Homo sapiens.

PN EP508417-A2.

PD 14-OCT-1992.

PF 09-APR-1992; 92EP-00106093.

PR 12-APR-1991; 91JP-00079996.

PR 17-APR-1991; 91JP-00085396.

PR 07-FEB-1992; 92JP-00022321.

XX (TAKE) TAKEDA CHEM IND LTD.

PA (MIYA) MIYAKE M.

PI Ikeyama S, Koyama M, Senoo M, Miyake M;

XX WPI; 1992-341723/42.

DR N-PSDB; AAQ29182.

XX New monoclonal antibody M31-15 specific for metastasis-controlling
 PT peptide - useful for treating and preventing cancer and metastasis.

XX Claim 7; Fig 4; 3app; English.

XX The sequence is that of a cancer cell surface protein which is capable of
 CC suppressing the motility of cancer cells. It is specifically recognised
 CC by the monoclonal (MAB) antibody M31-15 which is useful for suppressing
 CC cancer metastasis. The polypeptide and MAB M31-15 are therefore useful in
 CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and
 CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 228 AA;

Query Match 100.0%; Score 207; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 3.8e-21;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLLKAIHYALNCCGLAGGVQFISDLCPPKDV 38
 |||||

Db 135 KDEPQRETLLKAIHYALNCCGLAGGVQFISDLCPPKDV 172

RESULT 12

ABB44581

```
ID ABB44581 standard; protein; 228 AA.
XX
AC ABB44581;
XX
DT 25-JAN-2002 (first entry)
XX
DE Human wound healing related polypeptide SEQ ID NO 38.
XX
KW Human; mouse; vulnery; dermatological; skin disorder; wound healing;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN CA2325226-A1.
XX
PD 17-MAY-2001.
XX
PF 16-NOV-2000; 2000CA-02325226.
XX
PR 17-NOV-1999; 99DE-01055349.
PR 17-DEC-1999; 99US-0172511P.
PR 20-JUN-2000; 2000DE-01030149.
XX
PA (SWIT-) SWITCH BIOTECH AG.
XX
PI Regenhogen J, Wolf E, Goppelt A, Werner S, Halle J;
XX WPI; 2001-433142/47.
XX
PT Use of novel polypeptide or its variant or nucleic acid encoding the
PT polypeptide for diagnosing and/or preventing and/or treating skin
PT disorders and/or treatment in wound healing or for identifying active
PT substances.
XX
PS Disclosure; Page 193-194; 265pp; English.
XX
CC The invention relates to the use of a polypeptide (ABB44544-ABB44601,
CC ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-
CC ABA81995, ABA82016-ABA82032) with vulnerary and/or dermatological
CC activity for the diagnosis, prevention and treatment of skin disorders
CC and treatment in wound healing or for the identification of
CC pharmacologically active substances. The nucleic acids are useful in gene
CC therapy. Note: The printed sequence listing for this specification was
CC incomplete, terminating part way through SEQ ID NO 106. The remaining
CC data was obtained from EPO data for an equivalent patent (EP1114862)
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDBPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38
DB 135 KDBPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 172
RESULT 13
ABU05059
ID ABU05059 standard; protein; 228 AA.
XX
AC ABU05059;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1725.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1725; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 207; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.8e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDBPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38
DB 135 KDBPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 172
RESULT 14
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX
AC ABU05052;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1718.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX
```

```

OS Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1718; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
XX
XX Query Match 100.0%; Score 207; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-21;
XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 172

RESULT 15
ABU05048
ID ABU05048 standard; protein; 228 AA.
AC ABU05048;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1714.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

```

```

OS Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1714; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
XX
XX Query Match 100.0%; Score 207; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-21;
XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
DB 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 172

Search completed: January 20, 2006, 17:16:06
Job time : 133.704 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:10:37 ; Search time 26.7407 Seconds
(without alignments)
117.486 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDBPQRETLKAIHYALNCCGLAGVQFISDIPCKXDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	227	1	US-08-254-493-1
2	207	100.0	227	1	US-08-253-751-6
3	207	100.0	227	1	US-08-453-925-6
4	207	100.0	227	2	US-08-403-253A-6
5	207	100.0	227	2	US-08-435-816A-6
6	207	100.0	227	2	US-09-350-202-6
7	207	100.0	227	2	US-08-592-711-6
8	207	100.0	227	2	US-09-349-915B-6
9	207	100.0	228	1	US-08-408-222B-1
10	201	97.1	79	2	US-08-630-172-8
11	201	97.1	79	2	US-09-375-419-8
12	157	75.8	29	1	US-08-254-493-5
13	157	75.8	29	1	US-08-408-222B-5
14	54	26.1	542	2	US-09-583-110-4474
15	54	26.1	546	2	US-09-107-433-3368
16	53.5	25.8	343	1	US-08-454-196-6
17	53.5	25.8	343	1	US-08-286-819A-4
18	53.5	25.8	343	2	US-08-980-357-4
19	53.5	25.8	343	2	US-09-064-033-6
20	53.5	25.8	343	2	US-09-291-046-6
21	53.5	25.8	343	2	US-09-357-375-4
22	53.5	25.8	2296	1	US-08-286-819A-27
23	53.5	25.8	2296	2	US-08-980-357-27
24	53.5	25.8	2296	2	US-09-357-375-27
25	52	25.1	416	2	US-09-252-991A-28499
26	52	25.1	422	2	US-09-252-991A-22959
27	51.5	24.9	547	2	US-08-461-722-2

28	51.5	24.9	547	2	US-08-336-251-2	Sequence 2, Appli
29	51.5	24.9	547	2	US-09-468-041-2	Sequence 2, Appli
30	51.5	24.9	547	4	PCT-US94-06362-2	Sequence 2, Appli
31	51.5	24.9	548	1	US-08-467-822-32	Sequence 32, Appli
32	51.5	24.9	548	2	US-09-472-971-3	Sequence 3, Appli
33	51.5	24.9	548	2	US-08-432-697-32	Sequence 32, Appli
34	51.5	24.9	548	2	US-08-466-248-32	Sequence 32, Appli
35	51	24.6	300	2	US-09-134-000C-5262	Sequence 5262, Ap
36	51	24.6	1836	2	US-10-162-012-24	Sequence 24, Appli
37	50.5	24.4	764	2	US-07-741-453A-54	Sequence 54, Appli
38	50.5	24.4	764	2	US-07-741-453A-60	Sequence 60, Appli
39	50	24.2	29	1	US-08-254-493-6	Sequence 6, Appli
40	50	24.2	29	1	US-08-408-222B-6	Sequence 6, Appli
41	50	24.2	434	2	US-09-516-143A-2	Sequence 2, Appli
42	50	24.2	434	2	US-09-984-205-2	Sequence 2, Appli
43	50	24.2	434	2	US-10-759-277-2	Sequence 2, Appli
44	50	24.2	434	2	US-09-930-440C-4	Sequence 4, Appli
45	50	24.2	462	2	US-09-248-796A-14397	Sequence 14397, A

ALIGNMENTS

RESULT 1
US-08-254-493-1
; Sequence 1, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0223321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-1

Query Match 100.0%; Score 207; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 38
|||||
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 171

RESULT 2

US-08-253-751-6
; Sequence 6, Application US/08253751

; Patent No. 5858358

; GENERAL INFORMATION:

; APPLICANT: June, Carl H.

; APPLICANT: Thompson, Craig B.

; APPLICANT: Nabel, Gary J.

; APPLICANT: Gray, Gary S.

; APPLICANT: Rennert, Paul D.

; APPLICANT: Freeman, Gordon J.

; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING

; TITLE OF INVENTION: PROLIFERATION OF T-CELLS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII TEXT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,751

; FILING DATE: 3 JUNE 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-002CPB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-253-751-6

Query Match 100.0%; Score 207; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 38
|||||
Db 134 KDEPQRETLKAIHYALNCCGLAGGVEQFISD1CPKDV 171

RESULT 3

US-08-453-925-6

; Sequence 6, Application US/08453925

; Patent No. 5883223

; GENERAL INFORMATION:

; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.

; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING

; TITLE OF INVENTION: PROLIFERATION OF T-CELLS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII TEXT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/453,925

; FILING DATE: 30 MAY 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/253,751

; FILING DATE: 3 JUNE 1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-002CPB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-435-816A-6

Query Match 100.0%; Score 207; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDICKPKDV 38
|||||
Db 134 KDEPQRETLKAHYALNCCGLAGGVEQFISDICKPKDV 171

RESULT 6

US-09-350-202-6
; Sequence 6, Application US/09350202
; Patent No. 6887466
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-350-202-6

Query Match 100.0%; Score 207; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDICKPKDV 38
|||||
Db 134 KDEPQRETLKAHYALNCCGLAGGVEQFISDICKPKDV 171

RESULT 7

US-08-592-711-6
; Sequence 6, Application US/08592711
; Patent No. 6905680
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-592-711-6

Query Match 100.0%; Score 207; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 38
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 171

RESULT 8

US-09-349-915B-6

; Sequence 6, Application US/09349915B

; Patent No. 6905681

; GENERAL INFORMATION:

; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

; Gray, Gary S., Rennert, Paul D.

; TITLE OF INVENTION: Methods For Selectively Stimulating

; Proliferation Of T-Cells

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: HALE AND DORR LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/349,915B

; FILING DATE: 01-Aug-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/403,253

; FILING DATE: March 10, 1995

; APPLICATION NUMBER: US 08/253,964

; FILING DATE: 3 JUNE 1994

; APPLICATION NUMBER: US 08/073,223

; FILING DATE: 4 JUNE 1993

; APPLICATION NUMBER: US 08/200,947

; FILING DATE: 23 FEB 1994

; APPLICATION NUMBER: US 07/864,805

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/247,505

; FILING DATE: 23 MAY 1994

; APPLICATION NUMBER: US 07/864,866

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 08/218,155

; FILING DATE: 25 MAR 1994

; APPLICATION NUMBER: US 07/864,807

; FILING DATE: 7 APR 1992

; APPLICATION NUMBER: US 07/902,467

; FILING DATE: 16 JUNE 1992

; APPLICATION NUMBER: US 07/275,433

; FILING DATE: 23 NOV 1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Suparko, Colleen

; REGISTRATION NUMBER: 39,850

; REFERENCE/DOCKET NUMBER: 36119-125 (US10)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 526-6564

; TELEFAX: (617) 526-5000

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-349-915B-6

Query Match 100.0%; Score 207; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 38
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKDV 171

RESULT 9

US-08-408-222B-1

; Sequence 1, Application US/08408222B

; Patent No. 5776727

; GENERAL INFORMATION:

; APPLICANT: Ikeyama, Shuichi

; APPLICANT: Koyama, Masaru

; APPLICANT: Miyake, Masayuki

; APPLICANT: Senoo, Masaharu

; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dike, Bronstein, Roberts & Cushman

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/408,222B

; FILING DATE: 22-MAR-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/254,493

; FILING DATE: 06-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP-079996-1991

; FILING DATE: 12-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP-085396-1991

; FILING DATE: 14-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP-022321-1992

; FILING DATE: 07-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Resnick, David S.

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41777-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; US-08-408-222B-1

Query Match 100.0%; Score 207; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGFISDIPCCKDV 38
|||||
Db 135 KDEPQRETLKAIHYALNCCGLAGVGFISDIPCCKDV 172

RESULT 10
US-08-630-172-8
; Sequence 8, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS: 41
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,172
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-172-8

Query Match 97.1%; Score 201; DB 2; Length 79;
Best Local Similarity 97.4%; Pred. No. 8.7e-23;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGFISDIPCCKDV 38
|||||
Db 23 KDEPQRETLKAIHYALNCCGLAGVGFISDIPCCKDV 60

RESULT 11
US-09-375-419-8
; Sequence 8, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS: 41
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.

; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-375-419-8

Query Match 97.1%; Score 201; DB 2; Length 79;
Best Local Similarity 97.4%; Pred. No. 8.7e-23;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGVGFISDIPCCKDV 38
|||||
Db 23 KDEPQRETLKAIHYALNCCGLAGVGFISDIPCCKDV 60

RESULT 12
US-08-254-493-5
; Sequence 5, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991

; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STEE UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-5

Query Match 75.8%; Score 157; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33
DB 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 13
US-08-408-222B-5
; Sequence 5, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masauyuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-408-222B-5

Query Match 75.8%; Score 157; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QRETLKAIHYALNCCGLAGGVEQFISDIC 33
DB 1 QRETLKAIHYALNCCGLAGGVEQFISDIC 29

RESULT 14
US-09-583-110-4474
; Sequence 4474, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4474
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4474

Query Match 26.1%; Score 54; DB 2; Length 542;
Best Local Similarity 35.5%; Pred. No. 14;
Matches 11; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISD 31
DB 390 KDAQSQDFMQAVSYQLNVEIGKNEVVQITSD 420

RESULT 15
US-09-107-433-3368
; Sequence 3368, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>

```

/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: <Unknown>
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/107,433
/   FILING DATE: 30-Jun-1998
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: 60/ 085131
/   FILING DATE: May 12, 1998
/   APPLICATION NUMBER: 60/051553
/   FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Ariniello, Pamela Deneke
/   REGISTRATION NUMBER: 40,489
/   REFERENCE/DOCKET NUMBER: GTC-011
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (781)893-5007
/   TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 3368:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 546 amino acids
/     TYPE: amino acid
/     TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/   ORGANISM: Streptococcus pneumoniae
/ FEATURE:
/   NAME/KEY: misc feature
/   LOCATION: (B) LOCATION 1...546
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3368:
US-09-107-433-3368

Query Match      26.1%; Score 54; DB 2; Length 546;
Best Local Similarity 35.5%; Pred. No. 14;
Matches 11; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY      1 KDEPQRETLKATHYALNCCGLAGGVQFI SD 31
Db      394 KDAQSDFMQAVSYQLNEVGKNEVVQITSD 424

```

Search completed: January 20, 2006, 17:23:44
 Job time : 27.7407 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:11:18 ; Search time 76.4691 Seconds
(without alignments)
207.633 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207
Sequence: 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	38	US-10-619-323-4	Sequence 4, Appli
2	207	100.0	227	US-08-592-711-6	Sequence 6, Appli
3	207	100.0	227	US-09-183-055-6	Sequence 6, Appli
4	207	100.0	227	US-09-350-202-6	Sequence 6, Appli
5	207	100.0	227	US-10-390-330-6	Sequence 6, Appli
6	207	100.0	227	US-10-473-127-1723	Sequence 1723, Ap
7	207	100.0	227	US-10-473-127-1726	Sequence 1726, Ap
8	207	100.0	228	US-10-156-136-39	Sequence 39, Appl
9	207	100.0	228	US-10-331-496A-41	Sequence 41, Appl
10	207	100.0	228	US-10-619-323-1	Sequence 1, Appli
11	207	100.0	228	US-10-794-899-97	Sequence 97, Appl
12	207	100.0	228	US-10-473-127-1714	Sequence 1714, Ap
13	207	100.0	228	US-10-473-127-1715	Sequence 1715, Ap
14	207	100.0	228	US-10-473-127-1716	Sequence 1716, Ap
15	207	100.0	228	US-10-473-127-1718	Sequence 1718, Ap
16	207	100.0	228	US-10-473-127-1719	Sequence 1719, Ap
17	207	100.0	228	US-10-473-127-1722	Sequence 1722, Ap
18	207	100.0	228	US-10-473-127-1725	Sequence 1725, Ap
19	207	100.0	228	US-10-789-378-18	Sequence 18, Appl
20	207	100.0	228	US-10-482-029-144	Sequence 144, App
21	207	100.0	228	US-10-852-335A-187	Sequence 187, Appl
22	207	100.0	228	US-11-041-419-39	Sequence 39, Appl
23	207	100.0	275	US-09-925-301-1381	Sequence 1381, Ap
24	207	100.0	275	US-10-106-698-5930	Sequence 5930, Ap
25	207	100.0	275	US-10-473-127-1720	Sequence 1720, Ap
26	207	100.0	275	US-10-473-127-1721	Sequence 1721, Ap
27	201	97.1	79	US-10-473-127-1724	Sequence 1724, Ap

28	191	92.3	226	4	US-10-205-194-162	Sequence 162, App
29	187	90.3	454	5	US-10-450-763-44426	Sequence 44426, A
30	138	61.8	30	5	US-10-473-127-1717	Sequence 1717, Ap
31	105	50.7	209	4	US-10-106-698-6825	Sequence 6825, Ap
32	103	49.8	74	4	US-10-425-113-240878	Sequence 240878, A
33	60.5	29.2	96	4	US-10-425-115-216442	Sequence 216442, A
34	60	29.0	22	4	US-10-619-323-7	Sequence 7, Appli
35	58	28.0	217	4	US-10-437-963-109106	Sequence 109106, A
36	56	27.1	198	4	US-10-424-599-266302	Sequence 266302, A
37	55	26.6	64	4	US-10-424-599-171926	Sequence 171926, A
38	55	26.6	373	6	US-11-097-143-15411	Sequence 15411, A
39	54.5	26.3	943	4	US-10-282-122A-48512	Sequence 48512, A
40	54	26.1	546	5	US-10-617-320-3368	Sequence 3368, Ap
41	53.5	25.8	151	5	US-10-488-074-56	Sequence 56, Appl
42	53.5	25.8	200	5	US-10-488-074-40	Sequence 40, Appl
43	53.5	25.8	343	4	US-10-186-886-23	Sequence 23, Appl
44	53.5	25.8	343	5	US-10-952-915-4	Sequence 4, Appli
45	53.5	25.8	2296	5	US-10-952-915-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-619-323-4
; Sequence 4, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Croseno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-4

Query Match 100.0%; Score 207; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
DB 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38

RESULT 2

US-08-592-711-6
; Sequence 6, Application US/08592711
; Publication No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennett, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/864,805
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-350-202-6

Query Match 100.0%; Score 207; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGVGEQFISDICPKKV 38
Db 134 KDEPQRETAKAIHYALNCCGLAGVGEQFISDICPKKV 171

RESULT 5
US-10-390-330-6
Sequence 6, Application US/10390330
Publication No. US20040001829A1
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.

APPLICANT: Rennett, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation
OF T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/390,330
FILING DATE: March 17, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,816A
FILING DATE: May 4, 1995
CLASSIFICATION:
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10 MARCH 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-390-330-6

Query Match 100.0%; Score 207; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGVGEQFISDICPKKV 38
Db 134 KDEPQRETAKAIHYALNCCGLAGVGEQFISDICPKKV 171

RESULT 6
US-10-473-127-1723
Sequence 1723, Application US/10473127

Publication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1723
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-10-473-127-1723

Query Match 100.0%; Score 207; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 171

RESULT 7
US-10-473-127-1726
Sequence 1726, Application US/10473127
Publication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1726
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match 100.0%; Score 207; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
Db 134 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 171

RESULT 8
US-10-156-136-39
Sequence 39, Application US/10156136
Publication No. US20030129696A1
GENERAL INFORMATION:
APPLICANT: Ni, et al.
TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/156,136
APPLICATION NUMBER: US/10/156,136
FILING DATE: 29-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,146
FILING DATE: <Unknown>
APPLICATION NUMBER: WO US98/00959
FILING DATE: 21-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF354PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-156-136-39

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 38
Db 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDICPKKDV 172

RESULT 9
US-10-331-496A-41
Sequence 41, Application US/10331496A
Publication No. US20030228305A1
GENERAL INFORMATION:
APPLICANT: FRANTZ, GRETCHEN
APPLICANT: HILLAN, KENNETH J.
APPLICANT: PHILLIPS, HEIDI S.
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH, VICTORIA
APPLICANT: SPENCER, SUSAN D.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WU, THOMAS D.
APPLICANT: ZHANG, ZEMIN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND


```

; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 38
Db 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 172

RESULT 10
US-10-619-323-1
; Sequence 1, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-619-323-1

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 38
Db 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 172

us-10-619-323-4.rapbm

RESULT 11
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97

Query Match 100.0%; Score 207; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 38
Db 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 172

RESULT 12
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 38
Db 135 KDEPQRETAKAIHYALNCCGLAGGVEQFISDPCPKDV 172

RESULT 13
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.

```

```
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715
```

```
Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 38
|||||
Db 135 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172
```

RESULT 14

```
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1716
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1716
```

```
Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 38
|||||
Db 135 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172
```

RESULT 15

```
US-10-473-127-1718
; Sequence 1718, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1718
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1718

Query Match 100.0%; Score 207; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 38
|||||
Db 135 KDEPQRETLKAIHYALNCCGLAGGVEQFISDIPCCKDV 172

Search completed: January 20, 2006, 17:26:38
Job time : 77.4691 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:16:18 ; Search time 6.5679 Seconds
(without alignments)
58.632 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 1013381 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pbp:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pbp:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pbp:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pbp:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pbp:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pbp:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pbp:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	228	6	US-10-821-234-1266
2	51	24.6	287	6	US-10-467-657-2768
3	50	24.2	434	7	US-11-123-013-4
4	46	22.2	207	6	US-10-467-657-8262
5	46	22.2	273	6	US-10-793-626-728
6	45.5	22.0	78	6	US-10-467-657-3038
7	45	21.7	212	7	US-11-124-368A-320
8	45	21.7	254	7	US-11-124-368A-318
9	45	21.7	303	5	US-09-978-360A-763
10	45	21.7	508	6	US-10-467-657-3444
11	43.5	21.0	391	6	US-10-467-657-5988
12	43.5	21.0	1071	6	US-10-467-657-1654
13	43	20.8	122	6	US-10-467-657-606
14	43	20.8	154	6	US-10-821-234-1469
15	43	20.8	432	7	US-11-084-624-20
16	43	20.8	2340	7	US-11-052-554A-171
17	42.5	20.5	425	7	US-11-037-243-92
18	42.5	20.5	798	6	US-10-770-726-64
19	42.5	20.5	1767	7	US-11-052-554A-372
20	42	20.3	269	6	US-10-995-561-535
21	42	20.3	278	7	US-11-009-658-8
22	42	20.3	303	6	US-10-995-561-534
23	42	20.3	1400	6	US-10-821-234-1045
24	41.5	20.0	366	6	US-10-524-647-126
25	41.5	20.0	371	6	US-10-467-962B-41

ALIGNMENTS

RESULT 1

US-10-821-234-1266
; Sequence 1266, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1266
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1266

Query Match 100.0%; Score 207; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.7e-24;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 38
DB 135 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICPKKDV 172

RESULT 2

US-10-467-657-2768
; Sequence 2768, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2768
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2768

Query Match      24.6%; Score 51; DB 6; Length 287;
Best Local Similarity 44.0%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 3 EPQRETAKAIHYALNCCGLAGGVEQ 27
Db 205 EFSRQSLKQAHYALQTEGLQNALAQ 229

RESULT 3
US-11-123-013-4
; Sequence 4, Application US/111123013
; Publication No. US20050287637A1
; GENERAL INFORMATION:
; APPLICANT: Betenbaugh, Michael J.
; APPLICANT: Lawrence, Shawn J.
; APPLICANT: Lee, Yuan C.
; APPLICANT: Coleman, Timothy A.
; TITLE OF INVENTION: Engineering Intracellular Sialylation Pathways
; FILE REFERENCE: 03940077bp
; CURRENT APPLICATION NUMBER: US/11/123,013
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US 60/122,582
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/169,624
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/227,579
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/516,793
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 09/930,440
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (169)..(169)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-123-013-4

Query Match      24.2%; Score 50; DB 7; Length 434;
Best Local Similarity 37.5%; Pred. No. 4.7;
Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 10 KAIHYALNCCGLAGGVEQFISDIC 33
Db 399 KAVGYICKNGGGAIREPAEHC 422

us-10-619-323-4.rapbn

RESULT 4
US-10-467-657-8262
; Sequence 8262, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8262
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8262

Query Match      22.2%; Score 46; DB 6; Length 207;
Best Local Similarity 36.0%; Pred. No. 8.2;
Matches 9; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 14 YALNCCGLAGGVEQFISDICPKDV 38
Db 136 FAQNCADLSGSFKQFCRFILDDSDI 160

RESULT 5
US-10-793-626-728
; Sequence 728, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 728
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-728

Query Match      22.2%; Score 46; DB 6; Length 273;
Best Local Similarity 34.1%; Pred. No. 11;
Matches 14; Conservative 6; Mismatches 11; Indels 10; Gaps 2;

QY 8 TLKATH-----YALNCCGLAGGV-----EQFISDICPKDV 38
Db 185 TYKAHACKTYNVNRLIVAGGVASNGKJRNALSEACKKEGI 225

RESULT 6
US-10-467-657-3038
; Sequence 3038, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3038
LENGTH: 78
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3038

Query Match 22.0%; Score 45.5; DB 6; Length 78;
Best Local Similarity 38.2%; Pred. No. 3.3;
Matches 13; Conservative 4; Mismatches 6; Indels 11; Gaps 3;

QY 6 RETLKAH-YAL-NCC-----GLAGGVEQF 28
|:||||| ||||| :|
Db 5 RKTWKAIHPYACPRCCCLPANTRTGMANSASF 38

RESULT 7
US-11-124-368A-320
Sequence 320, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 320
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-11-124-368A-320

Query Match 21.7%; Score 45; DB 7; Length 212;
Best Local Similarity 35.3%; Pred. No. 12;
Matches 12; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 5 QRETLKAHYALNCCGLAGGVEQFISDICKDV 38
|:||||| :|
Db 89 QGVTLVVDYRYPAGVFTGAKENFSLDWCKQPDV 122

RESULT 8
US-11-124-368A-318
Sequence 318, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 318
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-124-368A-318

Query Match 21.7%; Score 45; DB 7; Length 254;
Best Local Similarity 35.3%; Pred. No. 15;
Matches 12; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 5 QRETLKAHYALNCCGLAGGVEQFISDICKDV 38
|:||||| :|
Db 89 QGVTLVVDYRYPAGVFTGAKENFSLDWCKQPDV 122

RESULT 9
US-09-978-360A-763
Sequence 763, Application US/09978360A
Publication No. US20060009633A9
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 763
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: -20.-1
US-09-978-360A-763

Query Match 21.7%; Score 45; DB 5; Length 303;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 1; Indels 8; Gaps 1;
QY 15 ALNCCGLAGGVEQFISDICKP 34
|:||||| :|
Db 245 AVNNCCLAGG-----CP 256

```

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1654
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1654

Query Match      21.0%; Score 43.5; DB 6; Length 1071;
Best Local Similarity 35.7%; Pred. No. 1.2e+02;
Matches 15; Conservative 8; Mismatches 10; Indels 9; Gaps 3;

QY 1 KDEPQRETLKAIHYALNCCGLAG-----GVEQFISDICKP 35
Db 800 QDEIRRQT-KAMAYALGVVGLMNVQFAVDGV-VFVLEVNPR 839

RESULT 13
US-10-467-657-606
; Sequence 606, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 606
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-606

Query Match      20.8%; Score 43; DB 6; Length 122;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 20 GLAGGVEQFISDICKPKD 37
Db 25 GFDGGVEQFNDNRHKRD 42

RESULT 14
US-10-821-234-1469
; Sequence 1469, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
```

```

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3444
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3444

Query Match      21.7%; Score 45; DB 6; Length 508;
Best Local Similarity 31.0%; Pred. No. 32;
Matches 9; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 7 ETLKAIHYALNCCGLAGGVEQFISDICKP 35
Db 173 DPIRAVFVPIGGGLAAGVAAFIKQVRPE 201

RESULT 11
US-10-467-657-5988
; Sequence 5988, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5988
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5988

Query Match      21.0%; Score 43.5; DB 6; Length 391;
Best Local Similarity 39.5%; Pred. No. 40;
Matches 15; Conservative 3; Mismatches 9; Indels 11; Gaps 3;

QY 1 KDEPQRETLKAIHYALNCC---CGLAGGVE---QFISDI 32
Db 309 KADPRRCT-----QGLNCLTSCGLRDLGSKAGQFCIDI 341

RESULT 12
US-10-467-657-1654
; Sequence 1654, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
```

Search completed: January 20, 2006, 17:27:02
Job time : 6.5679 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:06:32 ; Search time 26.7407 Seconds
(without alignments)
136.729 Million cell updates/sec

Title: US-10-619-323-4

Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGVQVFISDICPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	228	1 A40402	CD9 antigen [valid
2	202	97.6	228	1 A42929	CD9 antigen - gree
3	191	92.3	226	1 S39262	CD9 antigen - rat
4	167	80.7	226	2 I49589	antigen - mouse
5	151	72.9	226	1 JX0221	CD9 antigen - bovi
6	56.5	27.3	172	2 T26914	hypothetical prote
7	56.5	27.3	203	2 T22537	hypothetical prote
8	56	27.1	363	2 S62537	probable RNA 3'-te
9	55	26.6	302	2 S78509	heterodisulfide re
10	54	26.1	302	2 D69118	hypothetical prote
11	54	26.1	342	2 A98021	hypothetical prote
12	53.5	25.8	343	1 CES0VM	vancomycin resist
13	53.5	25.8	764	2 JCS643	thyroid stimulat
14	52.5	25.4	548	2 B84932	60 kd chaperonin [
15	52.5	25.4	548	2 B42281	symblonin syml - p
16	52.5	25.4	1651	2 F88750	protein vit-6 [imp
17	52	25.1	894	2 B96557	probable receptor
18	52	25.1	933	2 A31930	cytotactin - chick
19	51.5	24.9	544	2 B82048	chaperonin, 60 Kd
20	51.5	24.9	548	1 BVRCGL	chaperonin groEL -
21	51.5	24.9	548	2 B86110	hypothetical prote
22	51.5	24.9	548	2 AE1045	GroEL protein [imp
23	51.5	24.9	548	2 D91269	chaperonin GroEL [
24	51	24.6	290	2 D81938	probable RNA polym
25	51	24.6	290	2 G81166	RNA polymerase sig
26	51	24.6	306	2 B70304	dihydroorotase den
27	51	24.6	336	2 D64621	hypothetical prote
28	51	24.6	560	2 T46189	calcium-dependent
29	51	24.6	644	2 S39356	transcription fact

ALIGNMENTS

RESULT 1

A40402

CD9 antigen (validated) - human

N:Alternate names: motility-related protein-1

C:Species: Homo sapiens (man)

C>Date: 06-Dec-1991 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C/Accession: A46123; A40402; JH0555; A39029; S10564

R:Rubinstein, E.; Benoit, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouche

Genomics 16, 132-138, 1993

A>Title: Organization of the human CD9 gene.

A/Reference number: A46123; MUID:93252369; PMID:8486348

A/Accession: A46123

A/Molecule type: DNA

A/Residues: 1-228 <LAN>

A/Cross-references: UNIPROT:P21926; UNIPARC:UPI00003B45A; GB:S60489; NID:G300112; PIDN

A/Experimental source: leukocyte

A/Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328

R:Miya, M.; Koyama, M.; Seno, M.; Ikeyama, S.

J. Exp. Med. 174, 1347-1354, 1991

A>Title: Identification of the motility-related protein (MRP-1), recognized by monoclon

A/Reference number: JH0555; MUID:92078943; PMID:1720807

A/Accession: JH0555

A/Molecule type: mRNA

A/Residues: 1-228 <LAN>

A/Cross-references: UNIPARC:UPI00003B45A; GB:L34068; GB:M61880; NID:G508495; PIDN:AAA5

A/Note: parts of this sequence, including the amino end of the mature protein, were con

R:Miya, M.; Koyama, M.; Seno, M.; Ikeyama, S.

J. Exp. Med. 174, 1347-1354, 1991

A>Title: Identification of the motility-related protein (MRP-1), recognized by monoclon

A/Reference number: JH0555; MUID:92078943; PMID:1720807

A/Accession: JH0555

A/Molecule type: mRNA

A/Residues: 1-228 <MIY>

A/Cross-references: UNIPARC:UPI00003B45A; GB:X60111; NID:G34768; PIDN:CAA42708.1; PID:

A/Experimental source: breast carcinoma

A/Note: this protein has the epitope defined by cell motility-inhibiting monoclonal ant

R:Bouchaix, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; U

J. Biol. Chem. 266, 117-122, 1991

A>Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.

A/Reference number: A39029; MUID:91093112; PMID:1840589

A/Accession: A39029

A/Molecule type: mRNA

A/Residues: 1-8,'S',10-66,'A',68-193,195-228 <BOU>

A/Cross-references: UNIPARC:UPI000017414B; GB:M38690

A/Note: parts of this sequence, including the amino end of the mature protein, were con

R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.

FEBS Lett. 264, 270-274, 1990

A>Title: Purification and partial characterization of CD9 antigen of human platelets.

A/Reference number: S10564; MUID:90292223; PMID:2358073

A/Accession: S10564

A/Molecule type: protein

probable phytoene
DNA-binding protei
major single-stran
sodium channel alp
sodium channel alp
sodium channel alp
sodium channel alp
D-alanine-D-alanin
thyrotropin recept
vitellogenin vit-6
probable RNA methy
probable enzyme yg
yGCA protein - Esc
heat shock protein
probable DNA relax
traf protein - Esc

A:Residues: 2-8 'X', 10-21 <HIG>
A:Cross-references: UNIPARC:UPI000017414C
C:Genetics:
A:Gene: CD9; MIC3
A:Cross-references: GDB:120582; OMIM:143030
A:Map position: 12p13-12p13
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status experimental <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 207; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDICPKKDV 38
Db 135 KDEPQRETLKAHYALNCCGLAGGVEQFISDICPKKDV 172

RESULT 2
A42929
CD9 antigen - green monkey
N/Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
A:Accession: A42929
R:Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsunooka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
expresses on toxin-sensitive cells.
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A:Status: nucleic acid sequence not shown
A:Residues: 1-228 <MIT>
A:Molecule type: mRNA
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:9218565; PIDN:
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52,53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.6%; Score 202; DB 1; Length 228;
Best Local Similarity 97.4%; Pred. No. 5.9e-20;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDICPKKDV 38
Db 135 KDEPQRETLKAHYALDCCGLAGGVEQFISDICPKKDV 172

RESULT 3
S39262
CD9 antigen - rat
N/Alternate names: platelet cell surface glycoprotein

C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
A:Accession: I56562; S39262
R:Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A:Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expressed
on the surface of platelets.
A:Reference number: I56562; MUID:95123481; PMID:7823164
A:Accession: I56562
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:g434314; PIDN:
C:Genetics:
A:Gene: CD9
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; transmembrane protein
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
F:54-80/Domain: transmembrane #status predicted <TM2>
F:81-84/Domain: intracellular #status predicted <CY2>
F:85-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
F:193-219/Domain: transmembrane #status predicted <TM4>
F:220-226/Domain: intracellular #status predicted <CY3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.3%; Score 191; DB 1; Length 226;
Best Local Similarity 92.1%; Pred. No. 1.8e-18;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDICPKKDV 38
Db 133 KDEPQRETLKAHYALNCCGIAGGVEQFISDICPKKQV 170

RESULT 4
I49589
antigen - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A:Accession: I49589
R:Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A:Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A:Reference number: I49589; MUID:94054345; PMID:8236164
A:Accession: I49589
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-226 <RES>
A:Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:g388911; PIDN:
C:Superfamily: CD9 antigen

Query Match 80.7%; Score 167; DB 2; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.4e-15;
Matches 30; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAHYALNCCGLAGGVEQFISDICPKKDV 38
Db 133 KDEPQRETLKAHYALDCCGIAGPLEQFISDTCPKKQL 170

RESULT 5
JX0221
CD9 antigen - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: JX0221
R:Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A:Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cells.
A:Reference number: JX0221; MUID:93054422; PMID:1339429
A:Accession: JX0221

A:Molecule type: mRNA
A:Residues: 1-226 <MAR>
A:Cross-references: UNIPROT:P09332; UNIPARC:UPI0000167C21; GB:M81720; NID:g162820; PIDN:
A:Experimental source: ocular ciliary epithelial cell
C:Superfamily: CD9 antigen
F:2-226/Product: CD9 antigen #status predicted <MAT>
P:2-11/Domain: intracellular #status predicted <CY1>
P:12-35/Domain: transmembrane #status predicted <TM1>
F:36-53/Domain: extracellular #status predicted <EX1>
P:54-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CY2>
P:81-109/Domain: transmembrane #status predicted <TM3>
F:110-192/Domain: extracellular #status predicted <EX2>
P:193-219/Domain: transmembrane #status predicted <TM4>
F:220-226/Domain: intracellular #status predicted <CY3>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.9%; Score 151; DB 1; Length 226;
Best Local Similarity 71.1%; Pred. No. 5.2e-13;
Matches 27; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KDEPQRRLKAHYALNCCLAGGVGEQFISSCPKDV 38
Ddb 133 KDEPQRRLKAHYALDCGLTGYPEQLFTTCPPKNL 170
|||||
|||:::

RESULT 6
T26914
hypothetical protein Y45F10B.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26914
R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20286
A:Accession: T26914
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-172 <WIL>
A:Cross-references: UNIPROT:O62466; UNIPARC:UPI000017BC79; EMBL:AL021487; PIDN:CAA16352
A:Experimental source: clone Y45F10B
C:Genetics:
A:Gene: CESP:Y45F10B.1
A:Map position: 4
A:Introns: 52/3; 85/3

Query Match 27.3%; Score 56.5; DB 2; Length 172;
Best Local Similarity 45.8%; Pred. No. 3;
Matches 11; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 6 RETLKAIHYALNCCLAGGVGEQFI 29
Ddb 76 KNTLDVHTSLKCCG-ANGCEDFL 98
:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~::~:

RESULT 7
T22537
hypothetical protein F53B2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22537
R:Smye, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19577
A:Accession: T22537
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-203 <WIL>
A:Cross-references: UNIPROT:Q20707; UNIPARC:UPI000017B9FE; EMBL:Z73908; PIDN:CAA98130.1;
A:Experimental source: clone F53B2
C:Genetics:
A:Gene: CESP:F53B2.2

A;Experimental source: strain Marburg
C;Genetics:
A;Gene: hdrB
C;Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidoreductase (EC 1.8.1.7) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes contains a heterodisulfide reductase.
C;Function:
A;Description: heterodisulfide reductase
C;Superfamily: Acidianus ambivalens succinate dehydrogenase chain C
C;Keywords: membrane-associated complex; oxido-reductase

Query Match 26.6%; Score 55; DB 2; Length 302;
Best Local Similarity 30.2%; Pred. No. 8.2;
Matches 13; Conservative 6; Mismatches 12; Indels 12; Gaps 2;

Oy 2 DEPORETL-----KAHY--ALNCCGLAGGVEQFISDI 32
| | | : : : : :
Db 165 DNPFRPILDEIVETGAKEVDYKDKMCCGGGVRSRLDLDV 207
| | | : : : : :
| | | : : : : :

RESULT 10
D69118
heterodisulfide reductase [EC 1.97.1.1-] chain B - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69118
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.; Kir, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional annotation
A;Reference number: A69000; PMID:98037514; PMID:9371463
A;Accession: D69118
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-302 <MTH>
A;Cross-references: UNIPROT:O27907; UNIPARC:UPI00000665F1; GB:AE000940; GB:AE000666; NITD:NC_008697
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1879
C;Superfamily: Acidianus ambivalens succinate dehydrogenase chain C
C;Keywords: membrane-associated complex; oxido-reductase

Query Match 26.1%; Score 54; DB 2; Length 302;
Best Local Similarity 30.2%; Pred. No. 11;
Matches 13; Conservative 6; Mismatches 12; Indels 12; Gaps 2;

Oy 2 DEPORETL-----KAHY--ALNCCGLAGGVEQFISDI 32
| | | : : : : :
Db 165 DNPFRPTLDELVEVTGAKEVDYKDKMCCGGGVRSRLDLDV 207
| | | : : : : :
| | | : : : : :

RESULT 11
A98021
hypothetical protein appA [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: A98021
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eberhart, K.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, J.P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; et al.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; PMID:21429245; PMID:11544234
A;Accession: A98021
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-542 <Kur>
A;Cross-references: UNIPROT:Q8DPF2; UNIPARC:UPI00000E35F9; GB:AE007317; PIDN:AAR99997.1; NCBI:U00096.3
A;Genetic:
A;Gene: appA

Query Match 26.1%; Score 54; DB 2; Length 542;

Query Match 25.8%; Score 53.5; DB 2; Length 764;
Best Local Similarity 41.7%; Pred. No. 32;
Matches 15; Conservative 3; Mismatches 11; Indels 7; Gaps 3;
QY 4 PORETLKAI--HYALNCCGLAGGVEQFISDICPKKD 37
DB 373 PORETLQAFDNHYDYTVCC--GGSEEMV--CTPKSD 403

RESULT 14
B84932
60 kD chaperonin [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: B84932
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: B84932
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-548 <STO>
A;Cross-references: UNIPARC:UPI000005E41D; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: mopA; BU019
C;Superfamily: chaperonin groEL

Query Match 25.4%; Score 52.5; DB 2; Length 548;
Best Local Similarity 34.3%; Pred. No. 32;
Matches 12; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 3 EPORETLKAIHYALNCCGLAGGVEQFISDICPKKD 37
DB 495 DPTKVTRSALQYAASVAGLMTTECMVTDL-PKED 528

RESULT 15
B42281
symbionin symL - pea aphid
C;Species: Acyrthosiphon pisum (pea aphid)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 26-Aug-1999
C;Accession: B42281; S70753; S24481
R;Ohtaka, C.; Nakamura, H.; Ishikawa, H.
J. Bacteriol. 174, 1869-1874, 1992
A;Title: Structures of chaperonins from an intracellular symbiont and their functional e
A;Reference number: A42281; MUID:92193273; PMID:1347769
A;Accession: B42281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-548 <OHT>
A;Cross-references: UNIPARC:UPI000005E41D; EMBL:X61150; NID:g5658; PIDN:CAA43460.1; PID:
A;Note: Sequence extracted from NCBI backbone (NCBIN:88668, NCBIP:88674)
R;Ohtaka, C.; Ishikawa, H.
J. Mol. Evol. 36, 121-126, 1993
A;Title: Accumulation of adenine and thymine in a groE-homologous operon of an intracell
A;Reference number: S70752; MUID:93164272; PMID:8433382
A;Accession: S70753
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-548 <OH2>
A;Cross-references: UNIPARC:UPI000005E41D; EMBL:X61150; NID:g5658; PIDN:CAA43460.1; PID:
C;Genetics:
A;Gene: symL
C;Superfamily: chaperonin groEL
C;Keywords: molecular chaperone

Query Match 25.4%; Score 52.5; DB 2; Length 548;
Best Local Similarity 34.3%; Pred. No. 32;
Matches 12; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 3 EPORETLKAIHYALNCCGLAGGVEQFISDICPKKD 37

Db 495 DPTKVTRSALQYAASVAGLMTTECMVTDL-PKED 528
Search completed: January 20, 2006, 17:22:36
Job time : 27.7407 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:05:21 ; Search time 144.494 Seconds
(without alignments)
185.545 Million cell updates/sec

Title: US-10-619-323-4
Perfect score: 207

Sequence: 1 KDEPQRETLKAIHYALNCCGLAGGVQFISDICPKKDV 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	227	1	P21926 homo sapien
2	207	100.0	227	1	Q5J7W6 homo sapien
3	202	97.6	227	1	P30409 cercopithec
4	194	93.7	225	1	P40239 felis silve
5	191	92.3	225	1	P40241 rattus norv
6	179	86.5	226	2	Q8MJ48 sus scrofa
7	168	81.2	225	1	Q8WNG3 sus scrofa
8	167	80.7	225	1	P40240 mus musculu
9	151	72.9	225	1	P30932 bos taurus
10	127	61.4	228	2	Q6GQES XENLA
11	120	58.0	224	2	Q91BC9 CHICK
12	100	48.3	228	2	Q6DKM9 XENLA
13	95	45.9	227	2	Q7ZUH9 BRARE
14	94	45.4	227	2	Q6NWG7 BRARE
15	92	44.4	227	2	Q61OH7 BRARE
16	89	43.0	182	2	Q56CY1 HUMAN
17	88	42.5	246	2	Q6P0W1 BRARE
18	80	38.6	227	2	Q4REW0 TETNG
19	77	37.2	236	2	Q7ZTR5 XENLA
20	74	35.7	230	2	Q8AYJ0 SALSA
21	72.5	35.0	237	2	Q6P351 XENTR
22	72	34.8	230	2	Q8AXJ1 ONCMY
23	71.5	34.5	237	2	Q6DCU4 XENLA
24	66	31.9	546	2	Q4YD19 PLABE
25	66	31.9	813	2	Q6IMB9 9APIC
26	64	30.9	236	2	Q9DD57 BRACHYDANIO
27	64	30.9	236	2	Q6PFI1 BRACHYDANIO
28	59	28.5	126	2	Q6DT38 9NOCA
29	58	28.0	767	2	Q8AAF9 BACTN
30	57.5	27.8	2424	2	Q4UB39 THEAN
31	57	27.5	199	2	Q4JWS2 CORJK

32	57	27.5	818	2	Q4XS13 PLACH
33	56.5	27.3	228	2	Q8AV92 PETMA
34	56.5	27.3	230	2	Q20707 CAEEL
35	56.5	27.3	235	2	Q4S1G3 TETNG
36	56.5	27.3	241	2	Q62466 CAEEL
37	56.5	27.3	1090	2	Q6CTA6 KJULA
38	56	27.1	108	2	Q4UU38 XANCP
39	56	27.1	108	2	Q8P9P4 XANCP
40	56	27.1	249	2	Q5TTA9 ANOGA
41	56	27.1	363	1	RCL1 SCHPO
42	55.5	26.8	87	2	Q8XKJ7 CLOPE
43	55	26.6	256	2	Q7ZUI6 BRARE
44	55	26.6	256	2	Q4SA96 TETNG
45	55	26.6	302	1	HDRB METTM

Q4xsi3	plasmodium
Q8av92	petromyzon
Q20707	caenorhabdi
Q4s1g3	tetraodon n
O62466	caenorhabdi
Q6cta6	kluyveromyc
Q4uu38	xanthomonas
Q8p9p4	xanthomonas
Q5tta9	anopheles g
Q9870	schizosacch
Q8xkj7	clostridium
Q7zui6	brachydanio
Q4sa96	tetraodon n
Q50755	methanobact

ALIGNMENTS

RESULT 1

ID	CD9_HUMAN	STANDARD;	PRT;	227 AA.
AC	P21926; Q96ES4;			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)			
DE	(MRP-1) (Tetraspanin-29) (TSPAN-29).			
GN	Name=CD9; Synonyms=MIC3, TSPAN29;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.			
RX	MEDLINE=91093112; PubMed=1840589;			
RA	Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E.,			
RA	Gagnon J., Uzan G.;			
RT	"Molecular cloning of the CD9 antigen. A new family of cell surface			
RT	proteins.";			
RL	J. Biol. Chem. 266:117-122(1991).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.			
RX	MEDLINE=9124846; PubMed=2037603;			
RA	Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A.,			
RA	Coughlin S.R., Phillips D.R., Jennings L.K.;			
RT	"cDNA cloning and expression of platelet p24/CD9. Evidence for a new			
RT	family of multiple membrane-spanning proteins.";			
RL	J. Biol. Chem. 266:10638-10645(1991).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;			
RA	Miyake M., Koyama M., Seno M., Ikegama S.;			
RT	"Identification of the motility-related protein (MRP-1), recognized by			
RT	monoclonal antibody M31-15, which inhibits cell motility.";			
RL	J. Exp. Med. 174:1347-1354(1991).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RC	TISSUE=Leukocyte;			
RX	MEDLINE=93252369; PubMed=8486348;			
RA	Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,			
RA	Uzan G., Boucheix C.;			
RT	"Organization of the human CD9 gene.";			
RL	Genomics 16:132-138(1993).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,			
RA	Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-			
RT	FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalil D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [7]
RP PROTEIN SEQUENCE OF 1-20.
RC TISSUE=Platelet;
RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;
RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;
RT "Purification and partial characterization of CD9 antigen of human
RT platelets.";
RL FEBS Lett. 264:270-274 (1990).
RN [8]
RP ROLE IN CELL MOTILITY AND METASTASIS.
RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;
RA Ikeyama S., Koyama M., Yamako M., Saeada R., Miyake M.;
RT "Suppression of cell motility and metastasis by transfection with
RT human motility-related protein (MRP-1/CD9) DNA.";
RL J. Exp. Med. 177:1231-1237 (1993).
RN [9]
RP ROLE IN CELL ADHESION.
RX PubMed=7511626;
RA Masellis-Smith A., Shaw A.R.;
RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B
RT cell adhesion to bone marrow fibroblasts through de novo recognition
RT of fibronectin.";
RL J. Immunol. 152:2768-2777 (1994).
RN [10]
RP ROLE IN GAMETE FUSION.
RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;
RA Higginbottom A., Takahashi Y., Bolling L., Conrod S.A., White J.M.,
RA Partridge L.J., Monk P.N.;
RT "Structural requirements for the inhibitory action of the CD9 large
RT extracellular domain in sperm/oocyte binding and fusion.";
RL Biochem. Biophys. Res. Commun. 311:208-214 (2003).
RN [11]
RP SUBUNIT.
RX PubMed=14556650; DOI=10.1042/BJ20031037;
RA Kovalenko O.V., Yang X., Kolesnikova T.V., Hemler M.E.;
RT "Evidence for specific tetraspanin homodimers: inhibition of
RT palmitoylation makes cysteine residues available for cross-linking.";
RL Biochem. J. 377:407-417 (2004).
RN [12]
RP PHOSPHORYLATION.
RX MEDLINE=93327758; PubMed=7687539;
RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,
RA Aruffo A., Ledbetter J.A.;
RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";
RL EMBO J. 12:2691-2696 (1993).
RN [13]
RP PALMITOYLATION, AND MUTAGENESIS OF CVS-8; CVS-77; CVS-78; CVS-86;
RP CVS-217 AND CVS-218.
RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;
RA Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,
RA Rubinstein E.;
RT "Differential stability of tetraspanin/tetraspanin interactions: role
RT of palmitoylation.";
RL FEBS Lett. 516:139-144 (2002).
RN [14]
RP INTERACTION WITH PTGFRN.
RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;
RA Charrin S., Le Naour F., Oualid M., Billard M., Faure G., Hanash S.M.,
RA Boucheix C., Rubinstein E.;
RT "The major CD9 and CD81 molecular partner. Identification and
RT characterization of the complexes.";
RL J. Biol. Chem. 276:14329-14337 (2001).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis.
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with
CC PTGFRN/CD9P1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and
CC epithelial cells.
CC -!- PTM: Protein exists in three forms with molecular masses between
CC 22 and 27 kDa, and is known to carry covalently linked fatty
CC acids.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; S60489; AAC60586.1; -; Genomic DNA.
CC EMBL; S60462; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60463; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60464; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60700; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60699; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60465; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S60472; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; S38690; AAC60586.1; JOINED; Genomic DNA.
CC EMBL; L34068; AAC59982.1; -; mRNA.
CC EMBL; X60111; CAA42708.1; -; mRNA.
CC EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL; L08119; AAA51954.1; ALT_SEQ; Genomic DNA.
CC EMBL; L08120; AAA51955.1; ALT_SEQ; Genomic DNA.
CC EMBL; L08121; AAA51956.1; -; Genomic DNA.
CC EMBL; L08122; AAA51957.1; -; Genomic DNA.
CC EMBL; L08123; AAA51958.1; -; Genomic DNA.
CC EMBL; L08124; AAA51959.1; -; Genomic DNA.
CC EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL; AY422198; AA087878.1; -; Genomic DNA.
CC EMBL; BC011988; AAH1988.1; -; mRNA.
CC PIR; A46123; A40402.
CC EMBL; ENSG00000010278; Homo sapiens.
CC HGNC; HGNC:1709; CD9.
CC H-InvDB; HIX0010357; -.
CC Reactome; P21926; -.
CC MIM; 143030; -.
CC GO; GO:0005887; C:integral to plasma membrane; NAS.
CC GO; GO:0005886; C:plasma membrane; NAS.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0007155; P:cell adhesion; IDA.
CC GO; GO:0006928; P:cell motility; IDA.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; NAS.
CC InterPro; IPR00301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; I.
CC PRINTS; PR00259; TMFOUR.

[illegible]

```

RN NUCLEOTIDE SEQUENCE [MRNA].
RP PubMed:7753050; DOI=10.1016/0161-5890(95)00008-3;
RA Willett B.J., Neil J.C.;
RT "cDNA cloning and eukaryotic expression of feline CD9.";
RL Mol. Immunol. 32:417-423(1995).
[2]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Morikawa S.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L35275; AAA92867.1; -; mRNA.
CC EMBL; D30786; BAA06452.1; -; mRNA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; F:protein binding; ISS.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC Pfam; PF00335; Tetraspanin; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4 1; 1.
CC Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
CC Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 93.7%; Score 194; DB 1; Length 225;
Best Local Similarity 89.5%; Pred. No. 8.6e-20;
Matches 34; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDEPQRETLKATHYALNCCGLAGGVEQFISDTCPKQDV 38
DB 132 KDEPQRETLKATHYALNCCGLAGGVEQFISDTCPKQDI 169

```

```

CD9 RAT
ID - CD9 RAT STANDARD; PRT; 225 AA.
AC P40241;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE [MRNA].
RP STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
RX MEDLINE=95123481; PubMed=7823164;
RA Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;
RT "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen
RL and is expressed in the nervous system.";
RL J. Neurosci. 15:562-573(1995).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9p1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X76489; CAA54027.1; -; mRNA.
CC PIR; I56562; S39262.
CC Ensembl; ENSRNOG0000019556; Rattus norvegicus.
CC RGD; 2318; Cd9.
CC GO; GO:0009986; C:cell surface; IDA.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC InterPro; IPR000301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; 1.
CC PRINTS; PR00259; TMFOUR.
CC PROSITE; PS00421; TM4 1; 1.
CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
CC Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).

```

```
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 25084 MW; 7889619F99A59C9D CRC64;

Query Match 92.3%; Score 191; DB 1; Length 225;
Best Local Similarity 92.1%; Pred. No. 2.4e-19;
Matches 35; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38
Db 132 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 169

RESULT 6
Q8MJ48_PIG PRELIMINARY; PRT; 226 AA.
ID Q8MJ48_PIG
AC Q8MJ48;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane protein CD9.
GN Name:CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCB1_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,
RA Kurilla-Mahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,
RA Down J.D., Sachs D.H., Goodell M.A.;
RT "Use of CD9 Expression to Enrich for Porcine Hematopoietic
RT Progenitors";
RL Exp. Hematol. 0:0-0(2002).
DR EMBL; AF525029; AAM81376.1; -; mRNA.
DR HSP; P60033; IGHQ.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR000301; Trasmem 4.
DR Pfam; PF00335; Tetraspanin; I.
DR PRINTS; PR00259; Tmpour.
DR PROSITE; PS00421; TM4_1; 1.
KW Transmembrane.
SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;

Query Match 86.5%; Score 179; DB 2; Length 226;
Best Local Similarity 81.6%; Pred. No. 1.4e-17;
Matches 31; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38
Db 133 KDEPQRETLKAIHYALDCCGLMGVEQLLADICPKQDV 170

RESULT 7
CD9_PIG STANDARD; PRT; 225 AA.
ID CD9_PIG
AC Q8WQ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name:CD9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCB1_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [RNA].
RC TISSUE=Smooth muscle;
RX PubMed=14610355; DOI=10.1159/000074170;
```

```
RA Yubero N., Jimenez-Marin A., Yerle M., Morera L., Barbancho M.J.,
RA Llanes D., Garrido J.J.;
RT "Molecular cloning, expression pattern and chromosomal mapping of pig
RT CD9 antigen.";
RL Cytogenet. Genome Res. 101:143-146(2003).
CC -1- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY072785; AAL68966.1; -; mRNA.
CC GO; GO:0005887; C: integral to plasma membrane; ISS.
CC GO; GO:0005515; P: protein binding; ISS.
CC GO; GO:0007155; P: cell adhesion; ISS.
CC GO; GO:0006928; P: cell motility; ISS.
CC GO; GO:0007342; P: fusion of sperm to egg plasma membrane; ISS.
CC GO; GO:0030913; P: paranodal junction formation; ISS.
CC GO; GO:0030168; P: platelet activation; ISS.
CC InterPro; IPR000301; Trasmem 4.
CC Pfam; PF00335; Tetraspanin; I.
CC PRINTS; PR00259; Tmpour.
CC DR PROSITE; PS00421; TM4_1; 1.
CC Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 225 AA; 25070 MW; FF280FE39BC11545 CRC64;

Query Match 81.2%; Score 168; DB 1; Length 225;
Best Local Similarity 76.3%; Pred. No. 5.6e-16;
Matches 29; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDEPQRETLKAIHYALNCCGLAGGVEQFISDICKPKDV 38
Db 132 KDEPQRETLKAIHYALDCCGLMGVEQLLADICPKQDV 169

RESULT 8
CD9_MOUSE STANDARD; PRT; 225 AA.
ID CD9_MOUSE
AC P40240;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
```

DT 13-SEP-2005 (rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=cd9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=BALB/C; TISSUE=Kidney.
RX MEDLINE=94054345; PubMed=8236164; DOI=10.1016/0049-3848(93)90162-H;
RA Rubinstein E., Billard M., Plaisance S., Prenant M., Boucheix C.;
RT "Molecular cloning of the mouse equivalent of CD9 antigen.";
RL Thromb. Res. 71:377-383(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Kidney.
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kogawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Brain.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP ROLE IN GAMETE FUSION.
RX PubMed=10700183; DOI=10.1038/73502;
RA Kaji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,
RA Tada N., Miyazaki S., Kudo A.;
RT "The gamete fusion process is defective in eggs of Cd9-deficient
mice.";
RL Nat. Genet. 24:279-282(2000).
RN [5]
RP ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.
RX PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;
RA Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,
RA Baba H.;
RT "Tetraspanin protein CD9 is a novel paranodal component regulating
paranodal junctional formation.";
RL J. Neurosci. 24:96-102(2004).
RN [6]
RP FUNCTION AS RECEPTOR FOR PSGL1.
RX PubMed=11805154; DOI=10.1084/jem.20011741;
RA Waterhouse R., Ha C., Dveksler G.S.;
RT "Murine CD9 is the receptor for pregnancy-specific glycoprotein 17.";
RL J. Exp. Med. 195:277-282(2002).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis. Acts as a receptor for PSGL1.
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTFGRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral
CC nervous system.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; L08115; AAA37405.1; -; mRNA.
CC EMBL; AK022251; BAB21965.1; -; mRNA.
CC EMBL; AK012793; BAB28473.1; -; mRNA.
CC EMBL; BC070474; AAH70474.1; -; mRNA.
CC PIR; I49589; I49589.
CC Ensembl; ENSMUSG0000030342; Mus musculus.
CC MGI; MGI:88348; Cd9.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0007155; P:cell adhesion; ISS.
CC GO; GO:0006928; P:cell motility; ISS.
CC GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
CC GO; GO:0030913; P:paranodal junction formation; ISS.
CC GO; GO:0030169; P:platelet activation; ISS.
CC InterPro; IPR000301; Transmem 4.
CC Pfam; PF00335; Tetraspanin; I.
CC PRINTS; PR00259; TMSOUR.
CC PROSITE; PS00421; TM4_1; 1.
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).

```
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 2BBE40B8D7C31BC0 CRC64;

Query Match 80.7%; Score 167; DB 1; Length 225;
Best Local Similarity 78.9%; Pred. No. 7.8e-16;
Matches 30; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KDBPQRETLKAIHYALNCCGLAGVEQFISDICKPKDV 38
|||||:|||||:|||||:|||||:|||||:
DB 132 KDBPQRETLKAIHYALNCCGLAGVEQFISDICKPKQL 169
|||||:|||||:|||||:|||||:|||||:

RESULT 9
CD9_BOVIN STANDARD; PRT; 225 AA.
ID CD9_BOVIN STANDARD; PRT; 225 AA.
AC P30932;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ocular ciliary epithelium;
RX MEDLINE=93054422; PubMed=1339429;
RA Martin-Alonso J.M., Hernando N., Ghosh S., Coca-Prados M.;
RT "Molecular cloning of the bovine CD9 antigen from ocular ciliary
epithelial cells";
RL J. Biochem. 112:63-67(1992).
CC -I- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
fusion. Involved in cell adhesion, cell motility and tumor
metastasis (By similarity).
CC -I- SUBUNIT: Forms both disulfide-linked homodimers and higher
homooligomers as well as heterooligomers with other members of the
tetraspanin family. Associates with CR2/CD21 and with PTCFRN/CD9p1
(BY similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- PTM: Phosphorylated on tyrosine following B-cell activation (By
similarity).
CC -I- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; M81720; AAA30439.1; -; mRNA.
DR PIR; JX0221.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005155; F:protein binding; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0006928; P:cell motility; ISS.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM 4.1; 1.
KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
```

```
KW Palmitate; Phosphorylation; Transmembrane.
INIT MET 0 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSMEM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSMEM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSMEM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 25127 MW; ECB67DB91A0858E7 CRC64;

Query Match 72.9%; Score 151; DB 1; Length 225;
Best Local Similarity 71.1%; Pred. No. 1.7e-13;
Matches 27; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 KDBPQRETLKAIHYALNCCGLAGVEQFISDICKPKDV 38
|||||:|||||:|||||:|||||:|||||:
DB 132 KDBPQRETLKAIHYALNCCGLAGVEQFISDICKPKNL 169
|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q6GQE5_XENLA PRELIMINARY; PRT; 228 AA.
ID Q6GQE5_XENLA PRELIMINARY; PRT; 228 AA.
AC Q6GQE5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC80123 protein.
GN Name=MGC80123;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
```

```

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC072800; AAH72800.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4 1; 1.
DR SEQUENCE 228 AA; 25155 MW; 9A826DBC2D9980A2 CRC64;

Query Match 61.4%; Score 127; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 5.8e-10;
Matches 20; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KDEPQRETIKAIHYALNCCGLAGGVEQFISDPCPK 36
Db 134 RDGPKLTKGIHFAMNCCGLATIDATLTDICPNK 169

RESULT 11
Q91BC9 CHICK
ID Q91BC9_CHICK PRELIMINARY; PRT; 224 AA.
AC Q91BC9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD9 antigen.
OS Name=CD9;
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RA Kobayashi T., Mekada E.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AB032767; BAA93011.1; -, mRNA.
DR HSP; P60333; IG8Q.
DR Ensembl; ENSGALG00000017274; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4 1; 1.
DR SEQUENCE 224 AA; 24969 MW; AE64BDF849516151 CRC64;

Query Match 58.0%; Score 120; DB 2; Length 224;
Best Local Similarity 64.5%; Pred. No. 6e-09;
Matches 20; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 RETLKAIHYALNCCGLAGGVEQFISDPCPK 36
Db 136 REILKAFPALNCCGIGTGLEQLMESCPCPK 166

RESULT 12
Q6DKM9 XENLA
ID Q6DKM9_XENLA PRELIMINARY; PRT; 228 AA.
AC Q6DKM9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC82181 protein.
GN Name=MGC82181;
OS Xenopus laevis (African clawed frog).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC071132; AAH71132.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4 1; 1.
DR SEQUENCE 228 AA; 24906 MW; 288ED8AC45D9664 CRC64;

Query Match 48.3%; Score 100; DB 2; Length 228;
Best Local Similarity 50.0%; Pred. No. 5.2e-06;
Matches 17; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 KDEPQRETIKAIHYALNCCGLAGGVEQFISDPCP 34
Db 134 KDSSLKETLKGIFHAFDCGNGVLDALTDCP 167

RESULT 13
Q7ZUH9 BRARE
ID Q7ZUH9_BRARE PRELIMINARY; PRT; 227 AA.
AC Q7ZUH9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD9 antigen, like.
GN Name=cd9l;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

```


GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:03:51 ; Search time 87.963 Seconds
(without alignments)
124.876 Million cell updates/sec

Title: US-10-619-323-5
Perfect score: 132
Sequence: 1 PKDVLFTVTKSCPDALKEVFDNK 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	25	ADJ57562	Human CD9
2	132	100.0	227	AAR86834	Human CD9
3	132	100.0	227	ABB78366	Amino aci
4	132	100.0	227	AAE14636	Human CD9
5	132	100.0	227	ABU05057	Human exp
6	132	100.0	227	ABU05060	Human exp
7	132	100.0	227	ABW00436	Human CD9
8	132	100.0	227	ADK9862	Human CD9
9	132	100.0	227	AD119366	Human CD9
10	132	100.0	227	AEA89005	Human CD9
11	132	100.0	228	AAR27525	Metastasi
12	132	100.0	228	ABB44581	Human wou
13	132	100.0	228	ABU05059	Human exp
14	132	100.0	228	ABU05052	Human exp
15	132	100.0	228	ABU05048	Human exp
16	132	100.0	228	ABU05056	Human exp
17	132	100.0	228	ABU05049	Human exp
18	132	100.0	228	ABU05050	Human exp
19	132	100.0	228	ABU05053	Human exp
20	132	100.0	228	ABW01519	Protein #
21	132	100.0	228	ADG89037	TAT278. 1
22	132	100.0	228	ADG32002	Human hom
23	132	100.0	228	ADJ57558	Human CD9
24	132	100.0	228	ADL26782	Human CD9

25	132	100.0	228	8	ADL2853	Human PRO
26	132	100.0	228	8	ADP23088	PRO polyp
27	132	100.0	228	8	ADR73450	Human CD9
28	132	100.0	228	9	ADV70263	Tumor-ass
29	132	100.0	228	9	ADY97163	Human CD9
30	132	100.0	228	9	ADY19604	PRO polyp
31	132	100.0	228	9	ADY14362	PRO polyp
32	132	100.0	228	9	AE98450	Human can
33	132	100.0	275	3	ABA43936	Human can
34	132	100.0	275	4	AAG75156	Human col
35	132	100.0	275	6	ABU05055	Human exp
36	132	100.0	275	6	ABU05054	Human exp
37	132	100.0	454	4	ABG14067	Novel hum
38	117.5	89.0	79	2	AAW35851	Human CD9
39	117.5	89.0	79	6	ABU05058	Human exp
40	98	74.2	226	7	ADB85281	Rat G9 su
41	95	72.0	18	8	ADJ57563	Human CD9
42	94	71.2	226	4	ABB44580	Mouse wou
43	94	71.2	226	5	ABB57234	Mouse isc
44	94	71.2	226	9	ADV25799	Mouse CD9
45	94	71.2	226	9	AEA55045	Mouse CD9

ALIGNMENTS

RESULT 1

ADJ57562
ID ADJ57562 standard; peptide; 25 AA.

XX
AC ADJ57562;

XX
DT 06-MAY-2004 (first entry)

XX
DE Human CD9 fibronectin-binding domain peptide fragment.

XX
KW Human; CD9; antithrombotic; antiarteriosclerotic; vasototropic;

XX
KW haemostatic; antiangiogenic; cytostatic.

XX
OS Homo sapiens.

XX
PN WO2004007685-A2.

XX
PD 22-JAN-2004.

XX
PF 14-JUL-2003; 2003WO-US022050.

XX
PR 12-JUL-2002; 2002US-0395864P.

XX
PA (UYTE-) UNIV TENNESSEE RES FOUND.

XX
PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;

XX
PI Crossano JT, Lu Y;

XX
DR WPI; 2004-122924/12.

XX
PT Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.

XX
PS Claim 7; SEQ ID NO 5; 126pp; English.

XX
CC The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of CD9-expressing cells; modifying pericellular fibronectin matrix assembly; modifying invasiveness of a cell through a collagen and/or laminin matrix; and modifying cell-to-cell interaction. The methods are based on the finding that increased CD9 expression is implicated in (i) decreased adhesiveness of cells to extracellular matrix (via alpha5-beta1

CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX Sequence 25 AA;

Query Match 100.0%; Score 132; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAIKEVFDNK 25
 DB 1 PKQVLETFVTKSCPDAIKEVFDNK 25

RESULT 2
 AAR86834
 ID AAR86834 standard; protein; 227 AA.

XX AAR86834;

DT 12-JUL-1996 (first entry)

XX Human CD9 sequence.

KW CD9 antigen; stimulated T cell; antibody; ligand; proliferation;
 KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;
 KW immune response; cancer; infectious disease; growth factor.

XX Homo sapiens.

EH Key Location/Qualifiers

FT Modified-site 51 /note= "Potential N-linked glycosylation site"

FT Modified-site 52 /note= "Potential N-linked glycosylation site"

FT Domain 111..194 /note= "Extracellular domain"

FT Domain 135..220 /note= "Transmembrane domain"

FT Domain 221..227 /note= "Cytoplasmic domain"

PN WO9533823-A1.

XX 14-DEC-1995.

XX 01-DEC-1994; 94WO-US013782.

XX 03-JUN-1994; 94US-00253751.

XX 03-JUN-1994; 94US-00253964.

XX (USNA) US SEC OF NAVY.

XX (UNMI) UNIV MICHIGAN.

XX (REPK) REPLIGEN CORP.

XX (DAND) DANA FARBEN CANCER INST INC.

XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;

XX WPI; 1996-040230/04.

XX Selectively inducing CD8 positive T cell proliferation - by activating

XX the T cells and stimulating CD9 cell surface ligand, useful for

XX immuno:therapy of, e.g. cancer.

XX Example 10; Page 38-39; 79pp; English.

CC This sequence represents CD9 from the surface of stimulated T cells. The
 CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an
 CC antibody or other ligand to stimulate the T cell population to
 CC proliferate and expand leading to a 100- to 10000-fold increase in cell
 CC number compared to the original population. The antigenic sequence fits
 CC the generic sequence given in AAR86827. This epitope is recognised by the
 CC monoclonal antibody (WAb) ES5.2D8. CD9 is a 27 kD accessory protein found
 CC on activated T cells. The epitope was recognised by screening a phage
 CC display library. Selective proliferation of an antigen-specific T cell
 CC population is useful in cases where the immune response is to be up
 CC regulated, e.g. in the treatment of cancer or infectious diseases. By
 CC causing proliferation of the T cell population by stimulating T cell
 CC epitope removes the need for exogenous growth factors or accessory cells
 XX Sequence 227 AA;

Query Match 100.0%; Score 132; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAIKEVFDNK 25
 DB 167 PKQVLETFVTKSCPDAIKEVFDNK 191

RESULT 3
 ABB78366

ID ABB78366 standard; protein; 227 AA.

XX ABB78366;

XX 16-DEC-2002 (first entry)

XX Amino acid sequence of CD9.

XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;
 KW immunotherapy; CD9.

XX Homo sapiens.

OS US2002115214-A1.

XX 22-AUG-2002.

XX 26-JAN-1996; 96US-00592711.

XX 23-NOV-1988; 88US-00275433.

XX 07-APR-1992; 92US-00864805.

XX 07-APR-1992; 92US-00864807.

XX 07-APR-1992; 92US-00864866.

XX 04-JUN-1993; 93US-00073223.

XX 03-JUN-1994; 94US-00253964.

XX 10-MAR-1995; 95US-00403253.

XX 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABEL/) NABEL G J.

XX (GRAY/) GRAY G S.

XX (RENN/) RENNERT P D.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-712476/77.

XX Inducing a population of T cells to proliferate, by activating population
 of T cells and stimulating an accessory molecule on the surface of the T
 cells with a ligand which binds the accessory molecule.

XX Example 10; Page 25; 88pp; English.

XX The specification describes method for inducing a population of T cells
 to proliferate. The method involves activating population of T cells,

stimulating an accessory molecule on T cell surface with a ligand protein) which binds the molecule, to induce proliferation of T cells, monitoring proliferation of T cells in response to continuing exposure to the ligand, and reactivating and restimulating T cells when rate of proliferation has decreased to induce further proliferation of the cells. The method is useful for inducing proliferation of T cells, for use in treatment of infectious disease, cancer and immunotherapy. The method allows for the expansion of a population of T cells in numbers sufficient to reconstitute an individual's total CD4+ or CD8+ T cell population. The resulting T cell population can be genetically transduced and used for immunotherapy or can be used in methods of in vitro analyses of infectious agents. A population of tumour-infiltrating lymphocytes can be obtained from an individual afflicted with cancer and the T cells stimulated to proliferate to sufficient numbers. The resulting T cell population can be genetically transduced to express tumour necrosis factor (TNF) or other factor and restored to the individual. CD4+ T cells expanded by this method are useful in the treatment of HIV infection in an individual. The present sequence represents CD9, an antigen present on the surface of activated T cells

Query Match 100.0%; Score 132; DB 5; Length 227;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTVTKSCPDAIKEVFDNK 25
 |||||
 Db 167 PKKDVLFTVTKSCPDAIKEVFDNK 191

RESULT 4
 AAEL14636
 ID AAEL14636 standard; protein; 227 AA.

XX AAEL14636;

DT 16-JUL-2002 (first entry)

DE Human CD9 antigen.

KW T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
 KW immunotherapy; human immunodeficiency virus; HIV infection; cytokine;
 KW human; CD9 antigen.

OS Homo sapiens.

PN US6352694-B1.

PD 05-MAR-2002.

PF 10-MAR-1995; 95US-00403253.

XX 03-JUN-1994; 94US-00253964.

XX (GEM) GENETICS INST INC.

PA (UNMI) UNIV MICHIGAN.

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,
 PT comprises activating T cells by contacting T cells in vitro with
 PT immobilised anti-CD3 antibody and stimulating accessory molecule on T
 PT cell surface.

XX Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to
 CC proliferate for use in therapy comprising activating T cells by
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
 CC on solid phase surface, and stimulating accessory molecule on T cell

CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a
 CC population of T cells to proliferate in sufficient numbers for use in
 CC therapy e.g., for treating cancer or an infectious disease. The method
 CC can be used to selectively expand the population of CD28+, CD4+, CD8+,
 CC CD28RA+ or CD28RO+ T cells for immunotherapy. The T cell population
 CC resulting by the method can be genetically transduced and used for
 CC immunotherapy or can be used for in vitro analysis of infectious agents
 CC such as human immunodeficiency virus (HIV). Proliferation of a population
 CC of CD4+ T cells obtained from an individual infected with HIV can be
 CC achieved and the cells rendered resistant to HIV infection. Following the
 CC expansion of the T cells to sufficient numbers, the expanded T cells are
 CC restored to the individual. Also CD4+ T cells expanded by the above
 CC mentioned is useful for treating HIV infection in an individual. A
 CC population of tumour-infiltrating lymphocytes can be obtained from an
 CC individual afflicted with cancer and the T cells stimulated to
 CC proliferate to sufficient numbers and restored to the individual. The
 CC supernatants from cultures of T cells expanded from above mentioned
 CC method are useful as a rich source of cytokines and can be used to
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a
 CC population of antigen specific T cells are useful in therapeutic
 CC conditions where it is desirable to upregulate an immune response. The T
 CC cell proliferation occurs in the absence of exogenous growth factors or
 CC accessory cells. The present sequence is human CD9 antigen which is
 CC expressed on surface of activated T cells

XX
 SQ Sequence 227 AA;

Query Match 100.0%; Score 132; DB 5; Length 227;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTVTKSCPDAIKEVFDNK 25
 |||||

Db 167 PKKDVLFTVTKSCPDAIKEVFDNK 191

RESULT 5

ABU05057

ID ABU05057 standard; protein; 227 AA.

XX ABU05057;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1723.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0359885P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

```

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1723; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 132; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETTFTVKSCPDPAIKEVFDNK 25
Db 167 PKKQVLETTFTVKSCPDPAIKEVFDNK 191

RESULT 6
ABU05060
ID ABU05060 standard; protein; 227 AA.
XX
AC ABU05060;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1726.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.

```

```

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1726; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227 AA;
Query Match 100.0%; Score 132; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETTFTVKSCPDPAIKEVFDNK 25
Db 167 PKKQVLETTFTVKSCPDPAIKEVFDNK 191

RESULT 7
ABW00436
ID ABW00436 standard; protein; 227 AA.
XX
AC ABW00436;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human CD9 antigenic protein.
XX
KW HIV infection; human immunodeficiency virus; therapy; antigen; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 111..194
FT /note= "Extracellular domain"
FT Domain 195..220
FT /note= "Transmembrane domain"
FT Domain 221..227
FT /note= "Cytoplasmic domain"
XX
PN US2003099643-A1.
XX
PD 29-MAY-2003.
XX
PF 08-JUL-1999; 99US-00350202.
XX
PR 23-NOV-1988; 88US-00275433.
PR 22-NOV-1989; 89WO-US005304.
PR 07-APR-1992; 92US-00864805.
PR 07-APR-1992; 92US-00864807.
PR 07-APR-1992; 92US-00864866.
PR 04-JUN-1993; 93US-00073223.
PR 03-JUN-1994; 94US-00253694.
PR 10-MAR-1995; 95US-00403253.

```

```

XX PA (JUNE/) JUNE C H.
XX PA (THOM/) THOMPSON C B.
XX PA (NABEL/) NABEL G J.
XX PA (GRAY/) GRAY G S.
XX PA (RENN/) RENNERT P D.
XX PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX DR WPI; 2003-801206/75.
XX XX
XX PT Treating HIV infection in individual by isolating T cells from
XX PT leukocytes, contacting T cells with anti-CD3 antibody for T cell
XX PT proliferation, separating antibody from T cells, monitoring proliferation
XX PT of T cells.
XX PS Example 10; Page 23; Opp; English.
XX XX
XX CC The present invention relates to a novel method of treating human
XX CC immunodeficiency virus (HIV) infection in an individual. The method
XX CC involves isolating population of CD4 T cells from leukocytes, contacting
XX CC population of CD4+ T cells with an anti-CD3 antibody for stimulating T
XX CC cell proliferation, separating antibody from T cells, monitoring
XX CC proliferation of T cells, restimulating T cells with antibody and
XX CC restoring T cells to individual. The present sequence is human CD9
XX CC antigenic protein. This sequence is used to illustrate the method of the
XX CC invention
XX SQ Sequence 227 AA;
XX
XX Query Match 100.0%; Score 132; DB 7; Length 227;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 PKQVLETFVTKSCPDAIKEVFDNK 25
DB 167 PKQVLETFVTKSCPDAIKEVFDNK 191
XX
XX RESULT 8
XX ADK69862
XX ID ADK69862 standard; protein; 227 AA.
XX AC ADK69862;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE Human CD9 protein.
XX XX
XX KW CD28-associated signal; immunotherapy; infectious disease; cancer;
XX KW leukopheresis; human.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US6534055-B1.
XX XX
XX PD 18-MAR-2003.
XX XX
XX PF 04-MAY-1995; 95US-00435816.
XX XX
XX PR 07-APR-1992; 92US-00864805.
XX PR 07-APR-1992; 92US-00864807.
XX PR 07-APR-1992; 92US-00864866.
XX PR 04-JUN-1993; 93US-00072223.
XX PR 03-JUN-1994; 94US-00253964.
XX PR 10-MAR-1995; 95US-00403253.
XX XX
XX PA (GEMY ) GENETICS INST INC.
XX XX
XX PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX DR WPI; 2003-531074/50.
XX XX
XX PT Expanding T cell populations, useful for preparing renewable sources of T
XX PT cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28
XX PT -associated signal on the surface of the cells with an anti-CD28
XX PT antibody, B7-1 or B7-2.
XX PS Example 10; SEQ ID NO 6; 82pp; English.
XX XX
XX CC The invention relates to a method for expanding a population of T cells
XX CC to about 100-100000-fold over the original T cell population, or to about
XX CC 10 log 1 0 to 12 log 1 2. The method comprises stimulating a CD28-
XX CC associated signal on the surface of the T cells with agent comprising an
XX CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a
XX CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T
XX CC cells) to proliferate. The method is particularly useful for preparing a
XX CC renewable source of CD4+ T cells. The expanded T cell population can be
XX CC genetically transduced, and used for immunotherapy to treat a variety of
XX CC human diseases (e.g. infectious diseases or cancer), or used in
XX CC diagnostic protocols. T cells were obtained from leukopheresis of a
XX CC normal donor, and purified with FICOLL density gradient centrifugation,
XX CC followed by magnetic immunobead sorting. The present sequence is CD9 used
XX CC in the exemplification of the invention.
XX SQ Sequence 227 AA;
XX
XX Query Match 100.0%; Score 132; DB 7; Length 227;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 PKQVLETFVTKSCPDAIKEVFDNK 25
DB 167 PKQVLETFVTKSCPDAIKEVFDNK 191
XX
XX RESULT 9
XX ADI19366
XX ID ADI19366 standard; protein; 227 AA.
XX AC ADI19366;
XX XX
XX DT 15-APR-2004 (first entry)
XX XX
XX DE Human CD9 protein.
XX XX
XX KW T cell; immunotherapy; therapy; HIV infection; cancer;
XX KW infectious disease; cytostatic; antimicrobial; human.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US2004001829-A1.
XX XX
XX PD 01-JAN-2004.
XX XX
XX PF 17-MAR-2003; 2003US-00390330.
XX XX
XX PR 23-NOV-1988; 88US-00275433.
XX PR 22-NOV-1989; 89WO-US005304.
XX PR 07-APR-1992; 92US-00864805.
XX PR 07-APR-1992; 92US-00864807.
XX PR 07-APR-1992; 92US-00864866.
XX PR 04-JUN-1993; 93US-00072223.
XX PR 03-JUN-1994; 94US-00253964.
XX PR 10-MAR-1995; 95US-00403253.
XX PR 04-MAY-1995; 95US-00435816.
XX XX
XX PA (JUNE/) JUNE C H.
XX PA (THOM/) THOMPSON C B.
XX PA (NABEL/) NABEL G J.
XX PA (GRAY/) GRAY G S.
XX PA (RENN/) RENNERT P D.
XX XX
XX PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
XX DR WPI; 2004-061648/06.
XX XX

```

XX Inducing a population of T cells to proliferate, for immunotherapy or
 PT treating HIV infection, cancer or infectious disease, comprises
 PT activating a population of T cells and stimulating an accessory molecule
 PT on the surface of the T cells.

XX Example 10; SEQ ID NO 6; 80pp; English.

XX The invention relates to a method for inducing a population of T cells to
 CC proliferate. The method comprising activating a population of T cells,
 CC and stimulating an accessory molecule on the surface of the T cells with
 CC a ligand that binds the accessory molecule. The invention is useful for
 CC immunotherapy, for treating HIV infection, cancer or infectious disease,
 CC or in diagnostic applications. The present sequence is human CD9 protein.

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 132; DB 8; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKKDVLEFTTVKSCPDAlKEVFDNK 25
 |||||
 Db 167 PKKDVLEFTTVKSCPDAlKEVFDNK 191

RESULT 10

AEA89005
 ID AEA89005 standard; protein; 227 AA.

AC AEA89005;

DT 25-AUG-2005 (first entry)

XX Human CD9 antigenic protein, SEQ ID NO: 6.

XX Cell therapy; immune stimulation; immunotherapy; diagnosis;
 KW infectious disease; antimicrobial; infection; cancer; cytostatic;
 KW neoplasm; CD9; antigen.

OS Homo sapiens.

XX US6905681-B1.

XX 14-JUN-2005.

XX 08-JUL-1999; 99US-00349915.

XX 03-JUN-1994; 94US-00253964.

XX 10-MAR-1995; 95US-00403253.

XX (GEMY) GENETICS INST INC.

PA (UNMI) UNIV MICHIGAN.

PA (USNA) US SEC OF NAVY.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2005-464777/47.

XX Ex vivo proliferation of T cell population for use in therapy, involves
 PT contacting population of T cells with surface having anti-CD3 antibody
 PT and anti-CD28 antibody for activating T cells and stimulating activated T
 PT cells, respectively.

XX Example 10; SEQ ID NO 6; 76pp; English.

XX The present invention relates to a method of including ex vivo
 CC proliferation of a population of T cells to sufficient numbers for use in
 CC therapy. The method involves contacting population of T cells with
 CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T
 CC cells and stimulating activated T cells, respectively. The invention is
 CC useful for treating cancer and infectious disease and also useful in cell
 CC therapy. The present sequence is the human CD9 antigenic protein. This

CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used
 CC to stimulate a CD8+ T cell population.

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 132; DB 9; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKKDVLEFTTVKSCPDAlKEVFDNK 25
 |||||

Db 167 PKKDVLEFTTVKSCPDAlKEVFDNK 191

RESULT 11

AAR27525

ID AAR27525 standard; protein; 228 AA.

XX AAR27525;

XX 25-MAR-2003 (revised)

DT 05-MAR-1993 (first entry)

XX Metastasis controlling peptide.

XX M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;
 KW lung; glioblastoma.

OS Homo sapiens.

XX EP508417-A2.

XX 14-OCT-1992.

XX 09-APR-1992; 92EP-00106093.

XX 12-APR-1991; 91JP-00079996.

XX 17-APR-1991; 91JP-00085396.

XX 07-FEB-1992; 92JP-00022321.

XX (TAKE) TAKEDA CHEM IND LTD.

PA (MIYA/) MIYAKE M.

XX Ikeyama S, Koyama M, Senoo M, Miyake M;

XX WPI; 1992-341723/42.

XX N-PSDB; AAQ29182.

XX New monoclonal antibody M31-15 specific for metastasis-controlling
 PT peptide - useful for treating and preventing cancer and metastasis.

XX Claim 7; Fig 4; 34pp; English.

XX The sequence is that of a cancer cell surface protein which is capable of
 CC suppressing the motility of cancer cells. It is specifically recognised
 CC by the monoclonal (Mab) antibody M31-15 which is useful for suppressing
 CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in
 CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and
 CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 228 AA;

Query Match 100.0%; Score 132; DB 2; Length 228;

Best Local Similarity 100.0%; Pred. No. 2.6e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PKKDVLEFTTVKSCPDAlKEVFDNK 25
 |||||

Db 168 PKKDVLEFTTVKSCPDAlKEVFDNK 192

RESULT 12

ABB44581

ABB44581 standard; protein; 228 AA.
ABB44581;
25-JAN-2002 (first entry)
Human wound healing related polypeptide SEQ ID NO 38.
Human; mouse; vulnery; dermatological; skin disorder; wound healing;
gene therapy.
Homo sapiens.
CA2325226-A1.
17-MAY-2001.
16-NOV-2000; 2000CA-02325226.
17-NOV-1999; 99DE-01055349.
17-DEC-1999; 99US-0172511P.
20-JUN-2000; 2000DE-01030149.
(SWIT-) SWITCH BIOTECH AG.
Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;
WPI; 2001-433142/47.
Use of novel polypeptide or its variant or nucleic acid encoding the
polypeptide for diagnosing and/or preventing and/or treating skin
disorders and/or treatment in wound healing or for identifying active
substances.
Disclosure; Page 193-194; 265pp; English.
The invention relates to the use of a polypeptide (ABB44544-ABB44601,
ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-
ABA81995, ABA82016-ABA82032) with vulnerary and/or dermatological
activity for the diagnosis, prevention and treatment of skin disorders
and treatment in wound healing or for the identification of
pharmacologically active substances. The nucleic acids are useful in gene
therapy. Note: The printed sequence listing for this specification was
incomplete, terminating part way through SEQ ID NO 106. The remaining
data was obtained from EPO data for an equivalent patent (EP1114862)
Sequence 228 AA;
Query Match 100.0%; Score 132; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKQVLETFVTKSCPDPAIKEVFDNK 25
DB 168 PKQVLETFVTKSCPDPAIKEVFDNK 192
RESULT 13
ABU05059
ID ABU05059 standard; protein; 228 AA.
XX AC ABU05059;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1725.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.
XX WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PF 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1725; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 132; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PKQVLETFVTKSCPDPAIKEVFDNK 25
DB 168 PKQVLETFVTKSCPDPAIKEVFDNK 192
RESULT 14
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX AC ABU05052;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1718.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

```

OS Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1718; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 228 AA;
XX
XX Query Match 100.0%; Score 132; DB 6; Length 228;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PKKDVLFTFTVKSCPDALKEVFDNK 25
XX |||||
XX Db 168 PKKDVLFTFTVKSCPDALKEVFDNK 192
XX
XX RESULT 15
XX ABU05048
XX ID ABU05048 standard; protein; 228 AA.
XX AC ABU05048;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1714.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

```

Search completed: January 20, 2006, 17:16:07
Job time : 88.963 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:10:37 ; Search time 17.5926 Seconds
(without alignments)
117.486 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKKDVLFTVTKSCPDPAKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	29	1	US-08-254-493-6
2	132	100.0	29	1	US-08-408-222B-6
3	132	100.0	227	1	US-08-254-493-1
4	132	100.0	227	1	US-08-253-751-6
5	132	100.0	227	1	US-08-453-925-6
6	132	100.0	227	2	US-08-403-253A-6
7	132	100.0	227	2	US-08-435-816A-6
8	132	100.0	227	2	US-09-350-202-6
9	132	100.0	227	2	US-08-592-711-6
10	132	100.0	227	2	US-09-349-915B-6
11	132	100.0	228	1	US-08-408-222B-1
12	117.5	89.0	79	2	US-08-630-172-8
13	117.5	89.0	79	2	US-09-375-419-8
14	51	38.6	303	2	US-09-134-001C-5215
15	50	37.9	1905	2	US-09-964-956-44
16	47	35.6	919	2	US-09-248-796A-17485
17	47	35.6	1018	1	US-08-452-052-2
18	46	34.8	156	2	US-09-393-627B-27
19	46	34.8	456	2	US-09-492-027-2
20	46	34.8	566	2	US-09-328-352-7811
21	46	34.8	608	2	US-09-310-275-2
22	46	34.8	608	2	US-09-082-077-5
23	46	34.8	608	2	US-09-925-637-70
24	45	34.1	293	2	US-09-134-000C-4231
25	45	34.1	690	2	US-09-902-540-10349
26	44	33.3	156	2	US-09-393-627B-26
27	44	33.3	400	2	US-09-583-110-5315

28 44 33.3 411 2 US-09-248-796A-15503 Sequence 15503, A
29 44 33.3 414 2 US-09-107-433-3551 Sequence 3551, Ap
30 44 33.3 542 1 US-08-701-380-2 Sequence 2, Appli
31 44 33.3 542 2 US-09-032-365A-13 Sequence 13, Appl
32 44 33.3 643 2 US-09-949-016-10023 Sequence 10023, A
33 44 33.3 1334 1 US-08-996-545-2 Sequence 2, Appli
34 44 33.3 1334 2 US-09-328-320-2 Sequence 2, Appli
35 44 33.3 1334 2 US-09-758-828-2 Sequence 2, Appli
36 43.5 33.0 1604 2 US-09-004-838-95 Sequence 95, Appl
37 43.5 33.0 1854 2 US-09-004-838-95 Sequence 108, App
38 43 32.6 311 2 US-09-634-955B-5 Sequence 5, Appli
39 43 32.6 311 2 US-09-816-760-5 Sequence 5, Appli
40 43 32.6 311 2 US-09-838-561-5 Sequence 5, Appli
41 43 32.6 369 2 US-09-198-452A-1048 Sequence 1048, Ap
42 43 32.6 369 2 US-09-438-185A-977 Sequence 977, App
43 43 32.6 511 2 US-09-134-078-21 Sequence 21, Appl
44 43 32.6 519 1 US-08-319-387-4 Sequence 4, Appli
45 42.5 32.2 312 2 US-09-134-001C-5583 Sequence 5583, Ap

ALIGNMENTS

RESULT 1
US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:


```

1 Sequence 6, Application US/08453925
2 Patent No. 5883223
3 GENERAL INFORMATION:
4 APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
5 APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.
6 TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
7 TITLE OF INVENTION: PROLIFERATION OF T-CELLS
8 NUMBER OF SEQUENCES: 10
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: LAHIVE & COCKFIELD
11 STREET: 60 STATE STREET, SUITE 510
12 CITY: BOSTON
13 STATE: MA
14 COUNTRY: USA
15 ZIP: 02109
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: ASCII TEXT
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/453,925
23 FILING DATE: 30 MAY 1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/253,751
26 FILING DATE: 3 JUNE 1994
27 APPLICATION NUMBER: US 08/073,223
28 FILING DATE: 4 JUNE 1993
29 APPLICATION NUMBER: US 08/200,947
30 FILING DATE: 23 FEB 1994
31 APPLICATION NUMBER: US 07/864,805
32 FILING DATE: 7 APR 1992
33 APPLICATION NUMBER: US 08/247,505
34 FILING DATE: 23 MAY 1994
35 APPLICATION NUMBER: US 07/864,866
36 FILING DATE: 7 APR 1992
37 APPLICATION NUMBER: 08/218,155
38 FILING DATE: 25 MAR 1994
39 APPLICATION NUMBER: US 07/864,807
40 FILING DATE: 7 APR 1992
41 APPLICATION NUMBER: US 07/902,467
42 FILING DATE: 16 JUNE 1992
43 APPLICATION NUMBER: US 07/275,433
44 FILING DATE: 23 NOV 1988
45 ATTORNEY/AGENT INFORMATION:
46 NAME: MANDRAGOURAS, AMY E.
47 REGISTRATION NUMBER: 36,207
48 REFERENCE/DOCKET NUMBER: RPI-002CPB
49 TELECOMMUNICATION INFORMATION:
50 TELEPHONE: (617) 227-7400
51 TELEFAX: (617) 227-5941
52 INFORMATION FOR SEQ ID NO: 6:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 227 amino acids
55 TYPE: amino acid
56 TOPOLOGY: linear
57 MOLECULE TYPE: protein
58 US-08-453-925-6

```

RESULT 6
US-08-403-253A-6
; Sequence 6, Application US/08403253A
; Patent No. 6332694
; GENERAL INFORMATION:

```
Query Match      100.0%; Score 132; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,253A
; FILING DATE: March 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-403-253A-6

Query Match 100.0%; Score 132; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAlKEVFDNK 25
Db 167 PKKDVLFTTVKSCPDAlKEVFDNK 191

RESULT 7
US-08-435-816A-6
; Sequence 6, Application US/08435816A
; Patent No. 6534055
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
```

```
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,816A
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-435-816A-6

Query Match 100.0%; Score 132; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAlKEVFDNK 25
Db 167 PKKDVLFTTVKSCPDAlKEVFDNK 191

RESULT 8
US-09-350-202-6
; Sequence 6, Application US/09350202
; Patent No. 6887466
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
```

APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-350-202-6

Query Match 100.0%; Score 132; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDPAKEVFDNK 25
|||
Db 167 PKKDVLETFVKSCPDPAKEVFDNK 191

RESULT 9
US-08-592-711-6
; Sequence 6, Application US/08592711
; Patent No. 6905680
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.

APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-711-6

Query Match 100.0%; Score 132; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDPAKEVFDNK 25
|||
Db 167 PKKDVLETFVKSCPDPAKEVFDNK 191

RESULT 10
US-09-349-915B-6
; Sequence 6, Application US/09349915B
; Patent No. 6905681

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-172-8

Query Match 89.0%; Score 117.5; DB 2; Length 79;
Best Local Similarity 96.0%; Pred. No. 3.3e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 PKKDVLFTFTVKSPDAIKEVFNK 25
Db 56 PKKDVLFTFTVKSPD-IKEVFNK 79

RESULT 13
US-09-375-419-8
Sequence 8, Application US/09375419
Patent No. 6264950
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,419
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-375-419-8

Query Match 89.0%; Score 117.5; DB 2; Length 79;
Best Local Similarity 96.0%; Pred. No. 3.3e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 PKKDVLFTFTVKSPDAIKEVFNK 25
Db 56 PKKDVLFTFTVKSPD-IKEVFNK 79

RESULT 14
US-09-134-001C-5215
Sequence 5215, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5215
LENGTH: 303
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5215

Query Match 38.6%; Score 51; DB 2; Length 303;
Best Local Similarity 73.3%; Pred. No. 5.6;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 FTVKSCPDAIKEVFD 23
Db 251 FWDKSSPDAIKEVFN 265

RESULT 15
US-09-964-956-44
Sequence 44, Application US/09964956
Patent No. 6875570
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigar, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: No. 6875570el Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/09/964,956
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,396
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/276,667
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/294,823
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/304,868
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 1905
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-964-956-44

Query Match 37.9%; Score 50; DB 2; Length 1905;
Best Local Similarity 55.0%; Pred. No. 71;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
Qy 1 PKQVLETFVKSQDAIKE 20
Db 343 PKESVLCFLTKKIDKIKE 362

Search completed: January 20, 2006, 17:23:45
Job time : 18.5926 secs


```
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 240878
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(74)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_15125C.1.pep
US-10-425-115-240878

Query Match          100.0%; Score 132; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDPAIKEVFDNK 25
Db 20 PKDVLFTFTVKSCPDPAIKEVFDNK 44

RESULT 3
US-08-592-711-6
; Sequence 6, Application US/08592711
; Publication No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
```

```
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy B.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 227 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-592-711-6

Query Match          100.0%; Score 132; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDPAIKEVFDNK 25
Db 167 PKDVLFTFTVKSCPDPAIKEVFDNK 191

RESULT 4
US-09-183-055-6
; Sequence 6, Application US/09183055
; Publication No. US20020076407A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,055
; FILING DATE: 30-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
```

/ FILING DATE: 16 JUNE 1992
/ APPLICATION NUMBER: US 07/275,433
/ FILING DATE: 23 NOV 1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Superko, Colleen
/ REGISTRATION NUMBER: 39,850
/ REFERENCE/DOCKET NUMBER: 36119-125US8
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 526-6564
/ TELEFAX: (617) 526-5000
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 227 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-183-055-6

Query Match 100.0%; Score 132; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDPAIKEVFNK 25
|||
DB 167 PKDVLFTFTVKSCPDPAIKEVFNK 191

RESULT 5
US-09-350-202-6
/ Sequence 6, Application US/09350202
/ Publication No. US2003009643A1
/ GENERAL INFORMATION:
/ APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
/ APPLICANT: Gray, Gary S., Rennert, Paul D.
/ TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/350,202
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/403,253
/ FILING DATE: March 10, 1995
/ APPLICATION NUMBER: US 08/253,964
/ FILING DATE: 3 JUNE 1994
/ APPLICATION NUMBER: US 08/073,223
/ FILING DATE: 4 JUNE 1993
/ APPLICATION NUMBER: US 08/200,947
/ FILING DATE: 23 FEB 1994
/ APPLICATION NUMBER: US 07/864,805
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 08/247,505
/ FILING DATE: 23 MAY 1994
/ APPLICATION NUMBER: US 07/864,866
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 08/218,155
/ FILING DATE: 25 MAR 1994
/ APPLICATION NUMBER: US 07/864,807
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 07/902,467

/ FILING DATE: 16 JUNE 1992
/ APPLICATION NUMBER: US 07/275,433
/ FILING DATE: 23 NOV 1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: RPI-002CP2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 742-4214
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 227 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-350-202-6

Query Match 100.0%; Score 132; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDPAIKEVFNK 25
|||
DB 167 PKDVLFTFTVKSCPDPAIKEVFNK 191

RESULT 6
US-10-390-330-6
/ Sequence 6, Application US/10390330
/ Publication No. US20040001829A1
/ GENERAL INFORMATION:
/ APPLICANT: June, Carl H.
/ APPLICANT: Thompson, Craig B.
/ APPLICANT: Nabel, Gary J.
/ APPLICANT: Gray, Gary S.
/ APPLICANT: Rennert, Paul D.
/ TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 60 State Street, Suite 510
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/390,330
/ FILING DATE: March 17, 2003
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,816A
/ FILING DATE: May 4, 1995
/ CLASSIFICATION:
/ APPLICATION NUMBER: US 08/403,253
/ FILING DATE: 10 MARCH 1995
/ APPLICATION NUMBER: US 08/253,964
/ FILING DATE: 3 JUNE 1994
/ APPLICATION NUMBER: US 08/073,223
/ FILING DATE: 4 JUNE 1993
/ APPLICATION NUMBER: US 08/200,947
/ FILING DATE: 23 FEB 1994
/ APPLICATION NUMBER: US 07/864,805
/ FILING DATE: 7 APR 1992
/ APPLICATION NUMBER: US 08/247,505
/ FILING DATE: 23 MAY 1994
/ APPLICATION NUMBER: US 07/864,866

```
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-390-330-6

Query Match 100.0%; Score 132; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 PKKDVLETFVTKSCPDAIKEVFDNK 25
Db 167 PKKDVLETFVTKSCPDAIKEVFDNK 191
```

```
RESULT 7
US-10-473-127-1723
; Sequence 1723, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1723
```

```
Query Match 100.0%; Score 132; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 PKKDVLETFVTKSCPDAIKEVFDNK 25
Db 167 PKKDVLETFVTKSCPDAIKEVFDNK 191
```

```
RESULT 8
```

```
US-10-473-127-1726
; Sequence 1726, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1726
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match 100.0%; Score 132; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 PKKDVLETFVTKSCPDAIKEVFDNK 25
Db 167 PKKDVLETFVTKSCPDAIKEVFDNK 191
```

```
RESULT 9
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,136
; FILING DATE: 29-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,146
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO US98/00959
; FILING DATE: 21-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF354PCT
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-156-136-39

Query Match 100.0%; Score 132; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFNK 25
DB 168 PKQDVLETFVTKSCPDPAIKEVFNK 192

RESULT 10

US-10-331-496A-41
Sequence 41, Application US/10331496A
Publication No. US20030228305A1
GENERAL INFORMATION:
APPLICANT: FRANTZ, GRETCHEN
APPLICANT: HILLAN, KENNETH J.
APPLICANT: PHILLIPS, HEIDI S.
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH, VICTORIA
APPLICANT: SPENCER, SUSAN D.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WU, THOMAS D.
APPLICANT: ZHANG, ZEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR

FILE REFERENCE: P5014R1-PCT
CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 60/345,444
PRIOR FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US 60/351,885
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/366,869
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US 60/366,284
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/368,679
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/405,645
PRIOR FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 95

SEQ ID NO 41
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapien

US-10-331-496A-41

Query Match 100.0%; Score 132; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFNK 25
DB 168 PKQDVLETFVTKSCPDPAIKEVFNK 192

RESULT 11

US-10-619-323-1
Sequence 1, Application US/10619323
Publication No. US20040136985A1
GENERAL INFORMATION:
APPLICANT: Longhurst, Lisa K.
APPLICANT: Jennings, Celia M.
APPLICANT: Cook, George A.
APPLICANT: Bao, Jianxiong
APPLICANT: Zhang, Chunxiang
APPLICANT: White, Melanie M.
APPLICANT: Crossno, Jr., Joseph T.
APPLICANT: Lu, Yi

TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
FILE REFERENCE: 20609/241
CURRENT APPLICATION NUMBER: US/10/619,323
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: 60/395,864
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapien

US-10-619-323-1

Query Match 100.0%; Score 132; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFNK 25
DB 168 PKQDVLETFVTKSCPDPAIKEVFNK 192

RESULT 12

US-10-794-899-97
Sequence 97, Application US/10794899
Publication No. US20040146516A1
GENERAL INFORMATION:
APPLICANT: Utah Ventures
FILE REFERENCE: 27110-715
CURRENT APPLICATION NUMBER: US/10/794,899
CURRENT FILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 97
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens

US-10-794-899-97

Query Match 100.0%; Score 132; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFNK 25
DB 168 PKQDVLETFVTKSCPDPAIKEVFNK 192

RESULT 13

US-10-473-127-1714
Sequence 1714, Application US/10473127
Publication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: US/10/473,127

```
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match          100.0%; Score 132; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETTTVKSCPDPAIKEVFDNK 25
Db      168 PKKDVLETTTVKSCPDPAIKEVFDNK 192

RESULT 14
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715

Query Match          100.0%; Score 132; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETTTVKSCPDPAIKEVFDNK 25
Db      168 PKKDVLETTTVKSCPDPAIKEVFDNK 192

RESULT 15
US-10-473-127-1716
; Sequence 1716, Application US/10473127
; Publication No. US20040236091A1
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:16:18 ; Search time 4.32099 Seconds
(without alignments)
58.632 Million cell updates/sec

Title: US-10-619-323-5
Perfect score: 132
Sequence: 1 PKKDVLETFVKSCPDAlKEVFDNK 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	228	6	US-10-821-234-1266
2	43	32.6	364	6	US-10-510-947-2
3	42.5	32.2	130	7	US-11-055-822-690
4	42.5	32.2	130	7	US-11-055-822-690
5	41	31.1	274	6	US-10-454-437-354
6	41	31.1	409	6	US-10-978-927-1
7	41	31.1	528	6	US-10-978-927-6
8	41	31.1	529	6	US-10-821-234-1520
9	41	31.1	529	6	US-10-978-927-9
10	41	31.1	529	6	US-10-978-927-13
11	41	31.1	645	6	US-10-763-712A-17
12	41	31.1	645	6	US-10-763-712A-105
13	41	31.1	662	7	US-11-137-131-2
14	41	31.1	662	7	US-11-137-131-4
15	41	31.1	870	7	US-11-165-211-48
16	41	31.1	870	7	US-11-165-226-58
17	40.5	30.7	924	6	US-10-467-657-4290
18	40	30.3	174	7	US-11-149-349-10
19	40	30.3	367	6	US-10-467-657-1440
20	40	30.3	898	7	US-11-145-631-11
21	40	30.3	1218	6	US-11-052-554A-123
22	39.5	29.9	959	6	US-10-467-962B-4
23	39.5	29.9	2197	7	US-11-075-185-8
24	39	29.5	219	7	US-11-074-176-106
25	39	29.5	351	6	US-10-981-873-27

26	39	29.5	440	6	US-10-606-302-9
27	39	29.5	932	7	US-11-188-743-17
28	39	29.5	932	7	US-11-188-743-18
29	38.5	29.2	397	6	US-10-858-730-29
30	38.5	29.2	397	7	US-11-103-957-47
31	38	28.8	176	7	US-11-134-703-6
32	38	28.8	176	7	US-11-134-703-8
33	38	28.8	246	7	US-11-134-703-10
34	38	28.8	246	7	US-11-134-703-12
35	38	28.8	257	6	US-10-642-272A-5
36	38	28.8	257	6	US-10-642-272A-6
37	38	28.8	268	7	US-11-134-703-4
38	38	28.8	268	7	US-11-134-703-18
39	38	28.8	468	7	US-11-054-385-12
40	38	28.8	741	6	US-10-793-626-1178
41	37.5	28.4	306	6	US-10-485-517-185
42	37.5	28.4	587	6	US-10-623-155-501
43	37.5	28.4	724	6	US-10-131-826A-60
44	37.5	28.4	852	6	US-10-467-657-5004
45	37.5	28.4	2204	6	US-10-495-083-8

ALIGNMENTS

RESULT 1

US-10-821-234-1266
; Sequence 1266, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1266
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1266

Query Match 100.0%; Score 132; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAlKEVFDNK 25
DB 168 PKKDVLETFVKSCPDAlKEVFDNK 192

RESULT 2

US-10-510-947-2
; Sequence 2, Application US/10510947
; Publication No. US20050255123A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Medina, Maria Fe C.
; APPLICANT: Kobinger, Gary
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor
; FILE REFERENCE: UPN-02811PCT
; CURRENT APPLICATION NUMBER: US/10/510,947
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/376,480
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/385,704


```

; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-137-131-2

Query Match          31.1%; Score 41; DB 7; Length 662;
Best Local Similarity 40.0%; Pred.No. 77;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCFDAKEV 21
       :|: : ||| | | | :
Db      295 EQDAVNFTFKYISPDAAKPI 314

RESULT 14
US-11-137-131-4
; Sequence 4, Application US/11137131
; Publication No. US20060003358A1
; GENERAL INFORMATION:
; APPLICANT: Braun, A.
; TITLE OF INVENTION: POLYMORPHIC KINASE ANCHOR PROTEINS AND
; FILE REFERENCE: 24736-2035
; CURRENT APPLICATION NUMBER: US/11/137,131
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/09/834,700
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/240,335
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-137-131-4

Query Match          31.1%; Score 41; DB 7; Length 662;
Best Local Similarity 40.0%; Pred.No. 77;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCFDAKEV 21
       :|: : ||| | | | :
Db      295 EQDAVNFTFKYISPDAAKPI 314

RESULT 15
US-11-165-211-48
; Sequence 48, Application US/11165211
; Publication No. US20050287626A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides
; FILE REFERENCE: 4093-14
; CURRENT APPLICATION NUMBER: US/11/165,211
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JP2004-189012
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-211-48

Query Match          31.1%; Score 41; DB 7; Length 870;
Best Local Similarity 47.6%; Pred.No. 11e+02;
Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCFDAKEVF 22

```

```

; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-137-131-2

Query Match          31.1%; Score 41; DB 7; Length 662;
Best Local Similarity 40.0%; Pred.No. 77;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCFDAKEV 21
       :| : ||| | | | :
Db      295 EQDAVNFTFKYISPDAAKPI 314

RESULT 14
US-11-137-131-4
; Sequence 4, Application US/11137131
; Publication No. US20060003358A1
; GENERAL INFORMATION:
; APPLICANT: Braun, A.
; TITLE OF INVENTION: POLYMORPHIC KINASE ANCHOR PROTEINS AND
; FILE REFERENCE: NUCLEIC ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/11/137,131
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/09/834,700
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/240,335
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-137-131-4

Query Match          31.1%; Score 41; DB 7; Length 662;
Best Local Similarity 40.0%; Pred.No. 77;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCFDAKEV 21
       :| : ||| | | | :
Db      295 EQDAVNFTFKYISPDAAKPI 314

RESULT 15
US-11-165-211-48
; Sequence 48, Application US/11165211
; Publication No. US20050287626A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides
; FILE REFERENCE: 4093-14
; CURRENT APPLICATION NUMBER: US/11/165,211
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JP2004-189012
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-211-48

Query Match          31.1%; Score 41; DB 7; Length 870;
Best Local Similarity 47.6%; Pred.No. 11e+02;
Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCFDAKEVF 22

```

```

; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-137-131-2

Query Match          31.1%; Score 41; DB 7; Length 662;
Best Local Similarity 40.0%; Pred.No. 77;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCPDAIKEV 21
       :| : ||| | | | :
Db      295 EQDAVNFTFKYISPDAAKPI 314

RESULT 14
US-11-137-131-4
; Sequence 4, Application US/11137131
; Publication No. US20060003358A1
; GENERAL INFORMATION:
; APPLICANT: Braun, A.
; TITLE OF INVENTION: POLYMORPHIC KINASE ANCHOR PROTEINS AND
; FILE REFERENCE: 24736-2035
; CURRENT APPLICATION NUMBER: US/11/137,131
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/09/834,700
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/240,335
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-137-131-4

Query Match          31.1%; Score 41; DB 7; Length 662;
Best Local Similarity 40.0%; Pred.No. 77;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCPDAIKEV 21
       :| : ||| | | | :
Db      295 EQDAVNFTFKYISPDAAKPI 314

RESULT 15
US-11-165-211-48
; Sequence 48, Application US/11165211
; Publication No. US20050287626A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides
; FILE REFERENCE: 4093-14
; CURRENT APPLICATION NUMBER: US/11/165,211
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JP2004-189012
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-211-48

Query Match          31.1%; Score 41; DB 7; Length 870;
Best Local Similarity 47.6%; Pred.No. 11e+02;
Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 KDVLETFVTKSCPDAIKEVF 22

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:06:32 ; Search time 17.5926 Seconds
(without alignments)
136.729 Million cell updates/sec

Title: US-10-619-323-5
Perfect score: 132
Sequence: 1 PKKDVLETFVKSCPDARKEVFDNK 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	228	1 A40402	CD9 antigen [valid
2	131	99.2	228	1 A42929	CD9 antigen - gree
3	98	74.2	226	1 S39262	CD9 antigen - rat
4	94	71.2	226	2 I49589	antigen - mouse
5	61	46.2	226	1 JX0221	CD9 antigen - bovi
6	54	40.9	64	2 H91000	hypothetical prote
7	54	40.9	64	2 B90779	hypothetical prote
8	52	39.4	439	2 T29587	hypothetical prote
9	52	39.4	435	2 S16559	cellulase (EC 3.2.
10	50	37.9	1905	2 I51553	Plexin - African c
11	49	37.1	159	2 AE2547	hypothetical prote
12	48.5	36.7	500	2 F71978	hypothetical prote
13	48	36.4	1057	2 T15720	hypothetical prote
14	47.5	36.0	439	2 T16414	hypothetical prote
15	47	35.6	68	1 Q1850L	hypothetical prote
16	47	35.6	300	2 G89915	conserved hypotet
17	47	35.6	480	2 C97121	p-loop ATPase doma
18	47	35.6	1020	2 S05944	neutrolin cell surf
19	47	35.6	1021	2 A57112	contactin precurs
20	46	34.8	294	2 G87166	enoyl-CoA hydrat
21	46	34.8	336	2 JC4102	hypothetical 36.9k
22	46	34.8	387	1 BRA0N1	41k fiber protein
23	46	34.8	423	2 E90569	conserved hypotet
24	46	34.8	502	2 T22045	hypothetical prote
25	46	34.8	608	2 C89760	two-component sens
26	46	34.8	820	2 T27909	hypothetical prote
27	46	34.8	828	2 C71951	probable flagellar
28	46	34.8	1048	1 YGVCAR	anGR protein - Vib
29	46	34.8	1139	2 S44800	F1089.8 protein -

30	46	34.8	1405	2 T04426	hypothetical prote
31	46	34.8	1980	2 S54307	myosin heavy chain
32	45.5	34.5	192	2 A85534	hypothetical prote
33	45.5	34.5	192	2 E90683	hypothetical prote
34	45.5	34.5	192	2 C64767	yail protein - Esc
35	45.5	34.5	1335	2 JQ1258	RNA-directed RNA p
36	45	34.1	25	2 PC4445	L-ascorbate peroxi
37	45	34.1	134	2 T30024	hypothetical prote
38	45	34.1	195	2 T03086	probable thymidine
39	45	34.1	372	1 VVVPK1	coat protein vpi -
40	45	34.1	483	2 D86486	protein F2839.5 [i
41	45	34.1	867	2 D75091	large helicase-rel
42	45	34.1	1217	2 T13996	pol protein - frui
43	44.5	33.7	231	2 E82652	phage-related repr
44	44.5	33.7	545	2 T02578	hypothetical prote
45	44.5	33.7	586	2 S66697	probable membrane

ALIGNMENTS

RESULT 1

A40402
CD9 antigen [validated] - human
N;Alternate names: motility-related protein-1
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1991 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A46123; A40402; JH0555; A39029; S10564
R;Rubinstein, B.; Benoit, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouche
Genomics 16, 132-138, 1993
A;Title: Organization of the human CD9 gene.
A;Reference number: A46123; MUID:93252369; PMID:8486348
A;Accession: A46123
A;Molecule type: DNA
A;Residues: 1-228 <RUB>
A;Cross-references: UNIPROT:P21926; UNIPARC:UPI000003B45A; GB:S60489; NID:g300112; PIDN
A;Experimental source: leukocyte
R;Lanza, P.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.
J. Biol. Chem. 266, 10638-10645, 1991
A;Title: CDNA cloning and expression of platelet p24/CD9. Evidence for a new family of
A;Reference number: A40402; MUID:91244846; PMID:2037603
A;Accession: A40402
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <LAN>
A;Cross-references: UNIPARC:UPI000003B45A; GB:I34068; GB:M61880; NID:G508495; PIDN:AAA5
R;Miyake, M.; Koyama, M.; Seno, M.; Ikeyama, S.
J. Exp. Med. 174, 1347-1354, 1991
A;Title: Identification of the motility-related protein (MRP-1), recognized by monoclon
A;Reference number: JH0555; MUID:92078843; PMID:1720807
A;Accession: JH0555
A;Molecule type: mRNA
A;Residues: 1-228 <MIY>
A;Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:g34768; PIDN:CAA42708.1; PID:
A;Experimental source: breast carcinoma
R;Bouchet, C.; Benoit, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uz
J. Biol. Chem. 266, 117-122, 1991
A;Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.
A;Reference number: A39029; MUID:91093112; PMID:1840589
A;Accession: A39029
A;Molecule type: mRNA
A;Residues: 1-8, 'S', '10-66, 'A', '68-193, '195-228 <BOU>
A;Cross-references: UNIPARC:UPI000174148; GB:M38690
R;Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahara, K.; Kurokawa, K.
FEBS Lett. 264, 270-274, 1990
A;Title: Purification and partial characterization of CD9 antigen of human platelets.
A;Reference number: S10564; MUID:90292223; PMID:2358073
A;Accession: S10564
A;Molecule type: protein

A;Residues: 2-8,'X',10-21 <HIG>
A;Cross-references: UNIPARC:UPI000017414C
C;Genetics:
A;Gene: GDB:CD9; MIC3
A;Cross-references: GDB:120582; OMIM:143030
A;Map position: 12p13-12p13
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-228/Product: CD9 antigen #status experimental <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-55/Domain: extracellular #status predicted <EX1>
F;56-82/Domain: transmembrane #status predicted <TM2>
F;83-86/Domain: intracellular #status predicted <CY2>
F;87-111/Domain: transmembrane #status predicted <TM3>
F;112-194/Domain: extracellular #status predicted <EX2>
F;195-221/Domain: transmembrane #status predicted <TM4>
F;222-228/Domain: intracellular #status predicted <CY3>
F;53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 132; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDAIKEVFQNK 25
|||||
Db 168 PKKQVLETFVKSCPDAIKEVFQNK 192

RESULT 2
A42929
CD9 antigen - green monkey
N;Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
A;Accession: A42929
R;Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A;Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
epitopes on toxin-sensitive cells.
A;Reference number: A42929; MUID:92394967; PMID:1522113
A;Accession: A42929
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-228 <MT>
A;Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:G218565; PIDN:
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-228/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-55/Domain: extracellular #status predicted <EX1>
F;56-82/Domain: transmembrane #status predicted <CY2>
F;83-86/Domain: intracellular #status predicted <CY2>
F;87-111/Domain: transmembrane #status predicted <TM3>
F;112-194/Domain: extracellular #status predicted <EX2>
F;195-221/Domain: transmembrane #status predicted <TM4>
F;222-228/Domain: intracellular #status predicted <CY3>
F;52,53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.2%; Score 131; DB 1; Length 228;
Best Local Similarity 96.0%; Pred. No. 9.7e-12;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDAIKEVFQNK 25
|||||
Db 168 PKKQVLETFVKSCPDAIKEVFQNK 192

RESULT 3
S39262
CD9 antigen - rat
N;Alternate names: platelet cell surface glycoprotein

C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: I56562; S39262
R;Kaprielian, Z.; Cho, K.O.; Hadjiargyrou, M.; Patterson, P.H.
J. Neurosci. 15, 562-573, 1995
A;Title: CD9, a major platelet cell surface glycoprotein, is a ROCA antigen and is expr
A;Reference number: I56562; MUID:95123481; PMID:7823164
A;Accession: I56562
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-226 <RES>
A;Cross-references: UNIPROT:P40241; UNIPARC:UPI00001708C6; EMBL:X76489; NID:G434314; PI
C;Genetics:
A;Gene: CD9
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-80/Domain: transmembrane #status predicted <TM2>
F;81-84/Domain: intracellular #status predicted <CY2>
F;85-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CY3>
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.2%; Score 98; DB 1; Length 226;
Best Local Similarity 76.0%; Pred. No. 7.1e-07;
Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDAIKEVFQNK 25
|||||
Db 166 PKKQVLESQVKSCPDIDEVFQSK 190

RESULT 4
I49589
antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49589
R;Rubinstein, E.; Billard, M.; Plaisance, S.; Prenant, M.; Boucheix, C.
Thromb. Res. 71, 377-383, 1993
A;Title: Molecular cloning of the mouse equivalent of CD9 antigen.
A;Reference number: I49589; MUID:94054345; PMID:8236164
A;Accession: I49589
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-226 <RES>
A;Cross-references: UNIPROT:P40240; UNIPARC:UPI0000003E37; GB:L08115; NID:G388911; PIDN:
C;Superfamily: CD9 antigen

Query Match 71.2%; Score 94; DB 2; Length 226;
Best Local Similarity 68.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKKQVLETFVKSCPDAIKEVFQNK 25
|||||
Db 166 PKKQLLESQVKCPCEAISEVFQNK 190

RESULT 5
JX0221
CD9 antigen - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: JX0221
R;Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cell
A;Reference number: JX0221; MUID:93054422; PMID:1339429
A;Accession: JX0221

A;Molecule type: mRNA
A;Residues: 1-226 <MAR>
A;Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:G162820; PIDN:
A;Experimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-226/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CV1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CT2>
F;81-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CV3>
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.2%; Score 61; DB 1; Length 226;
Best Local Similarity 36.0%; Pred. No. 0.2;
Matches 9; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDPAIKEVFNK 25
|||::: : |||::: : |||::: :
DB 166 PPKNLIDSLKTRCPPEAIDEIFRSK 190

RESULT 6
H91000
hypothetical protein ECs2976 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H91000
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 <HAY>
A;Cross-references: UNIPROT:Q8X5B8; UNIPARC:UPI000005FCE7; GB:BA000007; PIDN:BA036399.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs2976
C;Superfamily: phage lambda hypothetical 7.9K protein (nin region)

Query Match 40.9%; Score 54; DB 2; Length 64;
Best Local Similarity 50.0%; Pred. No. 0.64;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 8 TFTVKSCPDPAIKEVFNK 25
||||: |||: |||:
DB 2 TFTVKTIPTDMLVAYENQ 19

RESULT 7
B90779
hypothetical protein ECs1202 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B90779
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90779
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 <HAY>
A;Cross-references: UNIPROT:Q8X5B8; UNIPARC:UPI000005FCE7; GB:BA000007; PIDN:BA036425.1;

A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs1202
C;Superfamily: phage lambda hypothetical 7.9K protein (nin region)

Query Match 40.9%; Score 54; DB 2; Length 64;
Best Local Similarity 50.0%; Pred. No. 0.64;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 8 TFTVKSCPDPAIKEVFNK 25
||||: |||: |||:
DB 2 TFTVKTIPTDMLVAYENQ 19

RESULT 8
T29587
hypothetical protein F55F8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T29587
R;Gattung, S.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid F55F8.
A;Reference number: Z20647
A;Accession: T29587
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-439 <GAT>
A;Cross-references: UNIPROT:P91343; UNIPARC:UPI000013B8F3; EMBL:U80447; PIDN:AAB37809.1
A;Experimental source: strain Bristol N2; clone F55F8
C;Genetics:
A;Gene: CESP:F55F8.5
A;Map position: 1
A;Introns: 31/2; 64/1; 95/3; 131/2; 173/1; 204/3; 312/1; 354/1; 398/2

Query Match 39.4%; Score 52; DB 2; Length 439;
Best Local Similarity 44.0%; Pred. No. 8.4;
Matches 11; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 1 PKQDVLETFVTKSCPDPAIKEVFNK 25
|||::: : |||::: : |||::: :
DB 331 PKSDLL-----ISSCTDAIPRLYDPK 351

RESULT 9
S16559
cellulase (EC 3.2.1.4) - Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S16559
R;Cunningham, C.; McPherson, C.A.; Martin, J.; Harris, W.J.; Flint, H.J.
Mol. Gen. Genet. 228, 320-323, 1991
A;Title: Sequence of a cellulase gene from the rumen anaerobe Ruminococcus flavefaciens
A;Reference number: S16559; MUID:91360084; PMID:1886616
A;Accession: S16559
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <CUN>
A;Cross-references: UNIPROT:Q53302; UNIPARC:UPI000003B6E7; GB:S55178; NID:G234871; PIDN:
C;Superfamily: cellulase CCA; Clostridium cellulase repeat homology
C;Keywords: glycosidase; hydrolase

Query Match 39.4%; Score 52; DB 2; Length 455;
Best Local Similarity 41.4%; Pred. No. 8.7;
Matches 12; Conservative 4; Mismatches 7; Indels 6; Gaps 1;

QY 1 PKQDV-----LETFTVTKSCPDPAIKEVFD 23
|||::: : |||::: : |||::: :
DB 68 PSKPIPLDSAGLETFTVTCWCPASQELFD 96

RESULT 10
I51553

C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence revision 13-Jun-1983 #text_change 10-Sep-1999
C;Accession: F43011; B43017; A04396
R;Daniels, D.
submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A94614
A;Accession: F43011
A;Molecule type: DNA
A;Residues: 1-68 <DNA>
A;Cross-references: UNIPARC:UPI0000174BCA
R;Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
J. Mol. Biol. 162, 729-773, 1982
A;Title: Nucleotide sequence of bacteriophage lambda DNA.
A;Reference number: A92891; MUID:83189071; PMID:6221115
A;Accession: B43017
A;Molecule type: DNA
A;Residues: 1-68 <DNA>
A;Cross-references: UNIPARC:UPI0000174BCA; GB:J02459; GB:M17233; GB:M24325; GB:V00636; G
C;Genetics:
A;Map position: 88.74-89.16
C;Superfamily: phage lambda hypothetical 7.9K protein (nin region)

Query Match 35.6%; Score 47; DB 1; Length 68;
Best Local Similarity 44.4%; Pred. No. 7.3;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 8 TPTVKSCPDALKEVPDNK 25
||:||: ||: ||: ||: ||:
Db 2 TFSVKTIPTDMLVETGNG 19

Search completed: January 20, 2006, 17:22:37
Job time : 18.5926 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:05:21 ; Search time 95.0617 Seconds
(without alignments)
185.545 Million cell updates/sec

Title: US-10-619-323-5

Perfect score: 132

Sequence: 1 PKKDVLETFVKSCPAIKEVFDNK 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	227	1	CD9 HUMAN
2	132	100.0	228	2	Q5J7W6 HUMAN
3	131	99.2	227	1	CD9 CERAE
4	98	74.2	225	1	CD9 RAT
5	96	72.7	225	1	CD9 FELCA
6	94	71.2	225	1	CD9 MOUSE
7	89	67.4	226	2	Q8MJ48 PIG
8	87	65.9	227	2	Q4REW0 TETNG
9	86	65.2	225	1	CD9 PIG
10	84	63.6	227	2	Q6NKG7 BRARE
11	70	53.0	224	2	Q9IBC9 CHICK
12	62	47.0	228	2	Q6GQ85 XENLA
13	61	46.2	225	1	CD9 BOVIN
14	58	43.9	246	2	Q6P0W1 BRARE
15	55.5	42.0	236	2	Q7ZTR5 XENLA
16	55	41.7	230	2	Q8AYJ1 ONCMY
17	54	40.9	64	1	NINH BP933
18	54	40.9	64	1	NINH BPVT2
19	54	40.9	64	2	Q8X5E8 9VIRU
20	54	40.9	64	2	Q7AK37 ECO57
21	53.5	40.5	398	2	Q6OKA7 CAERAR
22	53.5	40.5	896	2	Q8IEE9 PLAEMODI
23	53	40.2	642	2	Q6CQB0 KLJULA
24	52	39.4	439	1	YMG3M CAEEL
25	52	39.4	448	2	Q8NET3 HUMAN
26	52	39.4	452	2	Q96PV4 HUMAN
27	52	39.4	455	2	Q53302 RUMFL
28	52	39.4	759	2	Q51433 RUMFL
29	52	39.4	994	2	Q6CEH0 YARLI
30	51.5	39.0	1235	2	Q51783 ENTHI
31	51	38.6	64	1	NINH BP119

32	51	38.6	64	2	Q777W6 9VIRU	Q777W6 bacterioph
33	51	38.6	64	2	Q7Y277 9CAUD	Q7Y277 phage phi 4
34	51	38.6	228	2	Q6DKM9 XENLA	Q6DKM9 xenopus lae
35	51	38.6	298	2	Q8CSN0 STARP	Q8CSN0 staphylococ
36	51	38.6	298	2	Q5HPF1 STABQ	Q5HPF1 staphylococ
37	50	37.9	144	2	Q5Y296 NOCFA	Q5Y296 nocardia fa
38	50	37.9	373	2	Q4XUR1 PLACH	Q4XUR1 plasmodium
39	50	37.9	534	2	Q52F04 MAGGR	Q52F04 magnaporthe
40	50	37.9	1314	2	Q9C499 NEUCR	Q9C499 neurospora
41	50	37.9	1314	2	Q7RVZ9 NEUCR	Q7RVZ9 neurospora
42	50	37.9	1886	2	Q5U5A2 XENLA	Q5U5A2 xenopus lae
43	50	37.9	1905	2	Q91823 XENLA	Q91823 xenopus lae
44	49.5	37.5	206	2	Q5L954 BACFN	Q5L954 bacteroides
45	49.5	37.5	218	2	Q851Q5 ORYSA	Q851Q5 oryza sativ

ALIGNMENTS

RESULT 1

CD9_HUMAN STANDARD; PRT; 227 AA.
AC F21326; Q96ES4;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (Tetra-spanin-29) (Tspan-29).
DE Name=CD9; Synonyms=MIC3, TSPAN29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RX NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.
RA Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E., Gagnon J., Uzan G.;
RT "Molecular cloning of the CD9 antigen. A new family of cell surface proteins.";
RL J. Biol. Chem. 266:117-122(1991).
RN [2]
RX NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=91244846; PubMed=2037603;
RA Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A., Coughlin S.R., Phillips D.R., Jennings L.K.;
RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of multiple membrane-spanning proteins.";
RL J. Biol. Chem. 266:10638-10645(1991).
RN [3]
RX NUCLEOTIDE SEQUENCE.
MEDLINE=9207843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;
RA Miyake M., Koyama M., Seno M., Ikegama S.;
RT "Identification of the motility-related protein (MRP-1), recognized by monoclonal antibody M31-15, which inhibits cell motility.";
RL J. Exp. Med. 174:1347-1354(1991).
RN [4]
RX NUCLEOTIDE SEQUENCE [GENOMIC DNA].
TISSUE=Leukocyte;
RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M., Uzan G., Boucheix C.;
RT "Organization of the human CD9 gene.";
RL Genomics 16:132-138(1993).
RN [5]
RX NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattlesNP8, NHLBI HL6682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
[6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Ovary; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zerbey B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Skalska U., Smalusz D.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RP PROTEIN SEQUENCE OF 1-20.
RC TISSUE=Platelet;
RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;
RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;
RT "Purification and partial characterization of CD9 antigen of human
RT platelets.";
RL FEBS Lett. 264:270-274(1990).
[8]
RP ROLE IN CELL MOTILITY AND METASTASIS.
RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;
RA Ikegama S., Koyama M., Yamaoka M., Sasada R., Miyake M.;
RT "Suppression of cell motility and metastasis by transfection with
RT human motility-related protein (MRP-1/CD9) DNA.";
RL J. Exp. Med. 177:1231-1237(1993).
[9]
RP ROLE IN CELL ADHESION.
RX PubMed=7511626;
RA Masellis-Smith A., Shaw A.R.;
RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B
RT cell adhesion to bone marrow fibroblasts through de novo recognition
RT of fibronectin.";
RL J. Immunol. 152:2768-2777(1994).
[10]
RP ROLE IN GAMETE FUSION.
RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;
RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,
RA Partridge L.J., Monk P.N.;
RT "Structural requirements for the inhibitory action of the CD9 large
RT extracellular domain in sperm/oocyte binding and fusion.";
RL Biochem. Biophys. Res. Commun. 311:208-214(2003).
[11]
RP SUBUNIT.
RX PubMed=14556650; DOI=10.1042/BJ20031037;
RA Kovalev O.V., Yang X., Kolesnikova T.V., Hemler M.E.;
RT "Evidence for specific tetraspanin homodimers: inhibition of
RT palmitoylation makes cysteine residues available for cross-linking.";
RL Biochem. J. 377:407-417(2004).
[12]
RP PHOSPHORYLATION.
RX MEDLINE=93327758; PubMed=7687539;
RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,
RA Aruffo A., Ledbetter J.A.;
RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";
RL EMBO J. 12:2691-2696(1993).
[13]
RP PALMITOYLATION, AND MUTAGENESIS OF CYS-8; CYS-77; CYS-78; CYS-86;
RP CYS-217 AND CYS-218.
RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;
RA Charrin S., Manie S., Oualid M., Billard M., Boucheix C.,

RA Rubinstein E.;
RT "Differential stability of tetraspanin/tetraspanin interactions: role
RT of palmitoylation.";
RL FEBS Lett. 516:139-144(2002).
[14]
RP INTERACTION WITH PTGFRN.
RX MEDLINE=21216740; PubMed=11278880; DOI=10.1074/jbc.M011297200;
RA Charrin S., Le Nacur F., Oualid M., Billard M., Faure G., Hanash S.M.,
RA Boucheix C., Rubinstein E.;
RT "The major CD9 and CD81 molecular partner. Identification and
RT characterization of the complexes.";
RL J. Biol. Chem. 276:14329-14337(2001).
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis.
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with
CC PTGFRN/CD9P1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and
CC epithelial cells.
CC -!- PTM: Protein exists in three forms with molecular masses between
CC 22 and 27 kDa, and is known to carry covalently linked fatty
CC acids.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; S60489; AAC60586.1; -; Genomic DNA.
DR EMBL; S60462; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60463; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60464; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60700; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60699; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60465; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; S60472; AAC60586.1; JOINED; Genomic DNA.
DR EMBL; M38690; AAA80320.1; -; mRNA.
DR EMBL; L34068; AAA59982.1; -; mRNA.
DR EMBL; X60111; CAA42708.1; -; mRNA.
DR EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; L08119; AAA51954.1; ALT_SEQ; Genomic DNA.
DR EMBL; L08120; AAA51955.1; ALT_SEQ; Genomic DNA.
DR EMBL; L08121; AAA51956.1; -; Genomic DNA.
DR EMBL; L08122; AAA51957.1; -; Genomic DNA.
DR EMBL; L08123; AAA51958.1; -; Genomic DNA.
DR EMBL; L08124; AAA51959.1; -; Genomic DNA.
DR EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; AY422198; AAQ87878.1; -; Genomic DNA.
DR EMBL; BC011988; AAH11988.1; -; mRNA.
DR PIR; A46123; A40402.
DR ENSEMBL; ENSG0000010278; Homo sapiens.
DR HGNC; HGNC:1709; CD9.
DR H-InvDB; HIX0010357; -.
DR Reactome; P21926; -.
DR MIM; 143030; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0006928; P:cell motility; IDA.
DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
DR GO; GO:0030913; P:paranodal junction formation; ISS.
DR GO; GO:0030169; P:platelet activation; NAS.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; I.
DR PRINTS; PR00259; TMFOUR.

```

DR PROSITE; PS00421; TM4_1; 1.
KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;
Query Match 100.0%; Score 132; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.9e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDPAIKEVFDNK 25
Db 167 PKKDVLFTFTVKSCPDPAIKEVFDNK 191

RESULT 2
Q5J7W6 HUMAN
ID Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.
AC Q5J7W6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Growth-inhibiting gene 2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Kim J.W.;
RA "Identification of a human growth inhibition gene 2 (GIG2).";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY423720; AAS00483.1; -; mRNA.
SQ SEQUENCE 228 AA; 25416 MW; F68333E0C20611D8 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.9e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDPAIKEVFDNK 25
Db 168 PKKDVLFTFTVKSCPDPAIKEVFDNK 192

RESULT 3
CD9 CERAE
ID CD9 CERAE STANDARD; PRT; 227 AA.
AC P30409;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein) (DRAP27).
DE (DRAP27).
GN Names=CD9;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecoinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1];
RP NUCLEOTIDE SEQUENCE (MRNA).
RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;
RA Mitamura T., Iwamoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,
RA Mekada E.;
RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from
RT vero cells is the monkey homologue of human CD9 antigen: expression of
RT DRAP27 elevates the number of diphtheria toxin receptors on toxin-
RT sensitive cells.";
RL J. Cell Biol. 118:1389-1399(1992).
CC -1- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -1- FUNCTION: Expression of DRAP27 elevates the number of diphtheria
CC toxin receptors on toxin-sensitive cells.

-1- SUBUNIT: Forms both disulfide-linked homodimers and higher
homooligomers as well as heterooligomers with other members of the
tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
(BY similarity).
-1- PFM: Phosphorylated on tyrosine following B-cell activation (By
similarity).
-1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
EMBL; D10726; BAA01569.1; -; mRNA.
FIR; A42929; A42929.
GO; GO:0005887; C:integral to plasma membrane; ISS.
GO; GO:0005515; F:protein binding; ISS.
GO; GO:0007155; P:cell adhesion; ISS.
GO; GO:0006928; P:cell motility; ISS.
GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
GO; GO:0030913; P:paranodal junction formation; ISS.
GO; GO:0030168; P:platelet activation; ISS.
InterPro; IPR000301; Transmem 4.
PFAM; PF00335; Tetraspannin; 1.
PRINTS; PR00259; TMPOUR.
PROSITE; PS00421; TM4_1; 1.
Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
Palmitate; Phosphorylation; Transmembrane.
INIT MET 0
FT TOPO DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO DOM 33 54 Extracellular (Potential).
FT TRANSMEM 55 75 Potential.
FT TOPO DOM 76 86 Cytoplasmic (Potential).
FT TRANSMEM 87 110 Potential.
FT TOPO DOM 111 194 Extracellular (Potential).
FT TRANSMEM 195 220 Potential.
FT TOPO DOM 221 227 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 77 77 S-palmitoyl cysteine (By similarity).
FT LIPID 78 78 S-palmitoyl cysteine (By similarity).
FT LIPID 86 86 S-palmitoyl cysteine (By similarity).
FT LIPID 217 217 S-palmitoyl cysteine (By similarity).
FT LIPID 218 218 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;

Query Match 99.2%; Score 131; DB 1; Length 227;
Best Local Similarity 96.0%; Pred. No. 9.6e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDPAIKEVFDNK 25
Db 167 PKKDVLFTFTVKSCPDPAIKEVFDNK 191

RESULT 4
CD9 RAT
ID CD9 RAT STANDARD; PRT; 225 AA.
AC P40241;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE CD9 antigen.
GN Names=CD9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

```

RN  NUCLEOTIDE SEQUENCE [MRNA].
RP  STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
RC  MEDLINE=95123481; PubMed=7823164;
RA  Kaprielian Z., Cho K.O., Hadjiargyrou M., Patterson P.H.;
RT  "CD9, a major platelet cell surface glycoprotein, is a ROCA antigen
RL  and is expressed in the nervous system.";
CC  J. Neurosci. 15:562-573 (1995).
CC  -!- FUNCTION: Involved in platelet activation and aggregation.
CC  Regulates paranodal junction formation. Required for gamete
CC  fusion. Involved in cell adhesion, cell motility and tumor
CC  metastasis (By similarity).
CC  -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC  homooligomers as well as heterooligomers with other members of the
CC  tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC  (By similarity).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- TISSUE SPECIFICITY: Expressed in the peripheral nervous system.
CC  -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC  similarity).
CC  -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; X76489; CAAS44027.1; -; mRNA.
DR  PIR; I56562; S39262.
DR  Ensembl; ENSRNOG0000019556; Rattus norvegicus.
DR  RGD; 2318; Cd9.
DR  GO; GO:0009986; C:cell surface; IDA.
DR  GO; GO:0005887; C:integral to plasma membrane; ISS.
DR  GO; GO:0005515; F:protein binding; IPI.
DR  GO; GO:0007155; P:cell adhesion; ISS.
DR  GO; GO:0006928; P:cell motility; ISS.
DR  GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR  GO; GO:0030913; P:paranodal junction formation; ISS.
DR  GO; GO:0030168; P:platelet activation; ISS.
DR  InterPro; IPR000301; Transmem 4.
DR  Pfam; PF00335; Tetraspannin; I.
DR  PRINTS; PR00259; TMFOUR.
DR  PROSITE; PS00421; TM_1; 1.
KW  Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW  Palmitate; Phosphorylation; Transmembrane.
FT  INIT MET 0 0
FT  TOPO_DOM 1 11 Cytoplasmic (Potential).
FT  TRANSMEM 12 32 Potential.
FT  TOPO_DOM 33 52 Extracellular (Potential).
FT  TRANSMEM 53 73 Potential.
FT  TOPO_DOM 74 84 Cytoplasmic (Potential).
FT  TRANSMEM 85 108 Potential.
FT  TOPO_DOM 109 192 Extracellular (Potential).
FT  TRANSMEM 193 218 Potential.
FT  TOPO_DOM 219 225 Cytoplasmic (Potential).
FT  LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT  LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT  LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT  LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT  LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT  LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT  CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ  SEQUENCE 225 AA; 25084 MW; 7889619F99A59C9D CRC64;

Query Match 74.2%; Score 98; DB 1; Length 225;
Best Local Similarity 76.0%; Pred. No. 6.5e-06;
Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 PKQVLETTFKVSCPDAIKEVFNK 25
    |||||:|||||:|||||:
DB 165 PKQVLESFQVKSQCPDAIDVFHSK 189
    |||||:|||||:|||||:

```

```

RESULT 5
CD9_FELCA STANDARD; PRT; 225 AA.
ID CD9_FELCA AC P40239;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed:7753050; DOI=10.1016/0161-5890(95)00008-3;
RA Willett B.J., Neil J.C.;
RT "cDNA cloning and eukaryotic expression of feline CD9.";
RL Mol. Immunol. 32:417-423 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Morikawa S.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Involved in platelet activation and aggregation.
CC Regulates paranodal junction formation. Required for gamete
CC fusion. Involved in cell adhesion, cell motility and tumor
CC metastasis (By similarity).
CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
CC homooligomers as well as heterooligomers with other members of the
CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC  -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC  -----
DR  EMBL; I35275; AAA92867.1; -; mRNA.
DR  EMBL; D30786; BAA06452.1; -; mRNA.
DR  GO; GO:0005887; C:integral to plasma membrane; ISS.
DR  GO; GO:0005515; F:protein binding; ISS.
DR  GO; GO:0007155; P:cell adhesion; ISS.
DR  GO; GO:0006928; P:cell motility; ISS.
DR  GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR  GO; GO:0030913; P:paranodal junction formation; ISS.
DR  GO; GO:0030168; P:platelet activation; ISS.
DR  InterPro; IPR000301; Transmem 4.
DR  Pfam; PF00335; Tetraspannin; I.
DR  PRINTS; PR00259; TMFOUR.
DR  PROSITE; PS00421; TM_1; 1.
KW  Antigen; Cell adhesion; Fertilization; Lipoprotein; Palmitate;
KW  Phosphorylation; Transmembrane.
FT  INIT MET 0 0
FT  TOPO_DOM 1 11 Cytoplasmic (Potential).
FT  TRANSMEM 12 32 Potential.
FT  TOPO_DOM 33 52 Extracellular (Potential).
FT  TRANSMEM 53 73 Potential.
FT  TOPO_DOM 74 84 Cytoplasmic (Potential).
FT  TRANSMEM 85 108 Potential.
FT  TOPO_DOM 109 192 Extracellular (Potential).
FT  TRANSMEM 193 218 Potential.
FT  TOPO_DOM 219 225 Cytoplasmic (Potential).
FT  LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT  LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT  LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT  LIPID 84 84 S-palmitoyl cysteine (By similarity).

```

FT LPID 215 215 S-palmitoyl cysteine (By similarity).
 FT LPID 216 216 S-palmitoyl cysteine (By similarity).
 FT CONFLICT 82 82 S -> Y (in Ref. 2).
 SQ SEQUENCE 225 AA; 24927 MW; 5A049774501B03B3 CRC64;

Query Match 72.7%; Score 96; DB 1; Length 225;
 Best Local Similarity 68.0%; Pred. No. 1.3e-05;
 Matches 17; Conservative 4; Mismatches 0; Gaps 0;

QY 1 PKDVLFTFTVKSPDAIKVEFDNK 25
 ||||:||||:||||:||||:||||:||||
 DB 165 PQKDILSSITVKPCPEAIKEVFHNK 189

RESULT 6

CD9_MOUSE
 ID_CD9_MOUSE STANDARD; PRT; 225 AA.
 AC P40240;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen.
 GN Name=CD9;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=BALB/c; TISSUE=Kidney;
 RX MEDLINE=94054345; PubMed=8236164; DOI=10.1016/0049-3848(93)90162-H;
 RA Rubinstein E., Billard M., Plaisance S., Prenant M., Bouchaix C.;
 RT "Molecular cloning of the mouse equivalent of CD9 antigen."
 RL Thromb. Res. 71:377-383 (1993).
 RN [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kirogawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Waki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Varardo R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN [3]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Smailus D.E.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]

ROLE IN GAMETE FUSION.
 RP PubMed=10700183; DOI=10.1038/73502;
 RX Kaji K., Oda S., Shikano T., Ohnuki T., Uemateu Y., Sakagami J.,
 RT Tada N., Miyazaki S., Kudo A.;
 RT "The gamete fusion process is defective in eggs of Cd9-deficient
 RT mice."
 RL Nat. Genet. 24:279-282 (2000).
 RN [5]

ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.
 RP PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;
 RX Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,
 RA Baba H.;
 RT "Tetraspanin protein CD9 is a novel paranodal component regulating
 RT paranodal junctional formation."
 RL J. Neurosci. 24:96-102 (2004).
 RN [6]

FUNCTION AS RECEPTOR FOR PSG17.
 RP PubMed=11805154; DOI=10.1084/jem.20011741;
 RX Waterhouse R., Ha C., Dveksler G.S.;
 RT "Marine CD9 is the receptor for pregnancy-specific glycoprotein 17."
 RL J. Exp. Med. 195:277-282 (2002).

CC -1- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis. Acts as a receptor for PSG17.
 CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGPRN/CD9P1
 CC (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in the peripheral
 CC nervous system.
 CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).

CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR ENBL; L08115; AAA37405.1; -; mRNA.
 DR ENBL; AK002251; BAB21965.1; -; mRNA.
 DR ENBL; AK012793; BAB28473.1; -; mRNA.
 DR ENBL; BC070474; AAH70474.1; -; mRNA.
 DR PIR; I49589; I49589.
 DR Ensembl; ENSMUSG0000030342; Mus musculus.
 DR MGI; MGI:89348; CD9.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; ISS.

DR GO; GO:0006928; P:cell motility; ISS.
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
 DR GO; GO:0030913; P:paranodal junction formation; IDA.
 DR GO; GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraepannin; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.

KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein; Lipoprotein;
 Palmitate; Phosphorylation; Transmembrane.
 FT INIT MET 0 0
 By similarity.

FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT TOPO_DOM 74 84 Cytoplasmic (Potential).
 FT TRANSMEM 85 108 Extracellular (Potential).
 FT TOPO_DOM 109 192 Potential.
 FT TRANSMEM 193 218 Potential.
 FT TOPO_DOM 219 225 Cytoplasmic (Potential).
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 225 AA; 25127 MW; 2BBE408BD7C31BC0 CRC64;

Query Match 71.2%; Score 94; DB 1; Length 225;

Best Local Similarity 68.0%; Pred. No. 2.5e-05;

Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQVLETTFTVKSQCPDAIKEVFNK 25

DB 165 PKQLLESQVQPCPEAISEVFNK 189

RESULT 7

Q8MJ48_PIG PRELIMINARY; PRT; 226 AA.
 ID Q8MJ48;
 AC Q8MJ48;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transmembrane protein CD9.
 GN Name=CD9;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA Heinz M., Huang C.A., Emery D.W., Giovino M.A., LeGuern A.,
 RA Kurilla-Mahon B., Theodore P., Arn J.S., Sykes M., Mulligan R.C.,
 RA Down J.D., Sachs D.H., Goodell M.A.;
 RT "Use of CD9 Expression to Enrich for Porcine Hematopoietic
 Progenitors.";
 RL Exp. Hematol. 0:0-0(2002).
 DR EMBL; AF525029; AAM81376.1; -; mRNA.

DR HSP; P60033; 1G8Q.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000301; Transmem_4.

DR Pfam; PF00335; Tetraepannin; 1.

DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4_1; 1.

KW Transmembrane.

SQ SEQUENCE 226 AA; 25127 MW; 885C244477F95C23 CRC64;

Query Match

Best Local Similarity 67.4%; Score 89; DB 2; Length 226;

Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKQVLETTFTVKSQCPDAIKEVFNK 25

DB 166 PQKDVLLSLPMKPCPEAIEVFNK 190

RESULT 8

Q4REW0_TETNG

ID Q4REW0_TETNG PRELIMINARY; PRT; 227 AA.

AC Q4REW0;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Chromosome 13 SCAP15122, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG00035589001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=99883;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,

RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Bieumont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,

RA Crusad C., Duprat S., Bottier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

the early vertebrate proto-karyotype.";

RL Nature 431:946-957(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is

preliminary data.

DR EMBL; CAAE01015122; CAG13072.1; -; Genomic_DNA.

FT NON_TER 227 227

SQ SEQUENCE 227 AA; 25021 MW; 9CEE48C405F33996 CRC64;

Query Match 65.9%; Score 87; DB 2; Length 227;

Best Local Similarity 60.0%; Pred. No. 0.00027;

Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKQVLETTFTVKSQCPDAIKEVFNK 25

DB 167 PSRLLEQLITKSCPDIAEDVFSK 191

RESULT 9

CD9_PIG

ID CD9_PIG STANDARD; PRT; 225 AA.

AC Q8WQ03;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE CD9 antigen.

GN Name=CD9;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

OC Sus.

OX NCBI_TaxID=9823;

RN	[1]	NUCLEOTIDE SEQUENCE [MRNA].
RP		TISSUE=Smooth muscle;
RC		PubMed=14610355; DOI=10.1159/000074170;
RA		Yubero N., Jimenez-Marin A., Yerbe M., Morera L., Barbancho M.J.,
RA		Illanes D., Garrido J.J.;
RA		"Molecular cloning, expression pattern and chromosomal mapping of pig
RT		CD9 antigen.";
RL		Cytogenet. Genome Res. 101:143-146(2003).
CC	-!	FUNCTION: Involved in platelet activation and aggregation.
CC		Regulates paranodal junction formation. Required for gamete
CC		fusion. Involved in cell adhesion, cell motility and tumor
CC		metastasis (By similarity).
CC	-!	SUBUNIT: Forms both disulfide-linked homodimers and higher
CC		homooligomers as well as heterooligomers with other members of the
CC		tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
CC		(By similarity).
CC	-!	SUBCELLULAR LOCATION: Integral membrane protein.
CC	-!	PTM: Phosphorylated on tyrosine following B-cell activation (By
CC		similarity).
CC	-!	SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC		-----
CC		This Swiss-Prot entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use as long as its content is in no way modified and this statement is not
CC		removed.
CC		-----
DR		EMBL; AY02785; AAL68966.1; -; mRNA.
DR	GO:	GO:0005887; C:integral to plasma membrane; ISS.
DR	GO:	GO:0005515; P:protein binding; ISS.
DR	GO:	GO:0007155; P:cell adhesion; ISS.
DR	GO:	GO:0008928; P:cell motility; ISS.
DR	GO:	GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
DR	GO:	GO:0030913; P:paranodal junction formation; ISS.
DR	GO:	GO:0030168; P:platelet activation; ISS.
DR		InterPro; IPR000301; Transmem 4.
DR	Pfam:	PF00335; Tetraspanin; I.
DR	PRINTS:	PR00259; TMFOUR.
DR	PROSITE;	PS00421; TM4_1; 1.
KW	Antigen;	Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW	Palmitate;	Phosphorylation; Transmembrane.
FT	INIT MET	0 0 By similarity.
FT	TOPO_DOM	1 11 Cytoplasmic (Potential).
FT	TRANSMEM	12 32 Potential.
FT	TOPO_DOM	33 52 Extracellular (Potential).
FT	TRANSMEM	53 73 Potential.
FT	TOPO_DOM	74 84 Cytoplasmic (Potential).
FT	TRANSMEM	85 108 Potential.
FT	TOPO_DOM	109 192 Extracellular (Potential).
FT	TRANSMEM	193 218 Potential.
FT	TOPO_DOM	219 225 Cytoplasmic (Potential).
FT	LIPID	8 8 S-palmitoyl cysteine (By similarity).
FT	LIPID	75 75 S-palmitoyl cysteine (By similarity).
FT	LIPID	76 76 S-palmitoyl cysteine (By similarity).
FT	LIPID	84 84 S-palmitoyl cysteine (By similarity).
FT	LIPID	215 215 S-palmitoyl cysteine (By similarity).
FT	LIPID	216 216 S-palmitoyl cysteine (By similarity).
FT	CARBOHYD	49 49 N-linked (GLCNAC...) (Potential).
FT	CARBOHYD	50 50 N-linked (GLCNAC...) (Potential).
SQ	SEQUENCE	225 AA; 25070 MW; PF280FE39BC11545 CRC64;
	Query Match	65.2%; Score 86; DB 1; Length 225;
	Best Local Similarity	60.0%; Pred. No. 0.00037;
	Matches 15; Conservative	5; Mismatches 5; Indels 0; Gaps 0;

QGNWG7_BRARE PRELIMINARY; PRT; 227 AA.
QGNWG7;
AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein cd9.
DE Name=cd9;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Wild-type; Tissus=Eye, and Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RC Director MGC Project;
RA Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Wild-type; Tissus=Eye;
RC Director MGC Project;
RA Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC067597; AAH67597.1; -; mRNA.
DR EMBL; BC059691; AAH59691.1; -; mRNA.
DR ZFIN; ZDB-GENE-030131-1175; cd9.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem.4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25116 MW; 26E5BC25F4E638B8 CRC64;

Query Match 63.6%; Score 84; DB 2; Length 227;
Best Local Similarity 60.0%; Pred. No. 0.00073;
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAIKEVFDNK 25
|||.: : ||||| |||||
DB 167 PKKEGLDNLIIKCPDAIDEVFNK 191

RESULT 11
Q9IBC9_CHICK
ID Q9IBC9_CHICK PRELIMINARY; PRT; 224 AA.
AC Q9IBC9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 26, Last annotation update)

DT	01-OCT-2000	(TREMBLrel. 15, Created)
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)

DR GO: 0006928; P: cell motility; ISS.
DR GO: 0007342; P: fusion of sperm to egg plasma membrane; ISS.
DR GO: 0030913; P: paranodal junction formation; ISS.
DR GO: 0030168; P: platelet activation; ISS.
DR InterPro: IPR000301; Transmem 4.
DR Pfam: PF00335; Tetraspannin; 1.
DR PRINTS: PR00259; TMFOUR.
DR PROSITE: PS00421; TM4 1; 1.
DR Antigen: Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Transmembrane.
FT INIT MET 0 By similarity.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSDOM 12 32 Potential.
FT TOPO_DOM 33 52 Extracellular (Potential).
FT TRANSDOM 53 73 Potential.
FT TOPO_DOM 74 84 Cytoplasmic (Potential).
FT TRANSDOM 85 108 Potential.
FT TOPO_DOM 109 192 Extracellular (Potential).
FT TRANSDOM 193 218 Potential.
FT TOPO_DOM 219 225 Cytoplasmic (Potential).
FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 225 AA; 25127 MW; ECE67DB91A0859E7 CRC64;
Query Match 46.2%; Score 61; DB 1; Length 225;
Best Local Similarity 36.0%; Pred. No. 1.7;
Matches 9; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
QY 1 PKKDVLETFVTKSCPDPAKEVFDNK 25
Db 165 PPKNLIDSLKTRCPCEAIDIFRSK 189
RESULT 14
Q6P0W1 BRARE
ID Q6P0W1 BRARE PRELIMINARY; PRT; 246 AA.
AC Q6P0W1;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TEMBLrel. 30, Last annotation update)
DE Hypothetical protein zgc:65811.
GN CRPNames=zgc:65811;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney, and Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC TISSUE=Whole;
RP Director MGC Project;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065427; AAH65427.1; -; mRNA.
DR EMBL; BC056541; AAH56541.1; -; mRNA.
DR ZFIN; ZDB-GENE-040426-1428; zgc:65811.
DR GO: 0016021; C: integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 26087 MW; 73B6FALCAS9ABDC5 CRC64;
Query Match 43.9%; Score 58; DB 2; Length 246;
Best Local Similarity 41.7%; Pred. No. 5.1;
Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 PKKDVLETFVTKSCPDPAKEVFDN 24
Db 165 PDGNILKQLTFPSPSVIKDVFNS 188
RESULT 15
Q7ZTR5 XENLA
ID Q7ZTR5 XENLA PRELIMINARY; PRT; 236 AA.
AC Q7ZTR5;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TEMBLrel. 30, Last annotation update)
DE Cd81-prov protein.
GN Name=cdb1-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo, and Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC TISSUE=Embryo, and Lung;
RP NUCLEOTIDE SEQUENCE.

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:03:51 ; Search time 63.3333 Seconds
(without alignments)
124.876 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95
Sequence: 1 PKQVLETFVKSCPAI 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	ADJ57563	Adj57563 Human CD9
2	95	100.0	25	ADJ57562	Adj57562 Human CD9
3	95	100.0	227	AAR86834	Aar86834 Human CD9
4	95	100.0	227	ABB78366	Abb78366 Amino aci
5	95	100.0	227	AAE14636	Aae14636 Human CD9
6	95	100.0	227	ABU05057	Abu05057 Human exp
7	95	100.0	227	ABU05060	Abu05060 Human exp
8	95	100.0	227	ABW00436	Abw00436 Human CD9
9	95	100.0	227	ADK69862	Adk69862 Human CD9
10	95	100.0	227	ADI19366	Adi19366 Human CD9
11	95	100.0	227	AEA99005	Aea99005 Human CD9
12	95	100.0	228	AAR27525	Aar27525 Metaastai
13	95	100.0	228	ABBA4581	Abba4581 Human wou
14	95	100.0	228	ABU05059	Abu05059 Human exp
15	95	100.0	228	ABU05052	Abu05052 Human exp
16	95	100.0	228	ABU05048	Abu05048 Human exp
17	95	100.0	228	ABU05056	Abu05056 Human exp
18	95	100.0	228	ABU05049	Abu05049 Human exp
19	95	100.0	228	ABU05050	Abu05050 Human exp
20	95	100.0	228	ABU05053	Abu05053 Human exp
21	95	100.0	228	ABW01519	Abw01519 Protein #
22	95	100.0	228	ADG89037	Adg89037 TR1278. 1
23	95	100.0	228	ADG32002	Adg32002 Human hom
24	95	100.0	228	ADJ57558	Adj57558 Human CD9

25	95	100.0	228	8	ADL26782	Adl26782 Human CD9
26	95	100.0	228	8	ADL82853	Adl82853 Human PRO
27	95	100.0	228	8	ADP23088	Adp23088 PRO polyp
28	95	100.0	228	8	ADR73450	Adr73450 Human CD9
29	95	100.0	228	9	ADV70263	Adv70263 Tumor-ass
30	95	100.0	228	9	ADV97163	Adv97163 Human CD9
31	95	100.0	228	9	ADY19604	Ady19604 PRO polyp
32	95	100.0	228	9	ADY14362	Ady14362 PRO polyp
33	95	100.0	228	9	AE898450	Aeb98450 Human CD9
34	95	100.0	228	3	AA843936	Aab43936 Human can
35	95	100.0	275	4	AAG75156	Aag75156 Human col
36	95	100.0	275	6	ABU05055	Abu05055 Human exp
37	95	100.0	275	6	ABU05054	Abu05054 Human exp
38	95	100.0	454	4	ABG14067	Abg14067 Novel hum
39	87	91.6	79	2	AAW35851	Aaw35851 Human CD9
40	87	91.6	79	6	ABU05058	Abu05058 Human exp
41	79	83.2	226	7	ADB85281	Adb85281 Rat G9 eu
42	67	70.5	226	4	ABB44580	Abb44580 Mouse wou
43	67	70.5	226	5	ABB57234	Abb57234 Mouse isc
44	67	70.5	226	9	ADV25799	Adv25799 Mouse CD9
45	67	70.5	226	9	AEA55045	Aea55045 Mouse CD9

ALIGNMENTS

RESULT 1
ADJ57563
ID ADJ57563 standard; peptide; 18 AA.
XX
AC ADJ57563;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human CD9 fibronectin-binding domain peptide fragment.
XX
KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
KW haemostatic; antiangiogenic; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004007685-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-US022050.
XX
PR 12-JUL-2002; 2002US-0395864P.
XX (UYTE-) UNIV TENNESSEE RES FOUND.
XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM,
XX Crosseno JT, Lu Y;
XX WPI; 2004-122924/12.
XX Interfering with CD9 binding to fibronectin by binding a fibronectin-binding domain of the CD9 protein or polypeptide, useful in treating thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis and cancers.
XX Claim 7; SEQ ID NO 6; 126pp; English.
XX The present sequence is that of a peptide fragment from the fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an antibody that binds to it, is used in claimed methods for: interfering with CD9 binding to fibronectin; modifying adhesion, motility or spreading of a CD9-expressing cell on fibronectin; inhibiting proliferation or survival of CD9-expressing cells; modifying pericellular fibronectin matrix assembly; modifying invasiveness of a cell through a collagen and/or laminin matrix; and modifying cell-to-cell interaction. The methods are based on the finding that increased CD9 expression is implicated in (i) decreased adhesiveness of cells to extracellular matrix (via alphas5-beta-1

CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 95; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFYKSCPDAL 18
 |||||
 DB 1 PKKDVLETFYKSCPDAL 18

RESULT 2
 ADJ57562
 ID ADJ57562 standard; peptide; 25 AA.
 XX
 AC ADJ57562;

XX 06-MAY-2004 (first entry)

XX Human CD9 fibronectin-binding domain peptide fragment.

XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
 KW haemostatic; antiangiogenic; cytostatic.

XX Homo sapiens.

XX WO2004007685-A2.

XX 22-JAN-2004.

XX 14-JUL-2003; 2003WO-US022050.

XX 12-JUL-2002; 2002US-039864P.

XX (UYTE-) UNIV TENNESSEE RES FOUND.

XX Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;
 PI Crossno JT, Lu Y;

XX WPI; 2004-122924/12.

XX Interfering with CD9 binding to fibronectin by binding a fibronectin-
 CC binding domain of the CD9 protein or polypeptide, useful in treating
 CC thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
 CC and cancers.

XX Claim 7; SEQ ID NO 5; 126pp; English.

XX The present sequence is that of a peptide fragment from the fibronectin-
 CC binding domain of human CD9 ADJ57562. The peptide, or an antibody that
 CC binds to it, is used in claimed methods for: interfering with CD9 binding
 CC to fibronectin; modifying adhesion, motility or spreading of a CD9-
 CC expressing cell on fibronectin; inhibiting proliferation or survival of
 CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
 CC modifying invasiveness of a cell through a collagen and/or laminin matrix
 CC ; and modifying cell-to-cell interaction. The methods are based on the
 CC finding that increased CD9 expression is implicated in (i) decreased
 CC adhesiveness of cells to extracellular matrix (via alpha5-beta1
 CC integrin) and/or decreased cell invasiveness and/or decreased
 CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
 CC motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.

CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
 XX
 SQ Sequence 25 AA;

Query Match 100.0%; Score 95; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFYKSCPDAL 18
 |||||
 DB 1 PKKDVLETFYKSCPDAL 18

RESULT 3
 AAR86834
 ID AAR86834 standard; protein; 227 AA.
 XX
 AC AAR86834;

XX 12-JUL-1996 (first entry)

XX Human CD9 sequence.

XX CD9 antigen; stimulated T cell; antibody; ligand; proliferation;
 KW monoclonal antibody; ES5.2D8; 27 kD accessory protein; epitope;
 KW immune response; cancer; infectious disease; growth factor.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 51
 FT Modified-site 52

FT /note= "Potential N-linked glycosylation site"

FT /note= "Potential N-linked glycosylation site"

FT Domain 111..194

FT /note= "Extracellular domain"

FT Domain 195..220

FT /note= "Transmembrane domain"

FT Domain 221..227

FT /note= "Cytoplasmic domain"

XX WO9533823-A1.

XX 14-DEC-1995.

XX 01-DEC-1994; 94WO-US013782.

XX 03-JUN-1994; 94US-00253751.

XX 03-JUN-1994; 94US-00253964.

XX (USNA) US SEC OF NAVY.

XX (UNMI) UNIV MICHIGAN.

XX (REPK) REPLIGEN CORP.

XX (DAND) DANA FARBER CANCER INST INC.

XX June CH, Thompson CB, Nabel G, Gray GS, Rennert PD, Freeman GJ;

XX WPI; 1996-040230/04.

XX Selectively inducing CD8 positive T cell proliferation - by activating
 CC the T cells and stimulating CD9 cell surface ligand, useful for
 CC immuno:therapy of, e.g. cancer.

XX Example 10; Page 38-39; 79pp; English.

XX This sequence represents CD9 from the surface of stimulated T cells. The
 CC antigen at residues 31-37 of human CD9 (see AAR86832) is bound by an
 CC antibody or other ligand to stimulate the T cell population to
 CC proliferate and expand leading to a 100- to 10000-fold increase in cell
 CC number compared to the original population. The antigenic sequence fits

CC the generic sequence given in AAR86827. This epitope is recognised by the
 CC monoclonal antibody (MAB) ES5.2D8. CD9 is a 27 kD accessory protein found
 CC on activated T cells. The epitope was recognised by screening a phage
 CC display library. Selective proliferation of an antigen-specific T cell
 CC population is useful in cases where the immune response is to be up
 CC regulated, e.g. in the treatment of cancer or infectious diseases. By
 CC causing proliferation of the T cell population by stimulating T cell
 CC epitope removes the need for exogenous growth factors or accessory cells
 XX

XX Sequence 227 AA;

Query Match 100.0%; Score 95; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAI 18
 |||||
 DB 167 PKQVLETFVTKSCPDAI 184

RESULT 4

ID ABB78366
 AC ABB78366 standard; protein; 227 AA.

XX ABB78366;

XX 16-DEC-2002 (first entry)

XX Amino acid sequence of CD9.

XX T cell; T cell proliferation; infectious disease; cancer; immunotherapy;
 immunotherapy; CD9.

XX Homo sapiens.

XX US2002115214-A1.

XX 22-AUG-2002.

XX 26-JAN-1996; 96US-00592711.

XX 23-NOV-1988; 88US-00275433.

XX 07-APR-1992; 92US-00864805.

XX 07-APR-1992; 92US-00864807.

XX 07-APR-1992; 92US-00864866.

XX 04-JUN-1993; 93US-00073223.

XX 03-JUN-1994; 94US-00253964.

XX 10-MAR-1995; 95US-00403253.

XX 04-MAY-1995; 95US-00435816.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABE/) NABEL G J.

XX (GRAY/) GRAY G S.

XX (RENN/) RENNERT P D.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2002-712476/77.

XX Inducing a population of T cells to proliferate, by activating population
 of T cells and stimulating an accessory molecule on the surface of the T
 cells with a ligand which binds the accessory molecule.
 XX Example 10; Page 25; 88pp; English.

CC The method is useful for inducing proliferation of T cells, for use in
 CC treatment of infectious disease, cancer and immunotherapy. The method
 CC allows for the expansion of a population of T cells in numbers sufficient
 CC to reconstitute an individual's total CD4+ or CD8+ T cell population.
 CC The resulting T cell population can be genetically transduced and used
 CC for immunotherapy or can be used in methods of in vitro analyses of
 CC infectious agents. A population of tumour-infiltrating lymphocytes can be
 CC obtained from an individual afflicted with cancer and the T cells
 CC stimulated to proliferate to sufficient numbers. The resulting T cell
 CC population can be genetically transduced to express tumour necrosis
 CC factor (TNF) or other factor and restored to the individual. CD4+ T cells
 CC expanded by this method are useful in the treatment of HIV infection in
 CC an individual. The present sequence represents CD9, an antigen present on
 CC the surface of activated T cells
 XX

SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 5; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAI 18

|||||
 DB 167 PKQVLETFVTKSCPDAI 184

RESULT 5

AAE14636

ID AAE14636 standard; protein; 227 AA.

XX AAE14636;

XX 16-JUL-2002 (first entry)

XX Human CD9 antigen.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
 immunotherapy; human immunodeficiency virus; HIV infection; cytokine;
 human; CD9 antigen.

XX Homo sapiens.

XX US6352694-B1.

XX 05-MAR-2002.

XX 10-MAR-1995; 95US-00403253.

XX 03-JUN-1994; 94US-00253964.

XX (GEWY) GENETICS INST INC.

XX (UNMI) UNIV MICHIGAN.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
 WPI; 2002-314696/35.

XX Inducing T cell population to proliferate, useful in cancer therapy,
 comprises activating T cells by contacting T cells in vitro with
 immobilized anti-CD3 antibody and stimulating accessory molecule on T
 cell surface.

XX Example 10; Col 42; 71pp; English.

XX The invention relates to a method of inducing T cell population to
 CC proliferate for use in therapy comprising activating T cells by
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
 CC on solid phase surface, and stimulating accessory molecule on T cell
 CC surface in vitro with anti-CD28 antibody, or stimulatory form of natural
 CC ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a
 CC population of T cells to proliferate in sufficient numbers for use in
 CC therapy e.g., for treating cancer or an infectious disease. The method
 CC can be used to selectively expand the population of CD28⁺, CD4⁺, CD8⁺,

CC CD28RA⁺ or CD28RO⁺ T cells for immunotherapy. The T cell population
 CC resulting by the method can be genetically transduced and used for
 CC immunotherapy or can be used for in vitro analysis of infectious agents
 CC such as human immunodeficiency virus (HIV). Proliferation of a population
 CC of CD4⁺ T cells obtained from an individual infected with HIV can be
 CC achieved and the cells rendered resistant to HIV infection. Following the
 CC expansion of the T cells to sufficient numbers, the expanded T cells are
 CC restored to the individual. Also CD4⁺ T cells expanded by the above
 CC mentioned is useful for treating HIV infection in an individual. A
 CC population of tumour-infiltrating lymphocytes can be obtained from an
 CC individual afflicted with cancer and the T cells stimulated to
 CC proliferate to sufficient numbers and restored to the individual. The
 CC supernatants from cultures of T cells expanded from above mentioned
 CC method are useful as a rich source of cytokines and can be used to
 CC sustain T cells in vivo or ex vivo. Stimulating and expanding a
 CC population of antigen specific T cells are useful in therapeutic
 CC conditions where it is desirable to upregulate an immune response. The T
 CC cell proliferation occurs in the absence of exogenous growth factors or
 CC accessory cells. The present sequence is human CD9 antigen which is
 CC expressed on surface of activated T cells
 XX
 SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 5; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSCPDAI 18
 |||||
 Db 167 PKQVLETFVKSCPDAI 184

RESULT 6
 ABU05057
 ID ABU05057 standard; protein; 227 AA.

AC ABU05057;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1723.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

PI Chicx RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX Example 2; SEQ ID NO 1723; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 227 AA;

Query Match 100.0%; Score 95; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVKSCPDAI 18
 |||||
 Db 167 PKQVLETFVKSCPDAI 184

RESULT 7

ABU05060
 ID ABU05060 standard; protein; 227 AA.

AC ABU05060;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1726.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

PI Chicx RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX PS Example 2; SEQ ID NO 1726; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a

XX CC fragment of a kinase, phosphatase, protease, or protease inhibitor,

XX CC transporter, cytoskeletal protein, receptor or transcription factor. The

XX CC polypeptide is useful as an immunogenic composition for eliciting in a

XX CC mammal an immunogenic response directed against any of the purified

XX CC polypeptide. The purified polypeptide, or the antibody that binds to this

XX CC polypeptide, is useful for treating cancer. The polypeptide is also

XX CC useful for identifying compounds that binds to a naturally processed

XX CC class I or class II MHC-binding polypeptide. The polypeptides and

XX CC polynucleotides are particularly useful for treating or preventing

XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

XX CC lymphoma or leukaemia. These are also useful for screening agents for

XX CC treating the above mentioned diseases. This sequence represents an

XX CC expressed protein tag (EPT) isolated from human tissue for translational

XX CC profiling. Note: This sequence does not appear in the printed

XX CC specification but was obtained in electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
 |||||

DB 167 PKKDVLETFVKSCPDAI 184

RESULT 8

ID AEW00436 standard; protein; 227 AA.

XX AC AEW00436;

XX DT 15-JAN-2004 (first entry)

XX DE Human CD9 antigenic protein.

XX KW HIV infection; human immunodeficiency virus; therapy; antigen; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 111..194

FT /note= "Extracellular domain"

FT Domain 195..220

FT /note= "Transmembrane domain"

FT Domain 221..227

FT /note= "Cytoplasmic domain"

XX US2003099643-A1.

XX PN 29-MAY-2003.

XX PD 08-JUL-1999; 99US-00350202.

XX PP 23-NOV-1988; 88US-00275433.

XX PR 22-NOV-1989; 89WO-US005304.

XX PR 07-APR-1992; 92US-00864805.

XX PR 07-APR-1992; 92US-00864807.

XX PR 07-APR-1992; 92US-00864866.

XX PR 04-JUN-1993; 93US-00073223.

XX PR 03-JUN-1994; 94US-00253694.

XX PR 10-MAR-1995; 95US-00403253.

XX (JUNE/) JUNE C H.

XX (THOM/) THOMPSON C B.

XX (NABEL/) NABEL G J.

XX (GRAY/) GRAY G S.

PA (RENN/) RENNERT P D.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2003-801206/75.

XX Treating HIV infection in individual by isolating T cells from

XX leukocytes, contacting T cells with anti-CD3 antibody for T cell

XX proliferation, separating antibody from T cells, monitoring proliferation

XX of T cells.

XX Example 10; Page 23; Opp; English.

XX The present invention relates to a novel method of treating human

XX immunodeficiency virus (HIV) infection in an individual. The method

XX involves isolating population of CD4 T cells from leukocytes, contacting

XX population of CD4+ T cells with an anti-CD3 antibody for stimulating T

XX cell proliferation, separating antibody from T cells, monitoring

XX proliferation of T cells, restimulating T cells with antibody and

XX restoring T cells to individual. The present sequence is human CD9

XX antigenic protein. This sequence is used to illustrate the method of the

XX invention

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 95; DB 7; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18

|||||

DB 167 PKKDVLETFVKSCPDAI 184

RESULT 9

ID ADK69862

XX ADK69862 standard; protein; 227 AA.

XX AC ADK69862;

XX DT 06-MAY-2004 (first entry)

XX DE Human CD9 protein.

XX KW CD28-associated signal; immunotherapy; infectious disease; cancer;

XX leukopheresis; human.

XX OS Homo sapiens.

XX PN US6534055-B1.

XX PD 18-MAR-2003.

XX PF 04-MAY-1995; 95US-00435816.

XX PR 07-APR-1992; 92US-00864805.

XX PR 07-APR-1992; 92US-00864807.

XX PR 07-APR-1992; 92US-00864866.

XX PR 04-JUN-1993; 93US-00073223.

XX PR 03-JUN-1994; 94US-00253694.

XX PR 10-MAR-1995; 95US-00403253.

XX (GEMY) GENETICS INST INC.

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX WPI; 2003-531074/50.

XX Expanding T cell populations, useful for preparing renewable sources of T

XX cells (e.g. CD4+) for immunotherapy or diagnostics, by stimulating a CD28

XX -associated signal on the surface of the cells with an anti-CD28

XX antibody, B7-1 or B7-2.

XX Example 10; SEQ ID NO 6; 82pp; English.

XX

CC The invention relates to a method for expanding a population of T cells

CC to about 100-10000-fold over the original T cell population, or to about

CC 10 log 1.0 to 12 log 1.2. The method comprises stimulating a CD28-

CC associated signal on the surface of the T cells with agent comprising an

CC anti-CD28 antibody, B7-1 or B7-2. The method is useful for inducing a

CC population of T cells (e.g. CD4+, CD28+, CD8+, CD28RA+ or CD28RO+ T

CC cells) to proliferate. The method is particularly useful for preparing a

CC renewable source of CD4+ T cells. The expanded T cell population can be

CC genetically transduced, and used for immunotherapy to treat a variety of

CC human diseases (e.g. infectious diseases or cancer), or used in

CC diagnostic protocols. T cells were obtained from leukopheresis of a

CC normal donor, and purified with FICOLL density gradient centrifugation,

CC followed by magnetic immunobead sorting. The present sequence is CD9 used

CC in the exemplification of the invention.

XX

XX Sequence 227 AA;

SQ

Query Match 100.0%; Score 95; DB 7; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PKKDVLETTFTVKSCPDAl 18

Db 167 PKKDVLETTFTVKSCPDAl 184

|||||

RESULT 10

AD119366

ID AD119366 standard; protein; 227 AA.

XX

XX AD119366;

XX

DT 15-APR-2004 (first entry)

XX

XX Human CD9 protein.

XX

XX T cell; immunotherapy; therapy; HIV infection; cancer;

KW infectious disease; cytostatic; antimicrobial; human.

KW

XX Homo sapiens.

XX

XX US2004001829-A1.

PN

XX

PD 01-JAN-2004.

XX

XX

PF 17-MAR-2003; 2003US-00390330.

XX

XX 23-NOV-1988; 88US-00275433.

PR

XX 22-NOV-1989; 89WO-US005304.

PR

XX 07-APR-1992; 92US-00864805.

PR

XX 07-APR-1992; 92US-00864807.

PR

XX 07-APR-1992; 92US-00864866.

PR

XX 04-JUN-1993; 93US-00073223.

PR

XX 03-JUN-1994; 94US-00253964.

PR

XX 10-MAR-1995; 95US-00403253.

PR

XX 04-MAY-1995; 95US-00435816.

XX

XX (JUNE/) JUNE C H.

PA

XX (THOM/) THOMPSON C B.

PA

XX (NABE/) NABEL G J.

PA

XX (GRAY/) GRAY G S.

PA

XX (RENN/) RENNERT P D.

PA

XX

PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX

XX WPI; 2004-061648/06.

XX

XX Inducing a population of T cells to proliferate, for immunotherapy or

XX treating HIV infection, cancer or infectious disease, comprises

PT activating a population of T cells and stimulating an accessory molecule

PT on the surface of the T cells.

PT

XX Example 10; SEQ ID NO 6; 80pp; English.

XX

CC The invention relates to a method for inducing a population of T cells to

CC proliferate. The method comprising activating a population of T cells,

CC and stimulating an accessory molecule on the surface of the T cells with

CC a ligand that binds the accessory molecule. The invention is useful for

CC immunotherapy, for treating HIV infection, cancer or infectious disease,

CC or in diagnostic applications. The present sequence is human CD9 protein.

XX

XX Sequence 227 AA;

SQ

Query Match 100.0%; Score 95; DB 8; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PKKDVLETTFTVKSCPDAl 18

Db 167 PKKDVLETTFTVKSCPDAl 184

|||||

RESULT 11

AEA89005

ID AEA89005 standard; protein; 227 AA.

XX

XX AEA89005;

XX

DT 25-AUG-2005 (first entry)

XX

XX Human CD9 antigenic protein, SEQ ID NO: 6.

XX

XX Cell therapy; immune stimulation; immunotherapy; diagnosis;

KW infectious disease; antimicrobial; infection; cancer; cytostatic;

KW neoplasm; CD9; antigen.

KW

XX Homo sapiens.

XX

XX US6905681-B1.

PN

XX

PD 14-JUN-2005.

XX

XX 08-JUL-1999; 99US-00349915.

XX

XX 03-JUN-1994; 94US-00253964.

PR

XX 10-MAR-1995; 95US-00403253.

PR

XX (GEMY) GENETICS INST INC.

PA (UNMI) UNIV MICHIGAN.

PA (USNA) US SEC OF NAVY.

XX

XX June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

XX

XX WPI; 2005-464777/47.

DR

XX

XX Ex vivo proliferation of T cell population for use in therapy, involves

PT contacting population of T cells with surface having anti-CD3 antibody

PT and anti-CD28 antibody for activating T cells and stimulating activated T

PT cells, respectively.

PT

XX

XX Example 10; SEQ ID NO 6; 76pp; English.

XX

XX The present invention relates to a method of including ex vivo

CC proliferation of a population of T cells to sufficient numbers for use in

CC therapy. The method involves contacting population of T cells with

CC surface having anti-CD3 antibody and anti-CD28 antibody for activating T

CC cells and stimulating activated T cells, respectively. The invention is

CC useful for treating cancer and infectious disease and also useful in cell

CC therapy. The present sequence is the human CD9 antigenic protein. This

CC sequence is bound by an ES5.2D8 monoclonal antibody, which is to be used

CC to stimulate a CD8+ T cell population.

XX

XX Sequence 227 AA;

SQ

Query Match 100.0%; Score 95; DB 9; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAL 18
 DB 167 PKKDVLFTFTVKSCPDAL 184

RESULT 12
 AAR27525
 ID AAR27525 standard; protein; 228 AA.
 XX AC
 XX AAR27525;
 XX 25-MAR-2003 (revised)
 DT 05-MAR-1993 (first entry)
 XX XX
 DE Metastasis controlling peptide.
 XX M31-15 monoclonal antibody; cancer cell motility; prophylaxis; treatment;
 KW lung; glioblastoma.
 XX Homo sapiens.
 OS EP508417-A2.
 PN 14-OCT-1992.
 PD 09-APR-1992; 92EP-00106093.
 PF 12-APR-1991; 91JP-00079996.
 PR 17-APR-1991; 91JP-00085396.
 PR 07-FEB-1992; 92JP-00023221.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA (MIYA/) MIYAKE M.
 XX Ikeyama S, Koyama M, Senoo M, Miyake M;
 PI WPI; 1992-341723/42.
 XX N-PSDB; AAQ29182.
 DR New monoclonal antibody M31-15 specific for metastasis-controlling
 PT peptide - useful for treating and preventing cancer and metastasis.
 XX Claim 7; Fig 4; 34pp; English.
 PS The sequence is that of a cancer cell surface protein which is capable of
 CC suppressing the motility of cancer cells. It is specifically recognised
 CC by the monoclonal (Mab) antibody M13-15 which is useful for suppressing
 CC cancer metastasis. The polypeptide and Mab M31-15 are therefore useful in
 CC the prophylaxis and treatment of cancer, e.g. lung, glioblastoma and
 CC other metastatic cancers. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 228 AA;
 SQ

Query Match 100.0%; Score 95; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAL 18
 DB 168 PKKDVLFTFTVKSCPDAL 185

RESULT 13
 ABB44581
 ID ABB44581 standard; protein; 228 AA.
 XX AC
 XX ABB44581;
 XX DT 25-JAN-2002 (first entry)

XX Human wound healing related polypeptide SEQ ID NO 38.
 DE Human; mouse; vulnery; dermatological; skin disorder; wound healing;
 KW gene therapy.
 XX Homo sapiens.
 OS CA2325226-A1.
 PN 17-MAY-2001.
 PD 16-NOV-2000; 2000CA-02325226.
 PF 17-NOV-1999; 99DE-01055349.
 PR 17-DEC-1999; 99US-0172511P.
 PR 20-JUN-2000; 2000DE-01030149.
 XX (SWIT-) SWITCH BIOTECH AG.
 PA Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;
 PI WPI; 2001-433142/47.
 DR Use of novel polypeptide or its variant or nucleic acid encoding the
 PT polypeptide for diagnosing and/or preventing and/or treating skin
 PT disorders and/or treatment in wound healing or for identifying active
 PT substances.
 XX Disclosure; Page 193-194; 265pp; English.
 PS The invention relates to the use of a polypeptide (ABBA44544-ABBA44601,
 CC ABBA44606-ABBA44623) or its variant or encoding nucleic acid (ABBA81990-
 CC ABBA81995, ABBA82016-ABBA82032) with vulnery and/or dermatological
 CC activity for the diagnosis, prevention and treatment of skin disorders
 CC and treatment in wound healing or for the identification of
 CC pharmacologically active substances. The nucleic acids are useful in gene
 CC therapy. Note: The printed sequence listing for this specification was
 CC incomplete, terminating part way through SEQ ID NO 106. The remaining
 CC data was obtained from EPO data for an equivalent patent (EP1114862)
 XX Sequence 228 AA;
 SQ

Query Match 100.0%; Score 95; DB 4; Length 228;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAL 18
 DB 168 PKKDVLFTFTVKSCPDAL 185

RESULT 14
 ABU05059
 ID ABU05059 standard; protein; 228 AA.
 XX AC
 XX ABU05059;
 XX DT 29-JAN-2003 (first entry)
 XX Human expressed protein tag (EPT) #1725.
 DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX Homo sapiens.
 OS WO200278524-A2.
 PN 10-OCT-2002.
 PD

```

XX PF 28-MAR-2002; 2002WO-US009671.
XX XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX XX
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX XX
XX DR WPI; 2003-040607/03.
XX XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX XX
XX PS Example 2; SEQ ID NO 1725; 134pp; English.
XX CC
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;

Query Match 100.0%; Score 95; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAI 18
DB 168 PKKDVLFTTVKSCPDAI 185

RESULT 15
ABU05052
ID ABU05052 standard; protein; 228 AA.
XX AC ABU05052;
XX XX
XX DT 29-JAN-2003 (first entry)
XX XX
XX DE Human expressed protein tag (EPT) #1718.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX XX
XX PN WO200278524-A2.
XX XX
XX PD 10-OCT-2002.

```

```

XX PF 28-MAR-2002; 2002WO-US009671.
XX XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX XX
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX XX
XX DR WPI; 2003-040607/03.
XX XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX XX
XX PS Example 2; SEQ ID NO 1718; 134pp; English.
XX CC
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 228 AA;

Query Match 100.0%; Score 95; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAI 18
DB 168 PKKDVLFTTVKSCPDAI 185

Search completed: January 20, 2006, 17:16:07
Job time : 63.3333 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:10:37 ; Search time 12.6667 Seconds
(without alignments)
117.486 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95
Sequence: 1 PKKDVLETFVKSCPDAl 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/PGTUS COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	29	1	US-08-254-493-6
2	95	100.0	29	1	US-08-408-222B-6
3	95	100.0	227	1	US-08-254-493-1
4	95	100.0	227	1	US-08-253-751-6
5	95	100.0	227	1	US-08-453-925-6
6	95	100.0	227	2	US-08-403-253A-6
7	95	100.0	227	2	US-08-435-816A-6
8	95	100.0	227	2	US-09-350-202-6
9	95	100.0	227	2	US-08-592-711-6
10	95	100.0	227	2	US-09-349-915B-6
11	95	100.0	228	1	US-08-408-222B-1
12	87	91.6	79	2	US-08-630-172-8
13	87	91.6	79	2	US-09-375-419-8
14	47	49.5	1018	1	US-08-452-052-2
15	43	45.3	542	1	US-08-701-380-2
16	43	45.3	542	2	US-09-032-365A-13
17	43	45.3	1334	1	US-08-996-545-2
18	43	45.3	1334	2	US-09-328-320-2
19	43	45.3	1334	2	US-09-758-828-2
20	42	44.2	68	2	US-09-583-110-3271
21	42	44.2	97	2	US-10-039-836A-2
22	42	44.2	100	2	US-10-107-433-4841
23	42	44.2	160	2	US-09-949-016-10023
24	41	43.2	180	2	US-09-270-767-48380
25	41	43.2	520	2	US-10-104-047-2424
26	41	43.2	520	2	US-10-104-047-2730
27	40	42.1	103	2	US-09-603-208A-194

28	40	42.1	276	2	US-09-328-352-5682	Sequence 5682, Ap
29	40	42.1	411	2	US-09-248-796A-15503	Sequence 15503, A
30	40	42.1	456	2	US-09-492-027-2	Sequence 2, Appli
31	40	42.1	690	2	US-09-902-540-10349	Sequence 10349, A
32	40	42.1	1905	2	US-09-964-956-44	Sequence 44, Appl
33	39.5	41.6	65	2	US-09-149-476-645	Sequence 645, App
34	39	41.1	159	2	US-09-107-532A-3789	Sequence 3789, Ap
35	39	41.1	194	2	US-09-873-075A-1	Sequence 1, Appli
36	39	41.1	229	1	US-08-817-997A-2	Sequence 2, Appli
37	39	41.1	327	2	US-09-252-991A-25546	Sequence 25546, A
38	39	41.1	1018	1	US-08-408-093-6	Sequence 6, Appli
39	39	41.1	1018	1	US-08-408-420A-6	Sequence 6, Appli
40	39	41.1	1018	1	US-08-714-901-6	Sequence 6, Appli
41	39	41.1	1018	2	US-08-040-741-6	Sequence 6, Appli
42	39	41.1	1044	2	US-09-949-016-10321	Sequence 10321, A
43	38.5	40.5	426	2	US-09-134-000C-6758	Sequence 6758, Ap
44	38	40.0	129	2	US-09-250-124A-29	Sequence 29, Appl
45	38	40.0	166	2	US-09-621-976-5267	Sequence 5267, Ap

ALIGNMENTS

RESULT 1
US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0223321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-6

Query Match 100.0%; Score 95; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAl 18
Db 5 PKQVLETFVTKSCPDAl 22

RESULT 2

US-08-408-222B-6
; Sequence 6, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-408-222B-6

Query Match 100.0%; Score 95; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAl 18
Db 5 PKQVLETFVTKSCPDAl 22

RESULT 3

US-08-254-493-1
; Sequence 1, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-1

Query Match 100.0%; Score 95; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLETFVTKSCPDAl 18
Db 167 PKQVLETFVTKSCPDAl 184

RESULT 4

US-08-253-751-6
; Sequence 6, Application US/08253751
; Patent No. 5858358

GENERAL INFORMATION:

; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,751
; FILING DATE: 3 JUNE 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988

ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CPB
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-253-751-6

Query Match 100.0%; Score 95; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-253-751-6

QY 1 PKQVLETFVTKSCPDAI 18
Db 167 PKQVLETFVTKSCPDAI 184

RESULT 5

US-08-453-925-6

; Sequence 6, Application US/08453925
; Patent No. 5883223

GENERAL INFORMATION:

; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/453,925
; FILING DATE: 30 MAY 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,751
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988

ATTORNEY/AGENT INFORMATION:

; NAME: MANDRAGOURAS, AMY E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CPB
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-453-925-6

Query Match 100.0%; Score 95; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-453-925-6

QY 1 PKQVLETFVTKSCPDAI 18
Db 167 PKQVLETFVTKSCPDAI 184

RESULT 6

US-08-403-253A-6
; Sequence 6, Application US/08403253A
; Patent No. 6352694

GENERAL INFORMATION:

APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,253A
FILING DATE: March 10, 1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-002CP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-253A-6

Query Match 100.0%; Score 95; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFTVKSCPDAl 18
Db 167 PKQDVLETFTVKSCPDAl 184

RESULT 7

US-08-435-816A-6
Sequence 6, Application US/08435816A
Patent No. 6534055
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,816A
FILING DATE: May 4, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10 MARCH 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-002CP3
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-816A-6

Query Match 100.0%; Score 95; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFTVKSCPDAl 18
Db 167 PKQDVLETFTVKSCPDAl 184

RESULT 8

US-09-350-202-6
Sequence 6, Application US/09350202
Patent No. 6887466
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.

APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-350-202-6

Query Match 100.0%; Score 95; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDAl 18
Db 167 PKQDVLETFVTKSCPDAl 184

RESULT 9
US-08-592-711-6
; Sequence 6, Application US/08592711
; Patent No. 6905680
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.

APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-711-6

Query Match 100.0%; Score 95; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVTKSCPDAl 18
Db 167 PKQDVLETFVTKSCPDAl 184

RESULT 10
US-09-349-915B-6
; Sequence 6, Application US/09349915B
; Patent No. 6905681

```

;
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; TITLE OF INVENTION: Methods For Selectively Stimulating
; Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,915B
; FILING DATE: 01-Aug-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 36119-125 (US10)
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6564
; TELEFAX: (617) 526-5000
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
;
; US-09-349-915B-6
;
; Query Match 100.0%; Score 95; DB 2; Length 227;
; Best Local Similarity 100.0%; Pred. No. 2.5e-08;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; US-09-349-915B-6
;
; QY 1 PKQDVLETFVTKSCPDAI 18
; Db 167 PKQDVLETFVTKSCPDAI 184
;
; RESULT 11
; US-08-408-222B-1
; Sequence 1, Application US/08408222B
;
;
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masaharu
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
;
; US-08-408-222B-1
;
; Query Match 100.0%; Score 95; DB 1; Length 228;
; Best Local Similarity 100.0%; Pred. No. 2.6e-08;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 PKQDVLETFVTKSCPDAI 18
; Db 168 PKQDVLETFVTKSCPDAI 185
;
; RESULT 12
; US-08-630-172-8
; Sequence 8, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; LYMPHOCYTE VETO
;
;

```

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-172-8

Query Match 91.6%; Score 87; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPD 16
Db 56 PKQDVLETFVKSCPD 71

RESULT 13
US-09-375-419-8
Sequence 8, Application US/09375419
Patent No. 6264950
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,419
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-375-419-8

Query Match 91.6%; Score 87; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPD 16
Db 56 PKQDVLETFVKSCPD 71

RESULT 14
US-08-452-052-2
Sequence 2, Application US/08452052
Patent No. 5766922
GENERAL INFORMATION:
APPLICANT: Peles, Elior
TITLE OF INVENTION: FUNCTIONAL LIGANDS FOR THE AXONAL CELL
TITLE OF INVENTION: RECOGNITION MOLECULE CONTACTIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,052
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-452-052-2

Query Match 49.5%; Score 47; DB 1; Length 1018;
Best Local Similarity 60.0%; Pred. NO. 23;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPD 15
Db 890 PSSDVIEFTKAPP 904

RESULT 15
US-08-701-380-2

; Sequence 2, Application US/08701380
; Patent No. 5686598
; GENERAL INFORMATION:
; APPLICANT: NORTH, Michael
; APPLICANT: NISHINA, Patsy
; APPLICANT: NAGERT, Juergen
; TITLE OF INVENTION: GENES ASSOCIATED WITH RETINAL
; TITLE OF INVENTION: DYSTROPHIES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,380
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SHERWOOD, Pamela J.
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: A-63565/PJS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-8700
; TELEFAX: 415-494-8771
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-701-380-2

Query Match 45.3%; Score 43; DB 1; Length 542;
Best Local Similarity 56.2%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLFTTVKCPDA 17
| | | | |
Db 99 KDDPRETFVLVARAPDA 114

Search completed: January 20, 2006, 17:23:45
Job time : 12.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:11:18 ; Search time 36.2222 Seconds
(without alignments)
207.633 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95
Sequence: 1 PKKDVLETFVKSCPDAL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	4	US-10-619-323-6
2	95	100.0	25	4	US-10-619-323-5
3	95	100.0	74	4	US-10-425-115-240878
4	95	100.0	227	2	US-08-592-711-6
5	95	100.0	227	3	US-09-183-055-6
6	95	100.0	227	3	US-09-350-202-6
7	95	100.0	227	4	US-10-390-330-6
8	95	100.0	227	5	US-10-473-127-1723
9	95	100.0	227	5	US-10-473-127-1726
10	95	100.0	228	4	US-10-156-136-39
11	95	100.0	228	4	US-10-331-496A-41
12	95	100.0	228	4	US-10-619-323-1
13	95	100.0	228	4	US-10-794-899-97
14	95	100.0	228	5	US-10-473-127-1714
15	95	100.0	228	5	US-10-473-127-1715
16	95	100.0	228	5	US-10-473-127-1716
17	95	100.0	228	5	US-10-473-127-1718
18	95	100.0	228	5	US-10-473-127-1719
19	95	100.0	228	5	US-10-473-127-1722
20	95	100.0	228	5	US-10-473-127-1725
21	95	100.0	228	5	US-10-789-378-18
22	95	100.0	228	5	US-10-482-029-144
23	95	100.0	228	5	US-10-852-335A-187
24	95	100.0	228	6	US-11-041-419-39
25	95	100.0	275	3	US-09-925-301-1381
26	95	100.0	275	4	US-10-106-698-5930
27	95	100.0	275	5	US-10-473-127-1720

28	95	100.0	275	5	US-10-473-127-1721	Sequence 1721, Ap
29	95	100.0	454	5	US-10-450-763-44426	Sequence 44426, A
30	87	91.6	79	5	US-10-473-127-1724	Sequence 1724, Ap
31	79	83.2	226	4	US-10-205-194-162	Sequence 162, App
32	61	64.2	30	5	US-10-473-127-1717	Sequence 1717, Ap
33	49.5	52.1	258	4	US-10-437-963-169601	Sequence 169601, A
34	49	51.6	10	5	US-10-473-127-165	Sequence 165, App
35	47	49.5	1020	5	US-10-631-467-1637	Sequence 1637, Ap
36	44.5	46.8	423	4	US-10-282-122A-48428	Sequence 48428, A
37	44	46.3	54	4	US-10-425-115-339548	Sequence 339548, A
38	44	46.3	339	4	US-10-282-122A-48707	Sequence 48707, A
39	44	46.3	475	4	US-10-437-963-155174	Sequence 155174, A
40	43	45.3	364	4	US-10-353-856-14	Sequence 14, Appl
41	43	45.3	364	4	US-10-353-856-32	Sequence 32, Appl
42	43	45.3	364	4	US-10-353-856-42	Sequence 42, Appl
43	43	45.3	542	4	US-10-408-765A-2262	Sequence 2262, Ap
44	43	45.3	542	5	US-10-732-923-19513	Sequence 19513, A
45	43	45.3	542	5	US-10-732-923-19514	Sequence 19514, A

ALIGNMENTS

RESULT 1

US-10-619-323-6
; Sequence 6, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crosno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-6

Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PKKDVLETFVKSCPDAL 18
Db 1 PKKDVLETFVKSCPDAL 18

RESULT 2

US-10-619-323-5
; Sequence 5, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: White, Melanie M.
; APPLICANT: Crosno, Jr., Joseph T.

APPLICANT: Lu, Yi
TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
FILE REFERENCE: 20609/241
CURRENT APPLICATION NUMBER: US/10/619,323
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: 60/395,864
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CD9 peptide
US-10-619-323-5

Query Match 100.0%; Score 95; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 PKKDVLFTFTVKSCPDAI 18
|||||

Db 1 PKKDVLFTFTVKSCPDAI 18
|||||

RESULT 3
US-10-425-115-240878
Sequence 240878, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(S3222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 240878
LENGTH: 74
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(74)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_15125C.1.pep
US-10-425-115-240878

Query Match 100.0%; Score 95; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.8e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 PKKDVLFTFTVKSCPDAI 18
|||||

Db 20 PKKDVLFTFTVKSCPDAI 37
|||||

RESULT 4
US-08-592-711-6
Sequence 6, Application US/08592711
Publication No. US20020115214A1
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-711-6

Query Match 100.0%; Score 95; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 PKKDVLFTFTVKSCPDAI 18
|||||

Db 167 PKKDVLFTFTVKSCPDAI 184
|||||

RESULT 5
US-09-183-055-6
Sequence 6, Application US/09183055
Publication No. US20020076407A1
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating

Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,055
FILING DATE: 30-Oct-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
REFERENCE/DOCKET NUMBER: 36119-125US8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6564
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-183-055-6

Query Match 100.0%; Score 95; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18
|||||
Db 167 PKKDVLFTFTVKSCPDAl 184

RESULT 6

US-09-350-202-6
; Sequence 6, Application US/09350202
; Publication No. US20030099643A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.

TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,202
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-350-202-6

Query Match 100.0%; Score 95; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSCPDAl 18
|||||
Db 167 PKKDVLFTFTVKSCPDAl 184

RESULT 7

US-10-390-330-6
; Sequence 6, Application US/10390330
; Publication No. US20040001829A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.
APPLICANT: Remert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation
TITLE OF INVENTION: Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/390,330
FILING DATE: March 17, 2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,816A
FILING DATE: May 4, 1995
CLASSIFICATION:
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10 MARCH 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-390-330-6

Query Match 100.0%; Score 95; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAl 18
|||||
Db 167 PKKDVLFTTVKSCPDAl 184

RESULT 8
US-10-473-127-1723

Sequence 1723, Application US/10473127
Publication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1723
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-10-473-127-1723

Query Match 100.0%; Score 95; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAl 18
|||||
Db 167 PKKDVLFTTVKSCPDAl 184

RESULT 9

US-10-473-127-1726
Sequence 1726, Application US/10473127
Publication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1726
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-10-473-127-1726

Query Match 100.0%; Score 95; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLFTTVKSCPDAl 18
|||||

Db 167 PKDVLFTFTVKSCPDAl 184

RESULT 10
US-10-156-136-39
; Sequence 39, Application US/10156136
; Publication No. US20030129696A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
; TITLE OF INVENTION: Polynucleotides and Polypeptides Encoding Receptors
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,136
; FILING DATE: 29-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,146
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO US98/00959
; FILING DATE: 21-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF354PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-156-136-39

Query Match 100.0%; Score 95; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18
DB 168 PKDVLFTFTVKSCPDAl 185

RESULT 11
US-10-331-496A-41
; Sequence 41, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WO, THOMAS D.
; APPLICANT: ZHANG, ZEMIN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-12-30
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 41
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-41

Query Match 100.0%; Score 95; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18
DB 168 PKDVLFTFTVKSCPDAl 185

RESULT 12
US-10-619-323-1
; Sequence 1, Application US/10619323
; Publication No. US20040136985A1
; GENERAL INFORMATION:
; APPLICANT: Jennings, Lisa K.
; APPLICANT: Longhurst, Celia M.
; APPLICANT: Cook, George A.
; APPLICANT: Bao, Jianxiong
; APPLICANT: Zhang, Chunxiang
; APPLICANT: White, Melanie M.
; APPLICANT: Crossno, Jr., Joseph T.
; APPLICANT: Lu, Yi
; TITLE OF INVENTION: METHODS OF MODIFYING BEHAVIOR OF CD9-EXPRESSING CELLS
; FILE REFERENCE: 20609/241
; CURRENT APPLICATION NUMBER: US/10/619,323
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,864
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homosapien
US-10-619-323-1

Query Match 100.0%; Score 95; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKDVLFTFTVKSCPDAl 18
DB 168 PKDVLFTFTVKSCPDAl 185

```
RESULT 13
US-10-794-899-97
; Sequence 97, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-899-97

Query Match      100.0%; Score 95; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETFTVKSCPDAl 18
Db      168 PKKDVLETFTVKSCPDAl 185

RESULT 14
US-10-473-127-1714
; Sequence 1714, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1714
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1714

Query Match      100.0%; Score 95; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETFTVKSCPDAl 18
Db      168 PKKDVLETFTVKSCPDAl 185

RESULT 15
US-10-473-127-1715
; Sequence 1715, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1715
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1715

Query Match      100.0%; Score 95; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PKKDVLETFTVKSCPDAl 18
Db      168 PKKDVLETFTVKSCPDAl 185

Search completed: January 20, 2006, 17:26:39
Job time : 37.2222 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:16:18 ; Search time 3.11111 Seconds
(without alignments)
58.632 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95
Sequence: 1 PKQVLEFTVKSCPDAl 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	228	6	US-10-821-234-1266
2	43	45.3	364	6	US-10-510-947-2
3	40	42.1	367	6	US-10-467-657-1440
4	38	40.0	959	6	US-10-467-962B-4
5	36.5	38.4	342	6	US-11-129-143-63
6	36	37.9	34	6	US-10-816-768-31
7	36	37.9	98	6	US-10-816-768-42
8	36	37.9	112	7	US-11-082-884-1
9	36	37.9	405	6	US-10-873-528-62
10	36	37.9	645	6	US-10-821-234-1409
11	35.5	37.4	645	6	US-10-763-712A-17
12	35.5	37.4	645	6	US-10-763-712A-105
13	35	36.8	106	7	US-11-008-727-12
14	35	36.8	106	7	US-11-073-222-3
15	35	36.8	129	7	US-11-073-222-2
16	35	36.8	238	7	US-11-008-727-26
17	35	36.8	270	7	US-11-008-727-24
18	35	36.8	289	7	US-11-156-084-108
19	35	36.8	378	7	US-11-152-892-7
20	35	36.8	476	7	US-11-008-727-22
21	35	36.8	509	7	US-11-008-727-16
22	35	36.8	531	7	US-11-008-727-18
23	35	36.8	586	7	US-11-073-112-18
24	35	36.8	662	7	US-11-137-131-2
25	35	36.8	662	7	US-11-137-131-4

26 35 36.8 715 6 US-10-467-657-70 Sequence 70, Appl
27 35 36.8 715 6 US-10-467-657-3672 Sequence 3672, Ap
28 35 36.8 1218 7 US-11-052-554A-123 Sequence 123, App
29 34.5 36.3 130 7 US-11-055-822-690 Sequence 690, App
30 34.5 36.3 130 7 US-11-055-822-768 Sequence 768, App
31 34.5 36.3 924 6 US-10-467-657-4290 Sequence 4290, Ap
32 34 35.8 34 6 US-10-816-768-30 Sequence 30, Appl
33 34 35.8 98 6 US-10-816-768-41 Sequence 41, Appl
34 34 35.8 158 6 US-10-821-234-1453 Sequence 1453, Ap
35 34 35.8 210 7 US-11-103-957-49 Sequence 49, Appl
36 34 35.8 349 7 US-11-165-024-2 Sequence 2, Appl
37 34 35.8 383 7 US-11-186-284-183 Sequence 183, App
38 34 35.8 403 6 US-10-821-234-1490 Sequence 1490, App
39 34 35.8 422 6 US-10-821-234-1313 Sequence 1313, Ap
40 34 35.8 422 7 US-11-186-284-75 Sequence 75, Appl
41 34 35.8 467 7 US-11-156-084-115 Sequence 115, App
42 34 35.8 794 7 US-11-024-959-478 Sequence 478, Appl
43 34 35.8 870 7 US-11-165-211-48 Sequence 48, Appl
44 34 35.8 870 7 US-11-165-226-58 Sequence 58, Appl
45 34 35.8 1616 6 US-10-821-234-1497 Sequence 1497, Ap

ALIGNMENTS

RESULT 1
US-10-821-234-1266
; Sequence 1266, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1266
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1266

Query Match 100.0%; Score 95; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKQVLEFTVKSCPDAl 18
DB 168 PKQVLEFTVKSCPDAl 185

RESULT 2

US-10-510-947-2
; Sequence 2, Application US/10510947
; Publication No. US20050255123A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Medina, Maria Fe C.
; APPLICANT: Kobinger, Gary
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor
; FILE REFERENCE: UPN-02811PCT
; CURRENT APPLICATION NUMBER: US/10/510,947
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/376,480
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/385,704

```
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/427,752
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Ebola virus
US-10-510-947-2

Query Match          45.3%; Score 43; DB 6; Length 364;
Best Local Similarity 69.2%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KKDVLFTFTVKSC 14
   ||| ||| |||
Db 294 KNTSLEKFAVKSC 306

RESULT 3
US-10-467-657-1440
; Sequence 1440, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1440
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1440

Query Match          42.1%; Score 40; DB 6; Length 367;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 0;

QY 1 PKKDVLFTFTVKSCPD 16
   |.| ||| |. : : ||
Db 197 PKRTVLELFLKLNLPD 212

RESULT 4
US-10-467-962B-4
; Sequence 4, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 4
; LENGTH: 959
; TYPE: PRT

; ORGANISM: Arabidopsis thaliana
US-10-467-962B-4

Query Match          40.0%; Score 38; DB 6; Length 959;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 FTVKSCPDAL 18
   ||| ||| |||
Db 840 FTSKSVDPDAI 849

RESULT 5
US-11-129-143-63
; Sequence 63, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Rickettsia prowazekii
US-11-129-143-63

Query Match          38.4%; Score 36.5; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 2 KKDVLFTFTVKSC-CPD 16
   ||| :||| : ||
Db 106 KPDTIKTFTVRHVAPD 121

RESULT 6
US-10-816-768-31
; Sequence 31, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 31
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-10-816-768-31

Query Match          37.9%; Score 36; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLFTFTVKSC 14
   ||| : |||
Db 18 PKVEQLSNMVKSC 31
```

```

; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-62

Query Match      37.9%; Score 36; DB 6; Length 405;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      3 KDVLETFVTKSCPD 18
Db      177 QDVLETFVTHPTGI 192

RESULT 10
US-10-821-234-1409
; Sequence 1409, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1409
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1409

Query Match      37.9%; Score 36; DB 6; Length 645;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKDVLETFVTKSC 14
Db      542 PKDVLETFVAPWC 555

RESULT 11
US-10-763-712A-17
; Sequence 17, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison P.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; TITLE OF INVENTION: Production
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03

; PRIOR APPLICATION NUMBER: US/0816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 42
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta3
US-10-816-768-42

Query Match      37.9%; Score 36; DB 6; Length 98;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKDVLETFVTKSC 14
Db      82 PKVEQLSNMVKSC 95

RESULT 8
US-11-082-884-1
; Sequence 1, Application US/11082884
; Publication No. US20050272636A1
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Sarah et al.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF A REPRODUCTIVE DISORDER BY MEASURING
; TITLE OF INVENTION: OR INHIBITING INTERPERON-GAMMA
; FILE REFERENCE: 0641-0269PUS1
; CURRENT APPLICATION NUMBER: US/11/082,884
; CURRENT FILING DATE: 2005-03-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-082-884-1

Query Match      37.9%; Score 36; DB 7; Length 112;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 PKDVLETFVTKSC 14
Db      96 PKVEQLSNMVKSC 109

RESULT 9
US-10-873-528-62
; Sequence 62, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/F21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
```

```
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-763-712A-17

Query Match      37.4%; Score 35.5; DB 6; Length 645;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY      2 KKDVLFTFKVSC---PDAI 18
Db      604 KIEVLGTFVCVNGASPNVI 623

RESULT 12
US-10-763-712A-105
; Sequence 105, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; TITLE OF INVENTION: Production
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 645
; TYPE: PRT
; ORGANISM: T. maritima
US-10-763-712A-105

Query Match      37.4%; Score 35.5; DB 6; Length 645;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY      2 KKDVLFTFKVSC---PDAI 18
Db      604 KIEVLGTFVCVNGASPNVI 623

RESULT 13
US-11-008-727-12
; Sequence 12, Application US/11008727
; Publication No. US20050250185A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Macdonald, Lynn
; APPLICANT: Sleeman, Mark W.
; TITLE OF INVENTION: OGH Fusion Polypeptides and Therapeutic
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 2010A
; CURRENT APPLICATION NUMBER: US/11/008,727
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/529,036
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/548,415
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 106

; TYPE: PRT
; ORGANISM: homo sapiens
US-11-008-727-12

Query Match      36.8%; Score 35; DB 7; Length 106;
Best Local Similarity 38.5%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 KKDVLFTFKVSC 14
Db      84 RREELEIFTARAC 96

RESULT 14
US-11-073-222-3
; Sequence 3, Application US/11073222
; Publication No. US20050272635A1
; GENERAL INFORMATION:
; APPLICANT: KELLY, JAMES D.
; TITLE OF INVENTION: USE OF CORTICOTROPH-DERIVED
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE TO TREAT LIVER STEATOSIS
; FILE REFERENCE: 04-02
; CURRENT APPLICATION NUMBER: US/11/073,222
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,623
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-222-3

Query Match      36.8%; Score 35; DB 7; Length 106;
Best Local Similarity 38.5%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 KKDVLFTFKVSC 14
Db      84 RREELEIFTARAC 96

RESULT 15
US-11-073-222-2
; Sequence 2, Application US/11073222
; Publication No. US20050272635A1
; GENERAL INFORMATION:
; APPLICANT: KELLY, JAMES D.
; TITLE OF INVENTION: USE OF CORTICOTROPH-DERIVED
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE TO TREAT LIVER STEATOSIS
; FILE REFERENCE: 04-02
; CURRENT APPLICATION NUMBER: US/11/073,222
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,623
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-222-2

Query Match      36.8%; Score 35; DB 7; Length 129;
Best Local Similarity 38.5%; Pred. No. 30;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 KKDVLFTFKVSC 14
Db      107 RREELEIFTARAC 119
```

Search completed: January 20, 2006, 17:27:03
Job time : 3.11111 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:06:32 ; Search time 12.6667 Seconds
(without alignments)
136.729 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKKDVLETFVKSCPDAl 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	228	1 A40402	CD9 antigen [valid
2	94	98.9	228	1 A42929	CD9 antigen - gre
3	79	83.2	226	1 S3262	CD9 antigen - rat
4	67	70.5	226	2 I49589	antigen - mouse
5	48	50.5	1057	2 T15720	hypothetical prote
6	47	49.5	159	2 AE2547	hypothetical prote
7	47	49.5	1020	2 S05944	neuronal cell surf
8	47	49.5	1021	2 A57112	contactin precurs
9	44	46.3	226	1 JX0221	CD9 antigen - bovi
10	44	46.3	402	2 D70602	probable arginine
11	43	45.3	399	2 T16634	hypothetical prote
12	42	44.2	92	2 A98054	ferredoxin [import
13	42	44.2	581	2 G71520	proline-tRNA ligas
14	42	44.2	630	2 A49656	estrogen-responsi
15	41.5	43.7	1980	2 S54307	myosin heavy chain
16	41	43.2	68	2 H95186	ferredoxin [import
17	41	43.2	220	2 T26518	hypothetical prote
18	41	43.2	342	2 T08837	probable gamma-glu
19	41	43.2	398	2 JC4254	ribosomal protein
20	41	43.2	439	2 F81746	hypothetical prote
21	41	43.2	1018	2 JC4211	neural adhesion pr
22	41	43.2	1217	2 T13996	pol protein - frui
23	40.5	42.6	244	2 T41676	hypothetical prote
24	40	42.1	336	2 JC4102	hypothetical prote
25	40	42.1	367	2 A81974	probable DNA-direc
26	40	42.1	367	2 C81030	DNA polymerase III
27	40	42.1	439	2 T29587	hypothetical prote
28	40	42.1	823	2 T29644	hypothetical prote
29	40	42.1	836	2 B96716	probable serine/th

30	40	42.1	1160	2 T31688	Ca2+-transporting
31	40	42.1	1905	2 I51553	Plexin - African c
32	40	42.1	3396	2 T22613	hypothetical prote
33	39	41.1	64	2 H91000	hypothetical prote
34	39	41.1	64	2 B90779	hypothetical prote
35	39	41.1	175	2 F82486	conserved hypothet
36	39	41.1	201	2 B90114	hypothetical prote
37	39	41.1	211	2 B84066	hypothetical prote
38	39	41.1	274	2 B70020	conserved hypothet
39	39	41.1	294	2 G87366	enoyl-CoA hydratase
40	39	41.1	329	2 D86329	Fl4Pl.1 protein -
41	39	41.1	340	2 E72739	conserved hypothet
42	39	41.1	343	2 H84607	hypothetical prote
43	39	41.1	521	2 T01923	hypothetical prote
44	39	41.1	573	2 T48584	auxin-regulated pr
45	39	41.1	798	2 F98134	hypothetical prote

ALIGNMENTS

RESULT 1

A40402

CD9 antigen [validated] - human

N:Alternate names: motility-related protein-1

C:Species: Homo sapiens (man)

C>Date: 06-Dec-1991 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004

C:Accession: A46123; A40402; JH0555; A39029; S10564

R:Rubinstein, E.; Benoît, P.; Billard, M.; Plaisance, S.; Prenant, M.; Uzan, G.; Bouche

Genomics 16, 132-138, 1993

A:Title: Organization of the human CD9 gene.

A:Reference number: A46123; MUID:93252369; PMID:8486348

A:Accession: A46123

A:Molecule type: DNA

A:Residues: 1-228 <RUB>

A:Cross-references: UNIPROT:P21926; UNIPARC:UPI00003B45A; GB:S60489; NID:G300112; PIDN

A:Experimental source: leukocyte

A>Note: sequence extracted from NCBI backbone (NCBIN:131318, NCBIN:131326, NCBIN:131328,

R:Lanza, P.; Wolf, D.; Fox, C.F.; Kieffer, N.; Seyer, J.M.; Fried, V.A.; Coughlin, S.R.,

J. Biol. Chem. 266, 10638-10645, 1991

A:Title: cDNA cloning and expression of platelet p24/CD9. Evidence for a new family of

A:Reference number: A40402; MUID:91244846; PMID:2037603

A:Accession: A40402

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-228 <LAN>

A:Cross-references: UNIPARC:UPI000003B45A; GB:L34068; GB:M61880; NID:G508495; PIDN:AAA5

A>Note: parts of this sequence, including the amino end of the mature protein, were con

R:Miyake, M.; Koyama, M.; Seno, M.; Ikeyama, S.

J. Exp. Med. 174, 1347-1354, 1991

A:Title: Identification of the motility-related protein (MRP-1), recognized by monoclon.

A:Reference number: JH0555; MUID:92078843; PMID:1720807

A:Accession: JH0555

A:Molecule type: mRNA

A:Residues: 1-228 <MIY>

A:Cross-references: UNIPARC:UPI000003B45A; GB:X60111; NID:G34768; PIDN:CAA42708.1; PID

A:Experimental source: breast carcinoma

A>Note: this protein has the epitope defined by cell motility-inhibiting monoclonal ant

R:Bouchaix, C.; Benoît, P.; Frachet, P.; Billard, M.; Worthington, R.E.; Gagnon, J.; Uz

J. Biol. Chem. 266, 117-122, 1991

A:Title: Molecular cloning of the CD9 antigen. A new family of cell surface proteins.

A:Reference number: A39029; MUID:91093112; PMID:1840589

A:Accession: A39029

A:Molecule type: mRNA

A:Residues: 1-8, 'S', '10-66, 'A', '68-193, 195-228 <BOU>

A:Cross-references: UNIPARC:UPI000017414B; GB:IM38690

A>Note: parts of this sequence, including the amino end of the mature protein, were con

R:Higashihara, M.; Takahata, K.; Yatomi, Y.; Nakahata, K.; Kurokawa, K.

FEBS Lett. 264, 270-274, 1990

A:Title: Purification and partial characterization of CD9 antigen of human platelets.

A:Reference number: S10564; MUID:90292223; PMID:2358073

A:Accession: S10564

A:Molecule type: protein

A;Status: preliminary; translated from GB/EMBL/DBU
A;Molecule type: DNA
A;Residues: 1-1057 <LAT>
A;Cross-references: UNIPROT:Q18331; UNIPARC:UPI000007BC9F; EMBL:U49947; NID:g1208826; PIDN:10602
C;Genetics:
A;Gene: CESP:C30G4.3
A;Introns: 42/3; 66/2; 113/3; 150/1; 202/1; 239/3; 292/1; 345/3; 381/1; 404/2; 448/3; 53/3
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match 50.5%; Score 48; DB 2; Length 1057;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 DULETFTVKSCPD 16
| : : : : :
DB 926 DSIKFTVSHCPD 938

RESULT 6
AE2547
hypothetical protein all7664 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2547
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <KUR>
A;Cross-references: UNIPROT:Q8ZS48; UNIPARC:UPI00000CCDB2; GB:AP003602; PIDN:BAE77307.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all7664
A;Genome: plasmid

Query Match 49.5%; Score 47; DB 2; Length 159;
Best Local Similarity 61.5%; Pred. No. 3.4;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KQDVLETFVKSC 14
| : : : : :
DB 25 KQDGTFTVKNC 37

RESULT 7
S05944
neuronal cell surface protein F3 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S05944
R;Gennarini, G.; Cibelli, G.; Rougon, G.; Mattei, M.G.; Goridis, C.
J. Cell Biol. 109, 775-788, 1989
A;Title: The mouse neuronal cell surface protein F3: a phosphatidylinositol-anchored membrane protein
A;Reference number: S05944; MUID:89340657; PMID:2474555
A;Accession: S05944
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1020 <GEN>
A;Cross-references: UNIPROT:PI2960; UNIPARC:UPI0000028AF2; EMBL:X14943; NID:g50937; PIDN:10602
C;Genetics:
A;Map position: 15F
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;256-312/Domain: immunoglobulin homology <IMM>

Query Match 49.5%; Score 47; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCP 15
| : : : : :
DB 893 PSSDVIETFRKAPP 907

RESULT 8
A57112
contactin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: A57112
R;Peters, E.; Nativ, M.; Campbell, P.L.; Sakurai, T.; Martinez, R.; Lev, S.; Clary, D.O.
Cell 82, 251-260, 1995
A;Title: The carbonic anhydrase domain of receptor tyrosine phosphatase beta is a functionally distinct domain
A;Reference number: A57112; MUID:95354206; PMID:7628014
A;Accession: A57112
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1021 <PEL>
A;Cross-references: UNIPARC:UPI0000178925
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: membrane protein; phosphatidylinositol linkage
F;256-312/Domain: immunoglobulin homology <IMM>

Query Match 49.5%; Score 47; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCP 15
| : : : : :
DB 893 PSSDVIETFRKAPP 907

RESULT 9
JX0221
CD9 antigen - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: JX0221
R;Martin-Alonso, J.M.; Hernando, N.; Ghosh, S.; Coca-Prados, M.
J. Biochem. 112, 63-67, 1992
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cells
A;Reference number: JX0221; MUID:93054422; PMID:1339429
A;Accession: JX0221
A;Molecule type: mRNA
A;Residues: 1-226 <MAR>
A;Cross-references: UNIPROT:P30932; UNIPARC:UPI0000167C21; GB:M81720; NID:g162820; PIDN:10602
A;Experimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;2-226/Product: CD9 antigen #status predicted <MAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <TM1>
F;36-53/Domain: extracellular #status predicted <EX1>
F;54-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-109/Domain: transmembrane #status predicted <TM3>
F;110-192/Domain: extracellular #status predicted <EX2>
F;193-219/Domain: transmembrane #status predicted <TM4>
F;220-226/Domain: intracellular #status predicted <CY3>
F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.3%; Score 44; DB 1; Length 226;
Best Local Similarity 33.3%; Pred. No. 14;
Matches 6; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSCPDAI 18
| : : : : :
DB 166 PPKNLIDSLKTRPCPEAI 183

RESULT 10
D70602

probable arginine deiminase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70602
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70602
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-402 <COL>
A:Cross-references: UNIPROT:O05585; UNIPARC:UPI0000125D93; GB:Z94752; GB:AL123456; NID:9
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: arca
C:Superfamily: arginine deiminase arca

Query Match 46.3%; Score 44; DB 2; Length 402;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 DVLETFVKSCPDAI 18
DB 289 DTLEAFTIQTPDGV 303

RESULT 11
T16634
hypothetical protein M02F4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16634
R: Wu, X.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid M02F4.
A:Reference number: Z18550
A:Accession: T16634
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-399 <WUX>
A:Cross-references: UNIPROT:Q21472; UNIPARC:UPI000007B6B2; EMBL:U41548; NID:g1109912; PI
C:Genetics:
A:Gene: CESP:M02F4.1
A:Introns: 50/3; 234/3; 298/3; 336/1; 381/3

Query Match 45.3%; Score 43; DB 2; Length 399;
Best Local Similarity 45.0%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 PKQDVLE--TFTVKSCPDAI 18
DB 274 PREVLDPPLTCPCDPCI 293

RESULT 12
A98054
ferredoxin [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98054
R: Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A98054
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-92 <KUR>
A:Cross-references: UNIPROT:Q8DNY8; UNIPARC:UPI00000E3668; GB:AE007317; PIDN:AAL00262.1
C:Genetics:
A:Gene: fer

Query Match 44.2%; Score 42; DB 2; Length 92;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 PKQDVLETFVKSCP 15
DB 70 PSQDVLE--AVKNCP 82

RESULT 13
G71520
proline-trna ligase (EC 6.1.1.15) - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: G71520
R: Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: G71520
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-581 <ARN>
A:Cross-references: UNIPROT:P36431; UNIPARC:UPI0000136607; GB:AE001312; GB:AE001273; NID
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: proS
C:Superfamily: proline-trna synthetase
C:Keywords: aminoacyl-trna synthetase; ligase; protein biosynthesis

Query Match 44.2%; Score 42; DB 2; Length 581;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PKQDVLETFVKSC 14
DB 273 PKHKILTLVVKTC 286

RESULT 14
A49656
estrogen-responsive finger protein, efp (RING finger, coiled-coil domains) - human
C:Species: Homo sapiens (nan)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49656
R: Inoue, S.; Orimo, A.; Hosoi, T.; Kondo, S.; Toyoshima, H.; Kondo, T.; Ikegami, A.; Ouc
Proc. Natl. Acad. Sci. U.S.A. 90, 11117-11121, 1993
A:Title: Genomic binding-site cloning reveals an estrogen-responsive gene that encodes a
A:Reference number: A49656; MUID:94068555; PMID:8248217
A:Accession: A49656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-630 <INO>
A:Cross-references: UNIPROT:Q14258; UNIPARC:UPI000000D9E6; GB:D21205; NID:g458725; PIDN
A:Experimental source: placenta
A:Note: sequence extracted from NCBI backbone (NCBIN:140455, NCBIP:140456)
C:Superfamily: rfp transforming protein
C:Keywords: zinc
P:9-59/Domain: RING finger homology <RNG>

Query Match 44.2%; Score 42; DB 2; Length 630;
Best Local Similarity 52.9%; Pred. No. 80;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKDVLTFVKSCPDAI 18
DB 437 KAKVLEFLAKSRPELL 453

```

RESULT 15
S54307
myosin heavy chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54307
R;Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A;Title: A novel type of myosin implicated in signalling by rho family GTPases.
A;Reference number: S54307; MUID:95188874; PMID:7882973
A;Accession: S54307
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1980 <REI>
A;Cross-references: UNIPROT:Q63359; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:9639998; PID
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zeta
C;Keywords: nucleotide binding; P-loop
F;149-942/Domain: myosin motor domain homology <MMOT>
F;239-246/Region: nucleotide-binding motif A (P-loop)
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match      43.7%; Score 41.5; DB 2; Length 1980;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 9; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

QY      1 PKKDVLETTT---VKSCPDAI 18
Db      1191 FREDGLETWETAAPSCPQV 1211

```

Search completed: January 20, 2006, 17:22:38
Job time : 13.6667 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:05:21 ; Search time 68.4444 Seconds
(without alignments)
185.545 Million cell updates/sec

Title: US-10-619-323-6

Perfect score: 95

Sequence: 1 PKKDVLETFVKSCPDAL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	227	1	P21926 homo sapien
2	95	100.0	228	1	Q5J7W6 homo sapien
3	94	98.9	227	1	P30409 cercopithec
4	79	83.2	225	1	P40241 rattus norv
5	67	70.5	225	1	P40240 mus musculu
6	66	69.5	225	1	P40239 felis silve
7	63	66.3	227	2	Q6NWG7 brachydanio
8	62	65.3	227	2	Q4REW0 tetraodon n
9	58	61.1	226	2	Q8MJ48 sus scrofa
10	55	57.9	225	1	Q8Wmq3 sus scrofa
11	53.5	56.3	398	2	Q6OKA7 CABER
12	52	54.7	224	2	Q91BC9 CHICK
13	49.5	52.1	218	2	Q851Q5 ORYSA
14	48	50.5	144	2	Q5Y296 NOCPA
15	48	50.5	694	2	Q9SDY4_PETCR
16	48	50.5	1057	2	Q18331 CABEL
17	47	49.5	159	2	Q8ZS48 ANASP
18	47	49.5	1020	1	CNTN1 MOUSE
19	47	49.5	1021	1	CNTN1 RAT
20	46	48.4	178	2	Q46130 LEUMA
21	46	48.4	262	1	PYRK METKA
22	46	48.4	497	2	Q6B111 DEBHA
23	46	48.4	497	2	Q7RDN7 PLAYO
24	46	48.4	892	2	Q5AT76 EMENI
25	45.5	47.9	236	2	Q7ZTR5 XENLA
26	45	47.4	91	2	Q6OHW9 RAT
27	45	47.4	112	2	Q8EJ87 SHEON
28	45	47.4	150	2	Q5J183 PYRKO
29	45	47.4	331	2	Q8GP11 STAAU
30	45	47.4	365	2	Q51CE4 ENTHI
31	45	47.4	373	2	Q60119 rattus norv

RESULT 1

CD9_HUMAN

ID_CD9_HUMAN STANDARD; PRT; 227 AA.

AC P21926; Q96ES4;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein)

DE (MRP-1) (tetraspanin-29) (tspan-29).

GN Name=CD9; Synonym=MIC3, TSPAN29;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-4.

RX MEDLINE=91093112; PubMed=1840589;

RA Boucheix C., Benoit P., Frachet P., Billard M., Worthington R.E.,

RA Gagnon J., Uzan G.;

RT "Molecular cloning of the CD9 antigen. A new family of cell surface

proteins.";

RL J. Biol. Chem. 266:117-122(1991).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.

RX MEDLINE=91244846; PubMed=2037603;

RA Lanza F., Wolf D., Fox C.F., Kieffer N., Seyer J.M., Fried V.A.,

RA Coughlin S.R., Phillips D.R., Jennings L.K.;

RT "cDNA cloning and expression of platelet p24/CD9. Evidence for a new

family of multiple membrane-spanning proteins.";

RL J. Biol. Chem. 266:10638-10645(1991).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=92078843; PubMed=1720807; DOI=10.1084/jem.174.6.1347;

RA Miyake M., Koyama M., Seno M., Ikegawa S.;

RT "Identification of the motility-related protein (MRP-1), recognized by

monoclonal antibody M31-15, which inhibits cell motility.";

RL J. Exp. Med. 174:1347-1354(1991).

RN [4]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RX TISSUE=Leukocyte;

RC MEDLINE=93252369; PubMed=8486348;

RA Rubinstein E., Benoit P., Billard M., Plaisance S., Prenant M.,

RA Uzan G., Boucheix C.;

RT "Organization of the human CD9 gene.";

RL Genomics 16:132-138(1993).

RN [5]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,

RA Rajkumar N., Yi Q., Nickerson D.A.;

RT "seattlesnp. NHLBI HL66682 program for genomic applications, UW-

PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

RN [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [7]
 RP PROTEIN SEQUENCE OF 1-20.
 RC TISSUE=Platelet;
 RX MEDLINE=90292223; PubMed=2358073; DOI=10.1016/0014-5793(90)80265-K;
 RA Higashihara M., Takahata K., Yatomi Y., Nakahara K., Kurokawa K.;
 RT "Purification and partial characterization of CD9 antigen of human
 RT platelets.";
 RN FEBS Lett. 264:270-274(1990).
 [8]
 RP ROLE IN CELL MOTILITY AND METASTASIS.
 RX PubMed=8478605; DOI=10.1084/jem.177.5.1231;
 RA Ikegama S., Koyama M., Yamaoka M., Sasada R., Miyake M.;
 RT "Suppression of cell motility and metastasis by transfection with
 RL human motility-related protein (MRP-1/CD9) DNA.";
 RN J. Exp. Med. 177:1231-1237(1993).
 [9]
 RP ROLE IN CELL ADHESION.
 RX PubMed=7511626;
 RA Masellis-Smith A., Shaw A.R.;
 RT "CD9-regulated adhesion. Anti-CD9 monoclonal antibody induce pre-B
 RT cell adhesion to bone marrow fibroblasts through de novo recognition
 RT of fibronectin.";
 RN J. Immunol. 152:2768-2777(1994).
 [10]
 RP ROLE IN GAMETE FUSION.
 RX PubMed=14575715; DOI=10.1016/j.bbrc.2003.09.196;
 RA Higginbottom A., Takahashi Y., Bolling L., Coonrod S.A., White J.M.,
 RA Partridge L.J., Monk P.N.;
 RT "Structural requirements for the inhibitory action of the CD9 large
 RT extracellular domain in sperm/oocyte binding and fusion.";
 RN Biochem. Biophys. Res. Commun. 311:208-214(2003).
 [11]
 RP SUBUNIT.
 RX PubMed=14556650; DOI=10.1042/BJ20031037;
 RA Kovalevskaya O.V., Yang X., Kolesnikova T.V., Hemler M.E.;
 RT "Evidence for specific tetraspanin homodimers: inhibition of
 RT palmitoylation makes cysteine residues available for cross-linking.";
 RN Biochem. J. 377:407-417(2004).
 [12]
 RP PHOSPHORYLATION.
 RX MEDLINE=93327758; PubMed=7687539;
 RA Chalupny N.J., Kanner S.B., Schieven G.L., Wee S., Gilliland L.K.,
 RA Aruffo A., Ledbetter J.A.;
 RT "Tyrosine phosphorylation of CD19 in pre-B and mature B cells.";
 RN EMBO J. 12:2691-2696(1993).
 [13]
 RP PALMITOYLATION, AND MUTAGENESIS OF CVS-8; CVS-77; CVS-78; CVS-86;
 CVS-217 AND CVS-218.
 RX PubMed=11959120; DOI=10.1016/S0014-5793(02)02522-X;
 RA Charrin S., Manie S., Oualid M., Billard M., Boucheix S.,
 RA Rubinstein E.;
 RT "Differential stability of tetraspanin/tetraspanin interactions: role
 RT of palmitoylation.";
 RN FEBS Lett. 516:139-144(2002).
 [14]
 RP INTERACTION WITH PTGFRN.
 RX MEDLINE=21216740; PubMed=11279880; DOI=10.1074/jbc.M011297200;
 RA Charrin S., Le Nour F., Oualid M., Billard M., Faure G., Hanash S.M.,
 RA Boucheix C., Rubinstein E.;
 RT "The major CD9 and CD81 molecular partner. Identification and
 RT characterization of the complexes.";
 RN J. Biol. Chem. 276:14329-14337(2001).
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis.
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with
 CC PTGFRN/CD9P1.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed by a variety of hematopoietic and
 CC epithelial cells.
 CC -!- PTM: Protein exists in three forms with molecular masses between
 CC 22 and 27 kDa, and is known to carry covalently linked fatty
 CC acids.
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation.
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL; S60489; AACG0586.1; -; Genomic DNA.
 DR EMBL; S60462; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; S60463; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; S60464; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; S60700; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; S60699; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; S60465; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; S60472; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; M38590; AACG0586.1; JOINED; Genomic DNA.
 DR EMBL; L34068; AAA59982.1; -; mRNA.
 DR EMBL; X60111; CAA42708.1; -; mRNA.
 DR EMBL; L08118; -; NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL; L08119; AAA51954.1; ALT_SEQ; Genomic DNA.
 DR EMBL; L08120; AAA51955.1; ALT_SEQ; Genomic DNA.
 DR EMBL; L08121; AAA51956.1; -; Genomic DNA.
 DR EMBL; L08122; AAA51957.1; -; Genomic DNA.
 DR EMBL; L08123; AAA51958.1; -; Genomic DNA.
 DR EMBL; L08124; AAA51959.1; -; Genomic DNA.
 DR EMBL; L08125; -; NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL; AY422198; AAQ87878.1; -; Genomic DNA.
 DR EMBL; BC011988; AAH11988.1; -; mRNA.
 DR FIR; A46123; A40402.
 DR Ensembl; ENSG00000010278; Homo sapiens.
 DR HGNC; HGNC:1709; CD9.
 DR H-InvDB; HIX0010357; -.
 DR Reactome; P21926; -.
 DR MIM; 143030; -.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005886; C:plasma membrane; NAS.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0006928; P:cell motility; IDA.
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; IDA.
 DR GO; GO:0030913; P:paranodal junction formation; ISS.
 DR GO; GO:0030168; P:platelet activation; NAS.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; I.
 DR PRINTS; PR00259; TMFOUR.

DR PROSITE; PS00421; TM4_1; 1.
 KW Antigen; Cell adhesion; Direct protein sequencing; Fertilization;
 Query Match 100.0%; Score 95; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18
 |||||
 DB 167 PKKDVLETFVKSCPDAl 184

RESULT 2
 Q5J7W6 HUMAN PRELIMINARY; PRT; 228 AA.
 AC Q5J7W6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Growth-inhibiting gene 2 protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kim J.W.;
 RT "Identification of a human growth inhibition gene 2 (GIG2).";
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY423720; AA500483.1; -; mRNA.
 SQ SEQUENCE 228 AA; 25416 MW; F68333E0C20611D8 CRC64;

Query Match 100.0%; Score 95; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18
 |||||
 DB 168 PKKDVLETFVKSCPDAl 185

RESULT 3
 CD9 CERAE
 ID CD9 CERAE STANDARD; PRT; 227 AA.
 AC P30409;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen (27 kDa diphtheria toxin receptor-associated protein) (DRAP27).
 DE Names=CD9;
 GN Carcipothecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=92394967; PubMed=1522113; DOI=10.1083/jcb.118.6.1389;
 RA Mitamura T., Iwamoto R., Umata T., Yomo T., Urabe I., Tsuneoka M.,
 RA Mekada E.;
 RT "The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from
 RT vero cells is the monkey homologue of human CD9 antigen: expression of
 RT DRAP27 elevates the number of diphtheria toxin receptors on toxin-
 RT sensitive cells.";
 RL J. Cell Biol. 118:1389-1399(1992).
 CC -1- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis (By similarity).
 CC -1- FUNCTION: Expression of DRAP27 elevates the number of diphtheria
 CC toxin receptors on toxin-sensitive cells.

CC -1- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

EMBL; D10726; BAA01569.1; -; mRNA.
 DR PIR; A42929; A42929.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0007155; P:cell adhesion; ISS.
 DR GO; GO:0006928; P:cell motility; ISS.
 DR GO; GO:0007342; P:fusion of sperm to egg plasma membrane; ISS.
 DR GO; GO:0030913; P:paranodal junction formation; ISS.
 DR GO; GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraspannin; 1.
 DR PRINTS; PR00259; TMPOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
 KW Palmitate; Phosphorylation; Transmembrane.
 FT INIT MET 0 0 By similarity.
 FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 54 Extracellular (Potential).
 FT TRANSMEM 55 75 Potential.
 FT TOPO_DOM 76 86 Cytoplasmic (Potential).
 FT TRANSMEM 87 110 Potential.
 FT TOPO_DOM 111 194 Extracellular (Potential).
 FT TRANSMEM 195 220 Potential.
 FT TOPO_DOM 221 227 Cytoplasmic (Potential).
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
 FT LIPID 77 77 S-palmitoyl cysteine (By similarity).
 FT LIPID 78 78 S-palmitoyl cysteine (By similarity).
 FT LIPID 86 86 S-palmitoyl cysteine (By similarity).
 FT LIPID 217 217 S-palmitoyl cysteine (By similarity).
 FT LIPID 218 218 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 227 AA; 25300 MW; 8E3474E7A590374A CRC64;

Query Match 98.9%; Score 94; DB 1; Length 227;
 Best Local Similarity 94.4%; Pred. No. 3e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAl 18
 |||||
 DB 167 PKKDVLETFVKSCPDAl 184

RESULT 4
 CD9 RAT
 ID CD9 RAT STANDARD; PRT; 225 AA.
 AC P40241;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE CD9 antigen.
 GN Name=CD9;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [4]

RA ROLE IN GAMETE FUSION.
 RX PubMed=10700183; DOI=10.1038/73502;
 RX Kajji K., Oda S., Shikano T., Ohnuki T., Uematsu Y., Sakagami J.,
 RX Tada N., Miyazaki S., Kudo A.;
 RA "The gamete fusion process is defective in eggs of Cd9-deficient
 RT mice";
 RL Nat. Genet. 24:279-282(2000).
 RN [5]

RA ROLE IN PARANODAL FORMATION, AND TISSUE SPECIFICITY.
 RX PubMed=14715942; DOI=10.1523/JNEUROSCI.1484-03.2004;
 RX Ishibashi T., Ding L., Ikenaka K., Inoue Y., Miyado K., Mekada E.,
 RA Baba H.;
 RA "Tetraspanin protein Cd9 is a novel paranodal component regulating
 RT paranodal junctional formation";
 RL J. Neurosci. 24:96-102(2004).
 RN [6]

RA FUNCTION AS RECEPTOR FOR PSG17.
 RX PubMed=11805154; DOI=10.1084/jem.20011741;
 RX Waterhouse R., Ha C., Dvorkin G.S.;
 RA "Murine Cd9 is the receptor for pregnancy-specific glycoprotein 17";
 RL J. Exp. Med. 195:277-282(2002).
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis. Acts as a receptor for PSG17.
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the peripheral
 CC nervous system.
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; L08115; AAA37405.1; -; mRNA.
 DR EMBL; AK002251; BAB21965.1; -; mRNA.
 DR EMBL; AK012793; BAB28473.1; -; mRNA.
 DR EMBL; BC070474; AAB70474.1; -; mRNA.
 DR F01; I49589; I49589.
 DR Ensembl; ENSMUSG00000030342; Mus musculus.
 DR MGI; MGI:88348; Cd9.
 DR GO; GO:0005887; C: integral to plasma membrane; ISS.
 DR GO; GO:0005886; C: plasma membrane; TAS.
 DR GO; GO:0005515; P: protein binding; IPI.
 DR GO; GO:0007155; P: cell adhesion; ISS.
 DR GO; GO:0006928; P: cell motility; ISS.
 DR GO; GO:0007342; P: fusion of sperm to egg plasma membrane; IDA.
 DR GO; GO:0030913; P: paranodal junction formation; IDA.
 DR GO; GO:0030168; P: platelet activation; ISS.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; 1.
 DR PRINTS; PS00259; TMFOUR.
 DR PROSITE; PS00421; TM4 1; 1.
 KW Antigen; Cell adhesion; Fertilization; Glycoprotein; Lipoprotein;
 KW Palmitate; Phosphorylation; Transmembrane.
 FT INIT_MET 0 0 By similarity.
 FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.

FT TOPO_DOM 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT TOPO_DOM 74 84 Cytoplasmic (Potential).
 FT TRANSMEM 85 108 Potential.
 FT TOPO_DOM 109 192 Extracellular (Potential).
 FT TRANSMEM 193 218 Potential.
 FT TOPO_DOM 219 225 Cytoplasmic (Potential).
 FT LIPID 8 8 S-palmitoyl cysteine (By similarity).
 FT LIPID 75 75 S-palmitoyl cysteine (By similarity).
 FT LIPID 76 76 S-palmitoyl cysteine (By similarity).
 FT LIPID 84 84 S-palmitoyl cysteine (By similarity).
 FT LIPID 215 215 S-palmitoyl cysteine (By similarity).
 FT LIPID 216 216 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 225 AA; 25127 MW; 2BBE40B8D7C31B5C0 CRC64;
 Query Match 70.5%; Score 67; DB 1; Length 225;
 Best Local Similarity 66.7%; Pred. No. 0.01;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 PKQVLETFVKSQDAI 18
 DB 165 PKQQLLESFQVPCPEAI 182
 RESULT 6
 CD9_FELCA STANDARD; PRT; 225 AA.
 ID CD9_FELCA
 AC F40239;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE CD9 antigen.
 GN Name=CD9;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX PubMed=7753050; DOI=10.1016/0161-5890(95)00008-3;
 RA Willett B.J., Neil J.C.;
 RT "cDNA cloning and eukaryotic expression of feline CD9";
 RL Mol. Immunol. 32:417-423(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Morikawa S.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in platelet activation and aggregation.
 CC Regulates paranodal junction formation. Required for gamete
 CC fusion. Involved in cell adhesion, cell motility and tumor
 CC metastasis (By similarity).
 CC -!- SUBUNIT: Forms both disulfide-linked homodimers and higher
 CC homooligomers as well as heterooligomers with other members of the
 CC tetraspanin family. Associates with CR2/CD21 and with PTGFRN/CD9P1
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: Phosphorylated on tyrosine following B-cell activation (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; L35275; AAA92867.1; -; mRNA.
 DR EMBL; D30786; BAA06452.1; -; mRNA.
 DR GO; GO:0005887; C: integral to plasma membrane; ISS.
 DR GO; GO:0005515; P: protein binding; ISS.
 DR GO; GO:0007155; P: cell adhesion; ISS.


```
DE Hypothetical protein CBG24151.
GN Name=CBG24151;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]_TaxID=6238;
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100244; CAB56446.1; -; Genomic_DNA.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000535; MSP.
DR Pfam; PF00635; Motile_Sperm; 1.
DR PROSITE; PS0202; MSP; 1.
KW Cytoskeleton; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 398 AA; 44537 MW; EB3639FD23BD6FD2 CRC64;

Query Match 56.3%; Score 53.5; DB 2; Length 398;
Best Local Similarity 54.5%; Pred. No. 3.5;
Matches 12; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 1 PKKDVLETFVK-----SCPDA 17
Db ||| | | | | | | | | | | | | | | | |
24 PKKTVIETSKSLFSCPD 45

RESULT 12
Q9IBC9 CHICK
ID Q9IBC9_CHICK PRELIMINARY; PRT; 224 AA.
AC Q9IBC9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD9 antigen.
GN Name=CD9;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RA Kobayashi T., Mekada E.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032767; BAA93011.1; -; mRNA.
DR HSP; P60033; IG80.
DR Ensembl; ENSGALG0000017274; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 224 AA; 24969 MW; AE64BDF849516151 CRC64;

Query Match 54.7%; Score 52; DB 2; Length 224;
Best Local Similarity 55.6%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PKKDVLETFVKSCPDAI 18
Db ||| : | : | | | | | | | | | |
164 PKKTLPESTTMPCKAI 181

RESULT 13
Q851Q5_ORYSA
```

```
ID Q851Q5_ORYSA PRELIMINARY; PRT; 218 AA.
AC Q851Q5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative DNA-binding protein.
GN Name=OSJNBA0052F07.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP NUCLEOTIDE SEQUENCE.
DR EMBL; AC104321; AAC037525.1; -; Genomic_DNA.
DR Gramene; Q851Q5; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001025; BAH_1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF01426; BAH; 1.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00439; BAH; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
KW DNA-binding.
SQ SEQUENCE 218 AA; 25047 MW; D82DEFB3F116D057 CRC64;

Query Match 52.1%; Score 49.5; DB 2; Length 218;
Best Local Similarity 55.6%; Pred. No. 8.7;
Matches 10; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 PKKDVLETFVKSCPDAI 18
Db ||| | | | | | | | | | | | | | | | |
7 PKRVLESFTTKG-PDGV 23

RESULT 14
Q5YZ96 NOCPA
ID Q5YZ96_NOCPA PRELIMINARY; PRT; 144 AA.
AC Q5YZ96;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=nfal6490;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]_TaxID=37329;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD56495.1; -; Genomic_DNA.
```

Search completed: January 20, 2006, 17:21:31
Job time : 69.4444 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:38:26 ; Search time 29.2308 Seconds
(without alignments)
226.270 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192
Perfect score: 80
Sequence: 1 HKDEVIKEVQEPYKDYTNKL.....LEFTTVKSCPDAIKEVFNK 80

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/taa/5 COMB.pep.*
2: /cgn2_6/prodata/1/taa/6 COMB.pep.*
3: /cgn2_6/prodata/1/taa/H COMB.pep.*
4: /cgn2_6/prodata/1/taa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/taa/RE COMB.pep.*
6: /cgn2_6/prodata/1/taa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	227	1	US-08-254-493-1
2	80	100.0	227	1	US-08-253-751-6
3	80	100.0	227	1	US-08-453-925-6
4	80	100.0	227	2	US-08-403-253A-6
5	80	100.0	227	2	US-08-435-816A-6
6	80	100.0	227	2	US-09-350-202-6
7	80	100.0	227	2	US-08-592-711-6
8	80	100.0	227	2	US-09-349-915B-6
9	80	100.0	228	1	US-08-408-222B-1
10	47	58.8	79	2	US-08-630-172-8
11	47	58.8	79	2	US-09-375-419-8
12	30	37.5	30	1	US-08-254-493-4
13	30	37.5	30	1	US-08-408-222B-4
14	29	36.2	29	1	US-08-254-493-5
15	29	36.2	29	1	US-08-254-493-6
16	29	36.2	29	1	US-08-408-222B-5
17	29	36.2	29	1	US-08-408-222B-6
18	8	10.0	303	2	US-09-134-001C-5215
19	8	10.0	361	2	US-09-248-796A-16765
20	7	8.8	321	2	US-09-252-991A-26003
21	7	8.8	589	2	US-09-328-352-6901
22	7	8.8	770	2	US-09-252-991A-26865
23	7	8.8	781	2	US-09-252-991A-28926
24	7	8.8	919	2	US-09-248-796A-17485
25	7	8.8	1196	2	US-09-107-532A-3944
26	6	7.5	62	2	US-09-621-976-5649
27	6	7.5	75	2	US-09-489-039A-12814

28	7.5	76	2	US-09-107-532A-4420	Sequence 4420, Ap
29	7.5	90	2	US-09-397-787-17	Sequence 17, Appl
30	7.5	90	2	US-09-270-767-59503	Sequence 59503, A
31	7.5	100	2	US-09-583-110-3743	Sequence 3743, Ap
32	7.5	109	2	US-09-107-532A-5605	Sequence 5605, Ap
33	7.5	110	2	US-09-084-303B-200	Sequence 200, App
34	7.5	119	2	US-09-270-767-47551	Sequence 47551, A
35	7.5	120	2	US-09-949-016-8529	Sequence 8529, Ap
36	7.5	120	2	US-09-949-016-9471	Sequence 9471, Ap
37	7.5	122	2	US-09-134-001C-4533	Sequence 4533, Ap
38	7.5	123	2	US-09-949-016-10319	Sequence 10319, A
39	7.5	134	1	US-08-482-728A-14	Sequence 14, Appl
40	7.5	134	2	US-09-949-016-8720	Sequence 8720, Ap
41	7.5	144	2	US-09-107-433-3320	Sequence 3320, Ap
42	7.5	155	2	US-09-270-767-44087	Sequence 44087, A
43	7.5	155	2	US-09-248-796A-21136	Sequence 21136, A
44	7.5	156	2	US-09-902-540-10151	Sequence 10151, A
45	7.5	169	2	US-09-134-000C-3649	Sequence 3649, Ap
46	7.5	176	1	US-08-145-995A-4	Sequence 4, Appl
47	7.5	176	1	US-08-451-747-4	Sequence 4, Appl
48	7.5	176	2	US-09-134-852-4	Sequence 4, Appl
49	7.5	183	2	US-09-248-796A-15732	Sequence 15732, A
50	7.5	186	2	US-10-104-047-2159	Sequence 2159, Ap
51	7.5	194	2	US-09-489-039A-9776	Sequence 9776, Ap
52	7.5	196	2	US-09-543-681A-5304	Sequence 5304, Ap
53	7.5	202	2	US-09-248-796A-22355	Sequence 22355, A
54	7.5	207	2	US-09-134-001C-4488	Sequence 4488, Ap
55	7.5	222	1	US-08-090-048-1	Sequence 1, Appl
56	7.5	222	1	US-08-292-550-1	Sequence 1, Appl
57	7.5	222	1	US-07-927-661A-1	Sequence 1, Appl
58	7.5	245	2	US-09-252-991A-26304	Sequence 26304, A
59	7.5	248	2	US-09-252-991A-34788	Sequence 34788, A
60	7.5	252	2	US-09-252-991A-20598	Sequence 20598, A
61	7.5	261	2	US-08-975-762-72	Sequence 72, Appl
62	7.5	261	2	US-09-295-028-72	Sequence 72, Appl
63	7.5	261	2	US-09-106-582-72	Sequence 72, Appl
64	7.5	261	2	US-09-159-469-72	Sequence 72, Appl
65	7.5	265	2	US-09-693-542-72	Sequence 72, Appl
66	7.5	265	2	US-09-614-069-1	Sequence 1, Appl
67	7.5	265	2	US-09-855-323-16	Sequence 16, Appl
68	7.5	279	2	US-09-704-725-8	Sequence 8, Appl
69	7.5	281	2	US-09-270-767-35423	Sequence 35423, A
70	7.5	281	2	US-09-103-664A-5	Sequence 5, Appl
71	7.5	294	2	US-09-134-000C-5262	Sequence 5262, Ap
72	7.5	300	2	US-09-247-155-107	Sequence 107, App
73	7.5	303	2	US-09-903-190-107	Sequence 107, App
74	7.5	306	2	US-09-634-238-231	Sequence 231, App
75	7.5	307	2	US-09-134-000C-5830	Sequence 5830, Ap
76	7.5	312	2	US-09-107-532A-6219	Sequence 6219, Ap
77	7.5	314	2	US-09-551-826D-6	Sequence 6, Appl
78	7.5	316	2	US-09-551-826D-2	Sequence 2, Appl
79	7.5	318	2	US-09-551-826D-10	Sequence 10, Appl
80	7.5	319	2	US-09-615-192A-323	Sequence 323, App
81	7.5	324	2	US-09-304-967-81	Sequence 81, Appl
82	7.5	327	2	US-09-543-681A-6219	Sequence 6219, Ap
83	7.5	334	2	US-09-252-991A-27369	Sequence 27369, A
84	7.5	334	2	US-09-489-039A-14184	Sequence 14184, A
85	7.5	344	2	US-09-252-991A-16717	Sequence 16717, A
86	7.5	351	2	US-09-270-767-41311	Sequence 41311, A
87	7.5	351	2	US-09-270-767-56527	Sequence 56527, A
88	7.5	355	2	US-09-270-767-44300	Sequence 44300, A
89	7.5	362	2	US-10-164-595-68	Sequence 68, Appl
90	7.5	362	2	US-09-248-796A-14994	Sequence 14994, A
91	7.5	372	1	US-09-328-352-5630	Sequence 5630, Ap
92	7.5	386	1	US-08-455-968E-7	Sequence 7, Appl
93	7.5	387	1	US-08-823-516-140	Sequence 140, App
94	7.5	387	2	US-09-940-244-140	Sequence 140, App
95	7.5	387	2	US-09-381-212-140	Sequence 140, App
96	7.5	387	2	US-09-713-601A-140	Sequence 140, App
97	7.5	400	2	US-09-949-016-6387	Sequence 6387, Ap
98	7.5	403	2	US-08-311-731A-104	Sequence 104, App
99	7.5	405	2	US-09-769-787-62	Sequence 62, Appl

101	6	7.5	406	2	US-09-328-352-6564	Sequence 6564, Ap	174	6	7.5	691	2	US-09-252-991A-19506	Sequence 19506, A
102	6	7.5	410	2	US-09-949-016-8783	Sequence 8783, Ap	175	6	7.5	698	2	US-09-134-001C-3632	Sequence 3632, Ap
103	6	7.5	413	2	US-08-942-572-2	Sequence 2, Appli	176	6	7.5	700	2	US-09-252-991A-28344	Sequence 28344, A
104	6	7.5	413	2	US-09-614-069-13	Sequence 13, Appli	177	6	7.5	719	2	US-08-975-762-59	Sequence 59, Appli
105	6	7.5	413	2	US-09-614-069-14	Sequence 14, Appli	178	6	7.5	719	2	US-09-295-028-59	Sequence 59, Appli
106	6	7.5	413	2	US-09-821-803A-7	Sequence 7, Appli	179	6	7.5	719	2	US-09-106-582-59	Sequence 59, Appli
107	6	7.5	413	2	US-09-821-803A-8	Sequence 8, Appli	180	6	7.5	719	2	US-09-159-489-59	Sequence 59, Appli
108	6	7.5	416	2	US-09-252-991A-28396	Sequence 28396, A	181	6	7.5	719	2	US-09-693-542-59	Sequence 59, Appli
109	6	7.5	419	2	US-09-248-796A-17396	Sequence 17396, A	182	6	7.5	735	2	US-09-999-833A-74	Sequence 74, Appli
110	6	7.5	438	2	US-09-252-991A-16791	Sequence 16791, A	183	6	7.5	735	2	US-10-020-445A-74	Sequence 74, Appli
111	6	7.5	452	2	US-09-489-039A-12558	Sequence 12558, A	184	6	7.5	736	2	US-09-252-991A-31194	Sequence 31194, A
112	6	7.5	460	2	US-09-199-637A-132	Sequence 132, App	185	6	7.5	736	2	US-09-902-540-10958	Sequence 10958, A
113	6	7.5	460	2	US-09-949-016-7994	Sequence 7994, App	186	6	7.5	740	2	US-09-252-991A-20586	Sequence 20586, A
114	6	7.5	462	2	US-09-538-092-769	Sequence 769, App	187	6	7.5	745	1	US-08-887-518-3	Sequence 3, Appli
115	6	7.5	475	2	US-09-252-991A-29494	Sequence 29494, A	188	6	7.5	745	1	US-09-023-321-3	Sequence 4, Appli
116	6	7.5	475	2	US-09-252-991A-32378	Sequence 32378, A	189	6	7.5	745	1	US-08-890-853-4	Sequence 4, Appli
117	6	7.5	481	2	US-10-104-047-3799	Sequence 3799, Ap	190	6	7.5	745	1	US-09-032-475-3	Sequence 3, Appli
118	6	7.5	482	2	US-09-252-991A-19130	Sequence 19130, A	191	6	7.5	745	1	US-09-099-125A-4	Sequence 4, Appli
119	6	7.5	491	2	US-09-252-991A-22394	Sequence 22394, A	192	6	7.5	745	1	US-09-099-124A-4	Sequence 4, Appli
120	6	7.5	495	2	US-09-198-484-4	Sequence 4, Appli	193	6	7.5	745	2	US-09-032-476-4	Sequence 4, Appli
121	6	7.5	495	2	US-09-543-681A-5589	Sequence 5589, Ap	194	6	7.5	745	2	US-08-890-854-4	Sequence 4, Appli
122	6	7.5	495	2	US-09-902-540-15518	Sequence 5241, Ap	195	6	7.5	745	2	US-09-023-324-4	Sequence 4, Appli
123	6	7.5	499	2	US-09-252-991A-28010	Sequence 15518, A	196	6	7.5	745	2	US-09-168-629-2	Sequence 2, Appli
124	6	7.5	501	2	US-09-538-092-707	Sequence 707, App	197	6	7.5	745	2	US-08-910-820-10	Sequence 10, Appli
125	6	7.5	502	2	US-09-949-016-10218	Sequence 10218, A	198	6	7.5	745	2	US-08-810-131A-2	Sequence 2, Appli
126	6	7.5	504	1	US-08-441-139-18	Sequence 18, Appli	199	6	7.5	745	2	US-09-109-986-4	Sequence 4, Appli
127	6	7.5	508	2	US-08-956-171E-5241	Sequence 5241, Ap	200	6	7.5	745	2	US-09-844-908-10	Sequence 10, Appli
128	6	7.5	508	2	US-08-781-986A-5241	Sequence 5241, Ap	201	6	7.5	745	2	US-09-868-758-3	Sequence 3, Appli
129	6	7.5	509	2	US-09-134-000C-4807	Sequence 4807, Ap	202	6	7.5	745	2	US-09-796-872-2	Sequence 2, Appli
130	6	7.5	510	2	US-09-744-016A-5	Sequence 6, Appli	203	6	7.5	755	2	US-09-097-767A-38	Sequence 38, Appli
131	6	7.5	520	2	US-09-252-991A-23797	Sequence 23797, A	204	6	7.5	761	2	US-09-585-858-27	Sequence 27, Appli
132	6	7.5	521	1	US-08-557-122A-32	Sequence 32, Appli	205	6	7.5	761	2	US-10-270-878-27	Sequence 27, Appli
133	6	7.5	521	2	US-09-262-666-32	Sequence 32, Appli	206	6	7.5	811	2	US-09-540-236-2412	Sequence 2412, Ap
134	6	7.5	521	2	US-09-538-092-1283	Sequence 1283, Ap	207	6	7.5	815	2	US-09-328-352-4284	Sequence 4284, Ap
135	6	7.5	522	2	US-09-368-588-2	Sequence 2, Appli	208	6	7.5	879	2	US-09-872-733A-16	Sequence 16, Appli
136	6	7.5	523	2	US-09-744-016A-21	Sequence 21, Appli	209	6	7.5	903	2	US-09-543-681A-4186	Sequence 4186, Ap
137	6	7.5	529	2	US-09-949-016-10714	Sequence 10714, A	210	6	7.5	904	2	US-09-198-484-2	Sequence 2, Appli
138	6	7.5	529	6	5217865-2	Patent No. 5217865	211	6	7.5	909	2	US-09-949-016-6370	Sequence 6370, Ap
139	6	7.5	530	1	US-08-557-122A-35	Sequence 35, Appli	212	6	7.5	916	2	US-09-543-681A-5205	Sequence 5205, Ap
140	6	7.5	530	2	US-09-262-666-35	Sequence 35, Appli	213	6	7.5	916	2	US-09-489-039A-14125	Sequence 14125, A
141	6	7.5	533	2	US-09-744-016A-18	Sequence 18, Appli	214	6	7.5	952	2	US-09-252-991A-32183	Sequence 32183, A
142	6	7.5	534	2	US-09-103-664A-2	Sequence 2, Appli	215	6	7.5	971	2	US-09-248-796A-19531	Sequence 19531, A
143	6	7.5	536	2	US-10-104-047-2780	Sequence 2780, Ap	216	6	7.5	996	2	US-09-417-197-123	Sequence 123, App
144	6	7.5	541	2	US-09-107-532A-5648	Sequence 5648, Ap	217	6	7.5	997	2	US-09-417-197-121	Sequence 121, App
145	6	7.5	549	2	US-09-344-510B-2	Sequence 2, Appli	218	6	7.5	1003	1	US-07-991-867B-6	Sequence 6, Appli
146	6	7.5	550	2	US-09-344-510B-4	Sequence 4, Appli	219	6	7.5	1003	1	US-08-107-755A-6	Sequence 6, Appli
147	6	7.5	570	1	US-08-967-364-1	Sequence 1, Appli	220	6	7.5	1003	1	US-08-544-332-6	Sequence 6, Appli
148	6	7.5	570	1	US-09-368-408-1	Sequence 7, Appli	221	6	7.5	1003	2	US-09-370-861A-6	Sequence 6, Appli
149	6	7.5	570	2	US-09-368-408-7	Sequence 7, Appli	222	6	7.5	1011	2	US-09-602-362E-27	Sequence 27, Appli
150	6	7.5	570	2	US-09-368-408-7	Sequence 7, Appli	223	6	7.5	1012	2	US-09-344-510B-3	Sequence 1, Appli
151	6	7.5	572	2	US-09-252-991A-23996	Sequence 23996, A	224	6	7.5	1014	2	US-10-164-595-28	Sequence 28, Appli
152	6	7.5	572	2	US-09-252-991A-25086	Sequence 25086, A	225	6	7.5	1082	2	US-09-112-096-15	Sequence 15, Appli
153	6	7.5	586	2	US-08-419-810-12	Sequence 12, Appli	226	6	7.5	1095	2	US-09-636-215-778	Sequence 778, App
154	6	7.5	586	6	5405775-11	Patent No. 5405775	227	6	7.5	1095	2	US-09-636-215-780	Sequence 780, App
155	6	7.5	595	2	US-09-949-016-9801	Sequence 9801, Ap	228	6	7.5	1095	2	US-09-685-166A-778	Sequence 778, App
156	6	7.5	600	2	US-09-252-991A-21703	Sequence 21703, A	229	6	7.5	1095	2	US-09-685-166A-780	Sequence 780, App
157	6	7.5	618	2	US-09-252-991A-22418	Sequence 22418, A	230	6	7.5	1095	2	US-09-679-426-778	Sequence 778, App
158	6	7.5	630	2	US-09-902-540-11085	Sequence 11085, A	231	6	7.5	1095	2	US-09-657-279-780	Sequence 780, App
159	6	7.5	631	2	US-09-252-991A-20418	Sequence 20418, A	232	6	7.5	1095	2	US-09-657-279-780	Sequence 780, App
160	6	7.5	632	2	US-09-354-129-8	Sequence 8, Appli	233	6	7.5	1095	2	US-09-759-143-778	Sequence 778, App
161	6	7.5	632	2	US-09-504-357-8	Sequence 8, Appli	234	6	7.5	1095	2	US-09-759-143-780	Sequence 780, App
162	6	7.5	638	1	US-08-557-122A-38	Sequence 38, Appli	235	6	7.5	1095	2	US-09-651-236-778	Sequence 778, App
163	6	7.5	638	2	US-09-262-666-38	Sequence 38, Appli	236	6	7.5	1095	2	US-09-651-236-780	Sequence 780, App
164	6	7.5	645	2	US-09-538-092-920	Sequence 920, App	237	6	7.5	1095	2	US-09-657-279-778	Sequence 778, App
165	6	7.5	650	2	US-09-252-991A-32334	Sequence 32334, A	238	6	7.5	1095	2	US-09-657-279-780	Sequence 780, App
166	6	7.5	652	2	US-09-636-215-818	Sequence 818, App	239	6	7.5	1095	2	US-10-012-896-778	Sequence 778, App
167	6	7.5	652	2	US-09-685-166A-818	Sequence 818, App	240	6	7.5	1095	2	US-10-012-896-780	Sequence 780, App
168	6	7.5	652	2	US-09-678-426-818	Sequence 818, App	241	6	7.5	1231	2	US-09-071-035-420	Sequence 420, App
169	6	7.5	652	2	US-09-759-143-818	Sequence 818, App	242	6	7.5	1231	2	US-10-206-576-420	Sequence 420, App
170	6	7.5	652	2	US-09-651-236-818	Sequence 818, App	243	6	7.5	1239	2	US-10-076-622-577	Sequence 577, App
171	6	7.5	652	2	US-09-657-279-818	Sequence 818, App	244	6	7.5	1265	2	US-09-071-035-418	Sequence 418, App
172	6	7.5	652	2	US-10-012-896-818	Sequence 818, App	245	6	7.5	1265	2	US-10-206-576-418	Sequence 418, App
173	6	7.5	662	2	US-09-252-991A-31942	Sequence 31942, A	246	6	7.5	1278	2	US-09-134-000C-6043	Sequence 6043, Ap

247	6	7.5	1462	2	US-09-538-092-1043	Sequence 1043, Ap	320	5	6.2	20	2	US-09-724-062-65	Sequence 65, Appl
248	6	7.5	1462	2	US-09-949-002-381	Sequence 381, App	321	5	6.2	20	2	US-09-724-065-64	Sequence 64, Appl
249	6	7.5	1504	2	US-09-252-991A-26608	Sequence 26608, A	322	5	6.2	20	2	US-09-724-065-65	Sequence 65, Appl
250	6	7.5	1514	1	US-08-853-310-4	Sequence 4, Appli	323	5	6.2	20	2	US-09-724-481-64	Sequence 64, Appl
251	6	7.5	1524	2	US-09-949-002-495	Sequence 495, App	324	5	6.2	20	2	US-09-724-481-65	Sequence 65, Appl
252	6	7.5	1566	2	US-09-581-472B-2	Sequence 2, Appli	325	5	6.2	20	6	5204097-3	Patent No. 5204097
253	6	7.5	1581	2	US-09-110-517-2	Sequence 2, Appli	326	5	6.2	22	2	US-10-038-612-79	Sequence 79, Appl
254	6	7.5	1596	2	US-09-328-352-5542	Sequence 2, Appli	327	5	6.2	22	2	US-10-038-613-80	Sequence 80, Appl
255	6	7.5	1650	2	US-09-252-991A-21798	Sequence 21798, A	328	5	6.2	22	2	US-09-479-479-29	Sequence 29, Appl
256	6	7.5	1659	2	US-09-487-558B-118	Sequence 118, App	329	5	6.2	23	2	US-09-297-851-29	Sequence 29, Appl
257	6	7.5	1706	1	US-08-459-568-2	Sequence 2, Appli	330	5	6.2	23	2	US-09-200-757-5	Sequence 5, Appli
258	6	7.5	1706	1	US-08-399-411-2	Sequence 2, Appli	331	5	6.2	25	2	PCT-US95-13841-1	Sequence 1, Appli
259	6	7.5	1706	2	US-08-516-859A-2	Sequence 2, Appli	332	5	6.2	26	4	PCT-US95-13841-1	Sequence 2, Appli
260	6	7.5	1706	2	US-09-586-472-2	Sequence 2, Appli	333	5	6.2	28	2	US-09-058-459-2	Sequence 2, Appli
261	6	7.5	1706	2	US-09-528-706-2	Sequence 2, Appli	334	5	6.2	28	2	US-09-127-926-2	Sequence 2, Appli
262	6	7.5	1706	2	US-10-024-450-2	Sequence 2, Appli	335	5	6.2	28	2	US-09-714-357-2	Sequence 2, Appli
263	6	7.5	2220	2	US-09-949-016-9730	Sequence 9730, Ap	336	5	6.2	28	2	US-10-057-552-2	Sequence 2, Appli
264	6	7.5	2273	2	US-09-426-998-5	Sequence 5, Appli	337	5	6.2	28	2	US-09-827-960-2	Sequence 2, Appli
265	6	7.5	3052	1	US-08-557-122A-26	Sequence 26, Appl	338	5	6.2	28	2	US-09-837-886-2	Sequence 2, Appli
266	6	7.5	3522	2	US-09-262-666-26	Sequence 26, Appl	339	5	6.2	28	2	US-09-812-034-2	Sequence 2, Appli
267	6	7.5	3724	1	US-08-804-227C-10	Sequence 10, Appl	340	5	6.2	30	1	US-08-287-959-14	Sequence 14, Appl
268	6	7.5	3724	1	US-08-804-198-4	Sequence 4, Appli	341	5	6.2	31	2	US-09-227-357-398	Sequence 398, App
269	6	7.5	3913	2	US-09-949-016-10933	Sequence 10933, A	342	5	6.2	31	2	US-09-973-278-508	Sequence 508, App
270	6	7.5	4377	2	US-09-949-016-6978	Sequence 6978, Ap	343	5	6.2	39	2	US-09-270-767-58213	Sequence 58213, A
271	6	6.2	6	2	US-09-136-251-9	Sequence 9, Appli	344	5	6.2	42	4	PCT-US95-13841-25	Sequence 25, Appl
272	5	6.2	6	2	US-09-634-496-9	Sequence 9, Appli	345	5	6.2	42	4	PCT-US95-13841-29	Sequence 29, Appl
273	5	6.2	6	2	US-09-635-145A-9	Sequence 9, Appli	346	5	6.2	43	2	US-09-057-363C-59	Sequence 59, Appl
274	5	6.2	8	2	US-09-200-757-1	Sequence 1, Appli	347	5	6.2	43	2	US-09-265-107-59	Sequence 59, Appl
275	5	6.2	8	2	US-09-200-757-3	Sequence 3, Appli	348	5	6.2	43	2	US-09-270-767-62022	Sequence 62022, A
276	5	6.2	10	2	US-09-200-757-4	Sequence 4, Appli	349	5	6.2	43	4	PCT-US95-13841-30	Sequence 30, Appl
277	5	6.2	10	2	US-09-200-757-4	Sequence 4, Appli	350	5	6.2	46	1	US-08-639-857-30	Sequence 30, Appl
278	5	6.2	10	2	US-09-926-163B-18	Sequence 18, Appl	351	5	6.2	46	2	US-09-270-767-56973	Sequence 56973, A
279	5	6.2	10	2	US-10-394-980-398	Sequence 398, App	352	5	6.2	47	2	US-08-936-165A-345	Sequence 345, App
280	5	6.2	10	2	US-10-394-980-452	Sequence 452, App	353	5	6.2	47	2	US-09-904-615-88	Sequence 88, Appl
281	5	6.2	11	6	5204097-5	Patent No. 5204097	354	5	6.2	47	2	US-10-002-344A-178	Sequence 178, App
282	5	6.2	13	1	US-08-305-871A-28	Patent No. 5204097	355	5	6.2	47	2	US-10-054-988-88	Sequence 88, Appl
283	5	6.2	14	6	5204097-4	Patent No. 5204097	356	5	6.2	49	2	US-08-398-633-18	Sequence 18, Appl
284	5	6.2	15	2	US-09-490-702B-15	Sequence 15, Appl	357	5	6.2	49	2	US-08-480-070C-24	Sequence 24, Appl
285	5	6.2	15	2	US-09-767-460-15	Sequence 15, Appl	358	5	6.2	49	2	US-08-829-525-38	Sequence 38, Appl
286	5	6.2	16	2	US-08-602-999A-384	Sequence 384, App	359	5	6.2	49	2	US-08-829-525-38	Sequence 38, Appl
287	5	6.2	16	2	US-09-500-124-384	Sequence 384, App	360	5	6.2	51	6	5274075-11	Patent No. 5274075
288	5	6.2	17	2	US-09-479-479-23	Sequence 23, Appl	361	5	6.2	52	2	US-09-128-155-8	Sequence 8, Appli
289	5	6.2	17	2	US-09-297-851-23	Sequence 23, Appl	362	5	6.2	53	2	US-08-836-500A-8	Sequence 8, Appli
290	5	6.2	19	2	US-09-441-502B-90	Sequence 90, Appl	363	5	6.2	53	2	US-09-679-750-8	Sequence 8, Appli
291	5	6.2	19	2	US-09-441-502B-91	Sequence 91, Appl	364	5	6.2	54	2	US-09-270-767-36652	Sequence 36652, A
292	5	6.2	20	1	US-08-399-695-87	Sequence 87, Appl	365	5	6.2	54	2	US-09-270-767-51869	Sequence 51869, A
293	5	6.2	20	2	US-08-825-852-63	Sequence 63, Appl	366	5	6.2	54	2	US-09-513-999C-6743	Sequence 6743, Ap
294	5	6.2	20	2	US-08-825-852-64	Sequence 64, Appl	367	5	6.2	61	1	US-08-290-448A-57	Sequence 57, Appl
295	5	6.2	20	2	US-09-052-888-64	Sequence 64, Appl	368	5	6.2	61	1	US-08-290-448A-61	Sequence 61, Appl
296	5	6.2	20	2	US-09-052-888-65	Sequence 65, Appl	369	5	6.2	61	1	US-08-290-448A-57	Sequence 57, Appl
297	5	6.2	20	2	US-09-723-890-64	Sequence 64, Appl	370	5	6.2	61	1	US-08-290-448A-57	Sequence 57, Appl
298	5	6.2	20	2	US-09-723-890-65	Sequence 65, Appl	371	5	6.2	61	1	US-08-175-069A-57	Sequence 57, Appl
299	5	6.2	20	2	US-09-723-901-64	Sequence 64, Appl	372	5	6.2	61	1	US-08-175-069A-61	Sequence 61, Appl
300	5	6.2	20	2	US-09-723-901-65	Sequence 65, Appl	373	5	6.2	61	2	US-08-446-137B-12	Sequence 12, Appl
301	5	6.2	20	2	US-09-723-547-65	Sequence 65, Appl	374	5	6.2	61	2	US-08-461-939B-57	Sequence 57, Appl
302	5	6.2	20	2	US-09-723-547-65	Sequence 65, Appl	375	5	6.2	61	2	US-08-461-939B-61	Sequence 61, Appl
303	5	6.2	20	2	US-09-724-127-64	Sequence 64, Appl	376	5	6.2	61	2	US-08-464-000-57	Sequence 57, Appl
304	5	6.2	20	2	US-09-724-127-65	Sequence 65, Appl	377	5	6.2	61	2	US-08-464-000-61	Sequence 61, Appl
305	5	6.2	20	2	US-09-723-931-64	Sequence 64, Appl	378	5	6.2	61	2	US-09-248-796A-21602	Sequence 21602, A
306	5	6.2	20	2	US-09-723-931-65	Sequence 65, Appl	379	5	6.2	62	2	US-09-580-201A-16	Sequence 16, Appl
307	5	6.2	20	2	US-09-723-873-65	Sequence 65, Appl	380	5	6.2	62	2	US-09-902-540-10101	Sequence 10101, A
308	5	6.2	20	2	US-09-723-873-65	Sequence 65, Appl	381	5	6.2	63	2	US-09-128-155-4	Sequence 4, Appli
309	5	6.2	20	2	US-09-724-114-64	Sequence 64, Appl	382	5	6.2	63	2	US-09-497-431-47	Sequence 47, Appl
310	5	6.2	20	2	US-09-724-114-65	Sequence 65, Appl	383	5	6.2	63	2	US-09-248-796A-21203	Sequence 21203, A
311	5	6.2	20	2	US-09-723-913-64	Sequence 64, Appl	384	5	6.2	63	2	US-09-248-796A-22702	Sequence 22702, A
312	5	6.2	20	2	US-09-723-913-65	Sequence 65, Appl	385	5	6.2	63	2	US-09-248-796A-25412	Sequence 25412, A
313	5	6.2	20	2	US-09-723-912-65	Sequence 65, Appl	386	5	6.2	63	2	US-09-898-659-38	Sequence 38, Appl
314	5	6.2	20	2	US-09-723-912-65	Sequence 65, Appl	387	5	6.2	64	2	US-09-248-796A-24891	Sequence 24891, A
315	5	6.2	20	2	US-09-724-095-64	Sequence 64, Appl	388	5	6.2	65	1	US-08-981-012A-11	Sequence 11, Appl
316	5	6.2	20	2	US-09-724-095-64	Sequence 64, Appl	389	5	6.2	65	2	US-09-247-1551-108	Sequence 108, App
317	5	6.2	20	2	US-09-724-157-65	Sequence 65, Appl	390	5	6.2	65	2	US-09-337-501-10	Sequence 10, Appl
318	5	6.2	20	2	US-09-724-157-65	Sequence 65, Appl	391	5	6.2	65	2	US-09-621-976-4513	Sequence 4513, Ap
319	5	6.2	20	2	US-09-724-062-64	Sequence 64, Appl	392	5	6.2	65	2	US-09-479-040-29	Sequence 29, Appl

393	5	6.2	65	2	US-09-903-190-108	Sequence 108, App	466	5	6.2	89	2	US-08-821-324-26	Sequence 26, Appl
394	5	6.2	66	1	US-08-437-607A-44	Sequence 44, Appl	467	5	6.2	89	2	US-08-295-028-26	Sequence 26, Appl
395	5	6.2	66	2	US-08-446-137B-10	Sequence 10, Appl	468	5	6.2	89	2	US-09-106-582-26	Sequence 26, Appl
396	5	6.2	66	2	US-09-540-236-2981	Sequence 2981, Ap	469	5	6.2	89	2	US-09-159-469-26	Sequence 26, Appl
397	5	6.2	67	2	US-09-621-976-3394	Sequence 3394, Ap	470	5	6.2	89	2	US-09-489-039A-12673	Sequence 12673, A
398	5	6.2	67	2	US-09-465-559-22	Sequence 22, Appl	471	5	6.2	89	2	US-09-621-976-4646	Sequence 4646, Ap
399	5	6.2	67	2	US-09-248-796A-22622	Sequence 22622, A	472	5	6.2	89	2	US-09-334-477-4	Sequence 4, Appli
400	5	6.2	67	2	US-08-180-761B-3	Sequence 3, Appli	473	5	6.2	89	2	US-08-334-477-8	Sequence 8, Appli
401	5	6.2	68	1	US-09-248-796A-26169	Sequence 26169, A	474	5	6.2	89	2	US-09-693-542-26	Sequence 26, Appl
402	5	6.2	69	1	US-08-292-968-21	Sequence 21, Appl	475	5	6.2	89	2	US-09-513-999C-5953	Sequence 5953, Ap
403	5	6.2	69	1	US-08-467-974-21	Sequence 21, Appl	476	5	6.2	89	2	US-09-248-796A-24052	Sequence 24052, A
404	5	6.2	69	1	US-08-467-976-21	Sequence 21, Appl	477	5	6.2	91	2	US-09-543-681A-6313	Sequence 6313, Ap
405	5	6.2	69	2	US-08-467-976-21	Sequence 21, Appl	478	5	6.2	91	2	US-09-621-976-4864	Sequence 4864, Ap
406	5	6.2	69	2	US-09-082-514-21	Sequence 21, Appl	479	5	6.2	92	2	US-08-248-796A-16829	Sequence 16829, A
407	5	6.2	69	2	US-09-270-767-41728	Sequence 41728, A	480	5	6.2	92	2	US-09-248-796A-18539	Sequence 18539, A
408	5	6.2	70	2	US-09-328-352-5946	Sequence 5946, Ap	481	5	6.2	92	2	US-09-248-796A-25374	Sequence 25374, A
409	5	6.2	70	2	US-09-543-681A-4584	Sequence 4584, Ap	482	5	6.2	93	2	US-09-513-999C-5618	Sequence 5618, Ap
410	5	6.2	70	6	5204097-1	Patent No. 5204097	483	5	6.2	93	2	US-09-902-540-14770	Sequence 14770, A
411	5	6.2	71	2	US-09-621-976-4752	Sequence 4752, Ap	484	5	6.2	94	2	US-09-270-767-46508	Sequence 46508, A
412	5	6.2	72	2	US-08-836-500A-6	Sequence 6, Appli	485	5	6.2	94	2	US-08-270-767-62094	Sequence 62094, A
413	5	6.2	72	2	US-09-679-750-6	Sequence 6, Appli	486	5	6.2	95	2	US-09-902-540-10228	Sequence 10228, A
414	5	6.2	73	2	US-09-366-887A-24	Sequence 24, Appl	487	5	6.2	97	2	US-08-816-977-23	Sequence 23, Appl
415	5	6.2	73	2	US-09-248-796A-24220	Sequence 24220, A	488	5	6.2	97	2	US-08-816-977-27	Sequence 27, Appl
416	5	6.2	73	2	US-09-517-204-24	Sequence 24, Appl	489	5	6.2	97	2	US-09-366-887A-6	Sequence 6, Appli
417	5	6.2	74	2	US-09-134-000C-5163	Sequence 5163, Ap	490	5	6.2	97	2	US-09-252-991A-17020	Sequence 17020, A
418	5	6.2	75	2	US-09-540-236-3737	Sequence 3737, Ap	491	5	6.2	97	2	US-08-311-731A-77	Sequence 77, Appl
419	5	6.2	75	2	US-09-248-796A-25808	Sequence 25808, A	492	5	6.2	97	2	US-09-334-477-23	Sequence 23, Appl
420	5	6.2	75	2	US-09-513-999C-5127	Sequence 5127, Ap	493	5	6.2	97	2	US-09-334-477-27	Sequence 27, Appl
421	5	6.2	76	2	US-09-180-827-3	Sequence 3, Appli	494	5	6.2	97	2	US-09-545-894-14	Sequence 14, Appl
422	5	6.2	76	2	US-09-252-991A-32156	Sequence 32156, A	495	5	6.2	97	2	US-09-517-204-6	Sequence 6, Appli
423	5	6.2	76	2	US-09-583-110-3419	Sequence 3419, Ap	496	5	6.2	97	2	US-09-513-999C-5617	Sequence 5617, Ap
424	5	6.2	76	2	US-09-248-796A-24296	Sequence 24296, A	497	5	6.2	98	2	US-09-366-887A-7	Sequence 7, Appli
425	5	6.2	77	2	US-08-858-207A-285	Sequence 285, App	498	5	6.2	98	2	US-09-517-204-7	Sequence 7, Appli
426	5	6.2	77	2	US-09-134-001C-3386	Sequence 3386, Ap	499	5	6.2	99	2	US-09-583-110-3188	Sequence 3188, Ap
427	5	6.2	77	2	US-09-248-796A-23767	Sequence 23767, A	500	5	6.2	99	2	US-09-107-433-4418	Sequence 4418, Ap
428	5	6.2	77	2	US-09-248-796A-23996	Sequence 23996, A	501	5	6.2	99	2	US-09-902-540-10375	Sequence 10375, A
429	5	6.2	77	2	US-09-248-796A-27345	Sequence 27345, A	502	5	6.2	100	2	US-09-091-725-35	Sequence 35, Appl
430	5	6.2	79	2	US-09-621-976-4746	Sequence 4746, Ap	503	5	6.2	100	2	US-08-311-731A-235	Sequence 235, App
431	5	6.2	79	2	US-09-270-767-44291	Sequence 44291, A	504	5	6.2	101	1	US-08-264-244-1	Sequence 1, Appli
432	5	6.2	79	2	US-09-248-796A-24174	Sequence 24174, A	505	5	6.2	101	1	US-08-478-689-1	Sequence 1, Appli
433	5	6.2	80	2	US-09-149-476-578	Sequence 578, App	506	5	6.2	101	1	US-08-476-940-1	Sequence 1, Appli
434	5	6.2	80	2	US-09-252-991A-44876	Sequence 44876, A	507	5	6.2	101	1	US-08-704-872-1	Sequence 1, Appli
435	5	6.2	80	2	US-09-270-767-44007	Sequence 44007, A	508	5	6.2	101	1	US-08-577-464-2	Sequence 2, Appli
436	5	6.2	80	2	US-09-270-767-59415	Sequence 59415, A	509	5	6.2	101	1	US-08-967-038-1	Sequence 1, Appli
437	5	6.2	80	2	US-09-809-665A-129	Sequence 129, App	510	5	6.2	101	2	US-08-871-600A-1	Sequence 1, Appli
438	5	6.2	81	2	US-09-270-767-62025	Sequence 62025, A	511	5	6.2	101	2	US-09-198-452A-227	Sequence 227, App
439	5	6.2	81	2	US-09-248-796A-26750	Sequence 26750, A	512	5	6.2	101	2	US-09-248-796A-20677	Sequence 20677, A
440	5	6.2	82	2	US-09-198-452A-766	Sequence 766, App	513	5	6.2	101	2	US-09-438-185A-213	Sequence 213, App
441	5	6.2	82	2	US-09-438-185A-722	Sequence 722, App	514	5	6.2	101	2	US-10-004-381-12	Sequence 12, Appl
442	5	6.2	83	1	US-08-981-012A-5	Sequence 5, Appli	515	5	6.2	102	2	US-09-383-586-34	Sequence 34, Appl
443	5	6.2	83	2	US-09-337-501-5	Sequence 5, Appli	516	5	6.2	102	2	US-09-621-976-6356	Sequence 6356, Ap
444	5	6.2	83	2	US-09-489-039A-7547	Sequence 7547, Ap	517	5	6.2	102	2	US-09-583-110-2880	Sequence 2880, Ap
445	5	6.2	83	2	US-09-583-110-3302	Sequence 3302, Ap	518	5	6.2	102	2	US-09-823-038A-34	Sequence 34, Appl
446	5	6.2	83	2	US-09-270-767-33604	Sequence 33604, A	519	5	6.2	102	2	US-09-107-433-2659	Sequence 2659, Ap
447	5	6.2	83	2	US-09-270-767-48821	Sequence 48821, A	520	5	6.2	102	2	US-09-902-540-12779	Sequence 12779, A
448	5	6.2	83	2	US-09-513-999C-7784	Sequence 7784, Ap	521	5	6.2	103	2	US-09-543-681A-5086	Sequence 5086, App
449	5	6.2	84	1	US-08-981-012A-8	Sequence 8, Appli	522	5	6.2	104	2	US-08-946-329A-106	Sequence 106, App
450	5	6.2	84	2	US-09-337-501-8	Sequence 8, Appli	523	5	6.2	104	2	US-09-134-001C-4945	Sequence 4945, Ap
451	5	6.2	85	2	US-09-107-433-2973	Sequence 2973, Ap	524	5	6.2	104	2	US-09-107-532A-5958	Sequence 5958, Ap
452	5	6.2	85	2	US-09-720-583A-3	Sequence 3, Appli	525	5	6.2	104	2	US-09-562-914-106	Sequence 106, Appl
453	5	6.2	86	1	US-08-245-511-37	Sequence 37, Appl	526	5	6.2	105	1	US-08-264-244-3	Sequence 3, Appli
454	5	6.2	86	1	US-08-600-993A-37	Sequence 37, Appl	527	5	6.2	105	1	US-08-478-689-3	Sequence 3, Appli
455	5	6.2	86	2	US-09-134-001C-5329	Sequence 5329, Ap	528	5	6.2	105	1	US-08-476-940-3	Sequence 3, Appli
456	5	6.2	86	2	US-09-489-039A-8039	Sequence 8039, Ap	529	5	6.2	105	1	US-08-704-872-3	Sequence 3, Appli
457	5	6.2	86	2	US-09-513-999C-5489	Sequence 5489, Ap	530	5	6.2	105	2	US-08-967-038-3	Sequence 3, Appli
458	5	6.2	86	2	US-09-902-540-11924	Sequence 11924, A	531	5	6.2	105	2	US-08-871-600A-3	Sequence 3, Appli
459	5	6.2	87	2	US-09-543-681A-5167	Sequence 5167, Ap	532	5	6.2	106	2	US-09-583-110-4852	Sequence 4852, Ap
460	5	6.2	87	2	US-09-513-999C-5385	Sequence 5385, Ap	533	5	6.2	106	2	US-09-248-796A-22893	Sequence 22893, A
461	5	6.2	88	2	US-09-134-000C-6017	Sequence 6017, Ap	534	5	6.2	106	2	US-09-107-433-4219	Sequence 4219, Ap
462	5	6.2	88	2	US-09-902-540-15259	Sequence 15259, A	535	5	6.2	107	2	US-09-328-352-7927	Sequence 7927, Ap
463	5	6.2	89	2	US-08-816-977-8	Sequence 4, Appli	536	5	6.2	107	2	US-09-710-279-1586	Sequence 1586, Ap
464	5	6.2	89	2	US-08-816-977-8	Sequence 8, Appli	537	5	6.2	108	2	US-09-270-767-38340	Sequence 38340, A
465	5	6.2	89	2	US-08-975-762-26	Sequence 26, Appl	538	5	6.2	108	2	US-09-270-767-46712	Sequence 46712, A

539	5	6.2	108	2	US-09-270-767-53557	Sequence 53557, A	612	5	6.2	127	2	US-09-107-433-4263	Sequence 4263, Ap
540	5	6.2	108	2	US-09-513-999C-4860	Sequence 4860, Ap	613	5	6.2	128	2	US-09-134-000C-4010	Sequence 4010, Ap
541	5	6.2	109	2	US-09-276-071-2	Sequence 2, Appl	614	5	6.2	128	2	US-09-270-767-3311	Sequence 3311, A
542	5	6.2	109	2	US-09-328-352-7707	Sequence 7707, Ap	615	5	6.2	128	2	US-09-270-767-48328	Sequence 48328, A
543	5	6.2	109	2	US-09-732-210-295	Sequence 295, App	616	5	6.2	128	2	US-09-513-999C-8084	Sequence 8084, Ap
544	5	6.2	111	2	US-09-247-155-168	Sequence 168, App	617	5	6.2	129	2	US-09-328-352-6900	Sequence 6900, Ap
545	5	6.2	111	2	US-09-303-190-168	Sequence 168, App	618	5	6.2	129	2	US-09-489-039A-12730	Sequence 12730, A
546	5	6.2	112	2	US-09-395-689-6	Sequence 6, Appl	619	5	6.2	129	2	US-09-513-999C-4177	Sequence 4177, Ap
547	5	6.2	112	2	US-09-489-039A-11682	Sequence 11682, A	620	5	6.2	129	2	US-09-949-016-11574	Sequence 11574, A
548	5	6.2	112	2	US-09-248-796A-20732	Sequence 20732, A	621	5	6.2	130	1	US-08-686-878A-45	Sequence 45, Appl
549	5	6.2	112	2	US-09-248-796A-27648	Sequence 27648, A	622	5	6.2	130	2	US-09-175-928-44	Sequence 44, Appl
550	5	6.2	113	1	US-08-245-511-18	Sequence 18, Appl	623	5	6.2	130	2	US-09-107-532A-6322	Sequence 6322, Ap
551	5	6.2	113	1	US-08-600-993A-18	Sequence 18, Appl	624	5	6.2	130	2	US-09-134-000C-6498	Sequence 6498, Ap
552	5	6.2	113	2	US-09-732-210-679	Sequence 679, App	625	5	6.2	130	2	US-09-583-110-4053	Sequence 4053, Ap
553	5	6.2	113	2	US-09-732-210-681	Sequence 681, App	626	5	6.2	130	2	US-10-121-757B-6	Sequence 6, Appl
554	5	6.2	114	2	US-09-543-681A-6395	Sequence 6395, Ap	627	5	6.2	130	2	US-09-605-703B-2870	Sequence 2870, Ap
555	5	6.2	114	2	US-09-621-976-7553	Sequence 7553, Ap	628	5	6.2	131	2	US-08-903-223-428	Sequence 428, App
556	5	6.2	115	1	US-07-903-029-4	Sequence 4, Appl	629	5	6.2	131	2	US-08-956-171E-5224	Sequence 5224, Ap
557	5	6.2	115	1	US-07-903-029-5	Sequence 5, Appl	630	5	6.2	131	2	US-08-781-986A-5224	Sequence 5224, Ap
558	5	6.2	115	2	US-09-322-409-86	Sequence 86, Appl	631	5	6.2	131	2	US-09-903-540-10812	Sequence 10812, A
559	5	6.2	115	2	US-09-451-527-86	Sequence 86, Appl	632	5	6.2	132	2	US-09-465-559-4	Sequence 4, Appl
560	5	6.2	115	2	US-09-583-110-2719	Sequence 2719, Ap	633	5	6.2	132	2	US-09-270-767-38790	Sequence 38790, A
561	5	6.2	115	2	US-09-583-110-3822	Sequence 3822, Ap	634	5	6.2	132	2	US-09-270-767-54007	Sequence 54007, A
562	5	6.2	115	2	US-09-583-110-4727	Sequence 4727, Ap	635	5	6.2	133	2	US-09-134-001C-3883	Sequence 3883, Ap
563	5	6.2	115	2	US-09-583-110-5007	Sequence 5007, Ap	636	5	6.2	133	2	US-09-621-976-7559	Sequence 7559, Ap
564	5	6.2	115	2	US-09-583-110-5216	Sequence 5216, Ap	637	5	6.2	133	2	US-09-270-767-37757	Sequence 37757, A
565	5	6.2	115	2	US-09-248-796A-28204	Sequence 28204, A	638	5	6.2	133	2	US-09-270-767-52974	Sequence 52974, A
566	5	6.2	115	2	US-09-902-540-13670	Sequence 13670, A	639	5	6.2	133	2	US-09-513-999C-6374	Sequence 6374, Ap
567	5	6.2	116	2	US-09-252-991A-22983	Sequence 22983, A	640	5	6.2	134	2	US-09-322-409-81	Sequence 81, Appl
568	5	6.2	116	2	US-09-732-210-57	Sequence 57, Appl	641	5	6.2	134	2	US-09-451-527-81	Sequence 81, Appl
569	5	6.2	116	2	US-09-732-210-181	Sequence 181, App	642	5	6.2	134	2	US-09-371-615A-2	Sequence 2, Appl
570	5	6.2	116	2	US-09-732-210-670	Sequence 670, App	643	5	6.2	134	2	US-09-710-279-1382	Sequence 1382, Ap
571	5	6.2	117	2	US-09-270-767-36131	Sequence 36131, A	644	5	6.2	135	2	US-09-252-991A-18526	Sequence 18526, A
572	5	6.2	117	2	US-09-270-767-47131	Sequence 47131, A	645	5	6.2	135	2	US-09-134-000C-4757	Sequence 4757, Ap
573	5	6.2	117	2	US-09-270-767-51348	Sequence 51348, A	646	5	6.2	135	2	US-09-270-767-32007	Sequence 32007, Ap
574	5	6.2	117	2	US-09-513-999C-5619	Sequence 5619, Ap	647	5	6.2	135	2	US-09-270-767-56895	Sequence 56895, A
575	5	6.2	117	2	US-09-107-433-4108	Sequence 4108, Ap	648	5	6.2	135	2	US-09-248-796A-14667	Sequence 14667, A
576	5	6.2	117	2	US-09-107-433-4109	Sequence 4109, Ap	649	5	6.2	136	2	US-09-371-056-4	Sequence 4, Appl
577	5	6.2	117	2	US-09-107-433-4110	Sequence 4110, Ap	650	5	6.2	136	2	US-09-270-767-32542	Sequence 32542, A
578	5	6.2	117	2	US-09-107-433-4332	Sequence 4332, Ap	651	5	6.2	136	2	US-09-270-767-45958	Sequence 45958, A
579	5	6.2	118	1	US-08-588-258B-38	Sequence 38, Appl	652	5	6.2	136	2	US-09-270-767-47759	Sequence 47759, A
580	5	6.2	118	2	US-09-732-210-671	Sequence 671, App	653	5	6.2	136	2	US-09-903-540-10776	Sequence 10776, A
581	5	6.2	118	4	US-09-588-08295-38	Sequence 38, Appl	654	5	6.2	137	2	US-09-134-000C-6571	Sequence 6571, Ap
582	5	6.2	119	2	US-09-328-352-5915	Sequence 5915, Ap	655	5	6.2	137	2	US-09-134-000C-6671	Sequence 6671, Ap
583	5	6.2	119	2	US-09-732-210-333	Sequence 333, App	656	5	6.2	137	2	US-09-270-767-60694	Sequence 60694, A
584	5	6.2	119	2	US-09-732-210-334	Sequence 334, App	657	5	6.2	137	2	US-09-640-211A-710	Sequence 710, App
585	5	6.2	119	2	US-09-583-110-5006	Sequence 5006, Ap	658	5	6.2	138	2	US-09-134-001C-3691	Sequence 3691, Ap
586	5	6.2	119	2	US-09-270-767-31689	Sequence 31689, A	659	5	6.2	138	2	US-09-134-000C-6578	Sequence 6578, Ap
587	5	6.2	119	2	US-09-270-767-33386	Sequence 33386, A	660	5	6.2	138	2	US-09-134-000C-6680	Sequence 6680, Ap
588	5	6.2	119	2	US-09-270-767-46906	Sequence 46906, A	661	5	6.2	138	2	US-09-621-976-4421	Sequence 4421, Ap
589	5	6.2	119	2	US-09-270-767-48603	Sequence 48603, A	662	5	6.2	138	2	US-09-640-211A-712	Sequence 712, App
590	5	6.2	119	2	US-09-538-092-255	Sequence 255, App	663	5	6.2	139	2	US-09-134-001C-4413	Sequence 4413, Ap
591	5	6.2	119	2	US-09-538-092-316	Sequence 316, App	664	5	6.2	139	2	US-09-252-991A-20919	Sequence 20919, A
592	5	6.2	121	2	US-09-270-767-61497	Sequence 61497, A	665	5	6.2	139	2	US-09-621-976-4248	Sequence 4248, Ap
593	5	6.2	121	2	US-09-248-796A-25359	Sequence 25359, A	666	5	6.2	139	2	US-09-270-767-36731	Sequence 36731, A
594	5	6.2	121	2	US-09-893-737-182	Sequence 182, App	667	5	6.2	139	2	US-09-270-767-38088	Sequence 38088, A
595	5	6.2	122	2	US-09-732-210-974	Sequence 974, App	668	5	6.2	139	2	US-09-270-767-51948	Sequence 51948, A
596	5	6.2	122	2	US-09-489-039A-9305	Sequence 9305, Ap	669	5	6.2	139	2	US-09-270-767-53305	Sequence 53305, A
597	5	6.2	122	2	US-10-104-047-2393	Sequence 2393, Ap	670	5	6.2	140	2	US-09-330-914A-9	Sequence 9, Appl
598	5	6.2	122	2	US-10-104-047-2772	Sequence 2772, Ap	671	5	6.2	140	2	US-09-489-039A-12440	Sequence 12440, A
599	5	6.2	123	2	US-09-583-110-3923	Sequence 3923, Ap	672	5	6.2	140	2	US-09-270-767-33167	Sequence 33167, A
600	5	6.2	124	2	US-09-107-532A-5336	Sequence 5336, Ap	673	5	6.2	140	2	US-09-270-767-48384	Sequence 48384, A
601	5	6.2	124	2	US-09-270-767-59288	Sequence 59288, A	674	5	6.2	141	1	US-08-428-733A-11	Sequence 11, Appl
602	5	6.2	124	2	US-09-902-540-14445	Sequence 14445, A	675	5	6.2	141	2	US-09-270-767-31914	Sequence 31914, A
603	5	6.2	125	2	US-09-134-001C-5309	Sequence 5309, Ap	676	5	6.2	141	2	US-09-270-767-43497	Sequence 43497, A
604	5	6.2	125	2	US-09-328-352-5033	Sequence 5033, Ap	677	5	6.2	141	2	US-09-270-767-60164	Sequence 60164, A
605	5	6.2	125	6	5274075-4	Patent No. 5274075	678	5	6.2	141	2	US-09-248-796A-22756	Sequence 22756, A
606	5	6.2	126	2	US-09-540-236-3527	Sequence 3527, Ap	679	5	6.2	142	2	US-09-621-976-6716	Sequence 6716, Ap
607	5	6.2	126	2	US-09-471-276-1485	Sequence 1485, Ap	680	5	6.2	142	2	US-09-903-540-13948	Sequence 13948, A
608	5	6.2	127	2	US-09-134-001C-2937	Sequence 2937, Ap	681	5	6.2	143	1	US-08-259-696B-10	Sequence 10, Appl
609	5	6.2	127	2	US-09-322-409-125	Sequence 125, App	682	5	6.2	143	1	US-08-902-513-10	Sequence 10, Appl
610	5	6.2	127	2	US-09-451-527-195	Sequence 125, App	683	5	6.2	143	2	US-09-617-594A-8	Sequence 8, Appl
611	5	6.2	127	2	US-09-107-532A-5938	Sequence 5938, Ap	684	5	6.2	143	2	US-09-617-594A-10	Sequence 10, Appl

685	5	6.2	143	2	US-10-209-507-8	Sequence 8, Appli	758	5	6.2	158	2	US-10-054-295-82	Sequence 82, Appli
686	5	6.2	143	2	US-10-209-507-10	Sequence 10, Appli	759	5	6.2	158	2	US-10-054-295-85	Sequence 85, Appli
687	5	6.2	144	1	US-08-133-979A-11	Sequence 11, Appli	760	5	6.2	158	2	US-09-438-486A-82	Sequence 82, Appli
688	5	6.2	144	1	US-08-436-890-11	Sequence 11, Appli	761	5	6.2	158	2	US-09-438-486A-85	Sequence 85, Appli
689	5	6.2	144	1	US-08-451-213-11	Sequence 11, Appli	762	5	6.2	159	2	US-09-252-991A-21119	Sequence 21119, A
690	5	6.2	144	2	US-09-322-403-120	Sequence 120, Appl	763	5	6.2	159	2	US-09-270-767-56755	Sequence 56755, A
691	5	6.2	144	2	US-09-451-527-120	Sequence 120, Appl	764	5	6.2	159	2	US-09-142-108C-13	Sequence 13, Appli
692	5	6.2	144	2	US-09-732-210-613	Sequence 613, Appl	765	5	6.2	159	2	US-09-107-433-4990	Sequence 4990, Ap
693	5	6.2	144	2	US-09-589-260-9	Sequence 9, Appli	766	5	6.2	159	2	US-09-640-211A-659	Sequence 659, App
694	5	6.2	145	2	US-09-461-325-438	Sequence 438, App	767	5	6.2	160	2	US-09-370-838-187	Sequence 189, App
695	5	6.2	145	2	US-10-012-542-438	Sequence 438, App	768	5	6.2	160	2	US-09-252-991A-27416	Sequence 27416, A
696	5	6.2	145	2	US-09-583-110-3942	Sequence 3942, Ap	769	5	6.2	160	2	US-09-198-452A-1244	Sequence 1244, Ap
697	5	6.2	145	2	US-10-115-123-438	Sequence 438, App	770	5	6.2	160	2	US-09-583-110-3449	Sequence 3449, Ap
698	5	6.2	146	2	US-09-227-357-396	Sequence 396, App	771	5	6.2	160	2	US-09-854-133-189	Sequence 189, App
699	5	6.2	146	2	US-09-134-001C-3406	Sequence 3406, Ap	772	5	6.2	161	2	US-08-493-071-20	Sequence 20, Appl
700	5	6.2	146	2	US-09-107-433-3193	Sequence 3193, Ap	773	5	6.2	161	2	US-09-732-210-532	Sequence 532, App
701	5	6.2	146	2	US-09-973-278-506	Sequence 506, App	774	5	6.2	162	2	US-09-732-210-768	Sequence 768, App
702	5	6.2	147	2	US-09-383-586-35	Sequence 35, Appli	775	5	6.2	163	2	US-09-134-001C-4131	Sequence 4131, Ap
703	5	6.2	147	2	US-09-328-352-6302	Sequence 6302, Ap	776	5	6.2	163	2	US-09-270-767-59741	Sequence 59741, A
704	5	6.2	147	2	US-09-732-210-133	Sequence 133, App	777	5	6.2	163	2	US-09-902-540-10547	Sequence 10547, A
705	5	6.2	147	2	US-09-732-210-171	Sequence 171, App	778	5	6.2	163	2	US-09-902-540-11158	Sequence 11158, A
706	5	6.2	147	2	US-08-311-731A-359	Sequence 359, App	779	5	6.2	165	2	US-09-252-991A-21773	Sequence 21773, A
707	5	6.2	147	2	US-09-823-038A-35	Sequence 35, Appli	780	5	6.2	165	2	US-09-270-767-37910	Sequence 37910, A
708	5	6.2	148	2	US-09-328-352-7065	Sequence 7065, Ap	781	5	6.2	165	2	US-09-270-767-53127	Sequence 53127, A
709	5	6.2	148	2	US-09-732-210-677	Sequence 677, App	782	5	6.2	165	2	US-09-893-737-60	Sequence 60, Appl
710	5	6.2	149	2	US-09-732-210-843	Sequence 843, App	783	5	6.2	166	2	US-09-107-532A-5004	Sequence 5004, Ap
711	5	6.2	149	2	US-09-488-039A-3279	Sequence 3279, Ap	784	5	6.2	166	2	US-09-248-796A-17285	Sequence 17285, A
712	5	6.2	149	2	US-09-902-540-14114	Sequence 14114, A	785	5	6.2	167	2	US-09-128-155-7	Sequence 7, Appli
713	5	6.2	150	2	US-09-252-991A-27839	Sequence 27839, A	786	5	6.2	167	2	US-09-252-991A-21860	Sequence 21860, A
714	5	6.2	150	2	US-09-248-796A-14820	Sequence 14820, A	787	5	6.2	167	2	US-09-953-780-2	Sequence 2, Appli
715	5	6.2	150	2	US-09-248-796A-22720	Sequence 22720, A	788	5	6.2	167	2	US-09-393-862-2	Sequence 69, Appli
716	5	6.2	151	2	US-09-521-511C-9	Sequence 9, Appli	789	5	6.2	168	2	US-09-325-932A-69	Sequence 69, Appli
717	5	6.2	151	2	US-09-270-767-36318	Sequence 36318, A	790	5	6.2	168	2	US-09-513-999C-5125	Sequence 5125, Ap
718	5	6.2	151	2	US-09-270-767-49120	Sequence 49120, A	791	5	6.2	168	2	US-09-830-230A-632	Sequence 632, App
719	5	6.2	151	2	US-09-270-767-51535	Sequence 51535, A	792	5	6.2	169	2	US-09-134-000C-5112	Sequence 5112, Ap
720	5	6.2	151	2	US-09-461-912A-40	Sequence 40, Appl	793	5	6.2	169	2	US-09-902-540-12480	Sequence 12480, A
721	5	6.2	151	2	US-09-513-999C-7812	Sequence 7812, Ap	794	5	6.2	170	2	US-09-800-170-12	Sequence 12, Appl
722	5	6.2	151	2	US-09-902-540-10696	Sequence 10696, A	795	5	6.2	170	2	US-09-198-452A-336	Sequence 336, App
723	5	6.2	152	2	US-09-902-540-10243	Sequence 10243, A	796	5	6.2	170	2	US-09-917-340-33	Sequence 33, Appl
724	5	6.2	152	2	US-09-800-971-6	Sequence 6, Appli	797	5	6.2	170	2	US-09-270-767-43106	Sequence 43106, A
725	5	6.2	153	2	US-09-732-210-1611	Sequence 1611, Ap	798	5	6.2	171	2	US-09-248-796A-19456	Sequence 19456, A
726	5	6.2	153	2	US-09-270-767-59550	Sequence 59550, A	799	5	6.2	171	2	US-09-248-796A-27723	Sequence 27723, A
727	5	6.2	153	2	US-09-927-112-7	Sequence 7, Appli	800	5	6.2	172	2	US-09-252-991A-25750	Sequence 25750, A
728	5	6.2	154	2	US-09-252-991A-31799	Sequence 31799, A	801	5	6.2	172	2	US-09-489-039A-9531	Sequence 9531, Ap
729	5	6.2	154	2	US-09-270-767-34105	Sequence 34105, A	802	5	6.2	173	2	US-09-270-767-62091	Sequence 62091, A
730	5	6.2	154	2	US-09-270-767-49322	Sequence 49322, A	803	5	6.2	173	2	US-09-311-021-132	Sequence 132, App
731	5	6.2	155	2	US-08-336-553A-2	Sequence 2, Appli	804	5	6.2	174	1	US-07-778-156-7	Sequence 7, Appli
732	5	6.2	155	2	US-08-439-185-2	Sequence 2, Appli	805	5	6.2	174	1	US-08-822-261-4	Sequence 4, Appli
733	5	6.2	155	2	US-09-437-895-2	Sequence 2, Appli	806	5	6.2	174	1	US-08-423-166-7	Sequence 7, Appli
734	5	6.2	155	2	US-09-252-991A-18638	Sequence 18638, A	807	5	6.2	174	2	US-08-804-180C-4	Sequence 4, Appli
735	5	6.2	155	2	US-09-252-991A-26113	Sequence 26113, A	808	5	6.2	174	2	US-09-149-476-424	Sequence 424, App
736	5	6.2	155	2	US-09-710-279-3088	Sequence 3088, Ap	809	5	6.2	174	2	US-09-226-852-4	Sequence 4, Appli
737	5	6.2	155	2	US-09-710-279-3088	Sequence 573, App	810	5	6.2	174	2	US-09-543-681A-7764	Sequence 7764, Ap
738	5	6.2	156	2	US-10-101-464A-573	Sequence 1222, Ap	811	5	6.2	175	1	US-08-464-637-2	Sequence 2, Appli
739	5	6.2	156	2	US-09-710-279-1222	Sequence 30, Appl	812	5	6.2	175	1	US-08-401-530A-4	Sequence 4, Appli
740	5	6.2	157	2	US-09-125-619-30	Sequence 30, Appl	813	5	6.2	175	1	US-08-709-662-4	Sequence 4, Appli
741	5	6.2	157	2	US-09-270-767-35245	Sequence 35245, A	814	5	6.2	175	1	US-08-822-261-3	Sequence 3, Appli
742	5	6.2	157	2	US-09-270-767-35702	Sequence 36702, A	815	5	6.2	175	2	US-08-858-207A-363	Sequence 363, App
743	5	6.2	157	2	US-09-270-767-50462	Sequence 50462, A	816	5	6.2	175	2	US-09-134-001C-5626	Sequence 5626, Ap
744	5	6.2	157	2	US-09-270-767-51919	Sequence 51919, A	817	5	6.2	175	2	US-09-226-852-3	Sequence 3, Appli
745	5	6.2	157	2	US-10-222-566-30	Sequence 30, Appl	818	5	6.2	175	2	US-09-583-110-4664	Sequence 4664, Ap
746	5	6.2	157	2	US-10-143-024A-30	Sequence 30, Appl	819	5	6.2	175	2	US-09-270-767-42431	Sequence 42431, A
747	5	6.2	158	2	US-10-222-162-30	Sequence 30, Appl	820	5	6.2	175	2	US-09-769-787-97	Sequence 97, Appli
748	5	6.2	158	2	US-08-851-843A-82	Sequence 82, Appli	821	5	6.2	176	2	US-09-252-991A-28615	Sequence 28615, A
749	5	6.2	158	2	US-08-851-843A-85	Sequence 85, Appli	822	5	6.2	176	2	US-09-248-796A-19842	Sequence 19842, A
750	5	6.2	158	2	US-08-974-549A-228	Sequence 22, App	823	5	6.2	177	2	US-09-270-767-31778	Sequence 31778, A
751	5	6.2	158	2	US-08-854-050-82	Sequence 82, Appl	824	5	6.2	178	2	US-09-128-155-2	Sequence 2, Appli
752	5	6.2	158	2	US-08-854-050-85	Sequence 85, Appl	825	5	6.2	178	2	US-09-252-991A-24207	Sequence 24207, A
753	5	6.2	158	2	US-09-430-323-82	Sequence 82, Appl	826	5	6.2	179	2	US-08-836-500A-4	Sequence 4, Appli
754	5	6.2	158	2	US-09-430-323-85	Sequence 85, Appl	827	5	6.2	179	2	US-09-634-238-296	Sequence 296, App
755	5	6.2	158	2	US-09-402-181B-228	Sequence 228, App	828	5	6.2	179	2	US-09-732-210-70	Sequence 70, Appl
756	5	6.2	158	2	US-09-721-456-228	Sequence 22, App	829	5	6.2	179	2	US-09-543-681A-5087	Sequence 5087, Ap
757	5	6.2	158	2	US-09-766-253-82	Sequence 82, Appl	830	5	6.2	179	2	US-09-248-796A-18386	Sequence 18386, A

831	5	6.2	179	2	US-09-679-750-4	Sequence 4, Appli	904	5	6.2	197	1	US-08-188-582-24	Sequence 24, Appl
832	5	6.2	179	2	US-09-107-433-4882	Sequence 4882, Ap	905	5	6.2	197	1	US-08-646-715-24	Sequence 24, Appl
833	5	6.2	180	1	US-08-328-254-8	Sequence 8, Appli	906	5	6.2	197	2	US-09-125-612-25	Sequence 25, Appl
834	5	6.2	180	2	US-09-164-714-7	Sequence 7, Appli	907	5	6.2	197	2	US-10-222-566-25	Sequence 25, Appl
835	5	6.2	180	2	US-09-328-352-5483	Sequence 5483, Ap	908	5	6.2	197	2	US-10-143-024A-25	Sequence 25, Appl
836	5	6.2	180	2	US-09-583-110-3597	Sequence 3597, Ap	909	5	6.2	197	2	US-10-222-162-25	Sequence 25, Appl
837	5	6.2	180	2	US-09-548-473B-14	Sequence 14, Appli	910	5	6.2	197	2	US-09-605-703B-1592	Sequence 1592, Ap
838	5	6.2	181	1	US-08-766-551-1	Sequence 1, Appli	911	5	6.2	198	2	US-09-848-813-2	Sequence 2, Appli
839	5	6.2	181	2	US-09-252-991A-30203	Sequence 30203, A	912	5	6.2	198	2	US-09-270-767-60759	Sequence 60759, A
840	5	6.2	181	2	US-09-328-352-5118	Sequence 5118, Ap	913	5	6.2	198	2	US-09-270-767-41993	Sequence 41993, A
841	5	6.2	181	2	US-09-270-767-32378	Sequence 32378, A	914	5	6.2	199	2	US-09-270-767-57247	Sequence 57247, A
842	5	6.2	181	2	US-09-270-767-47595	Sequence 47595, A	915	5	6.2	200	2	US-09-134-000C-4738	Sequence 4738, Ap
843	5	6.2	181	2	US-09-270-767-59934	Sequence 59934, A	916	5	6.2	200	2	US-09-484-577A-22	Sequence 22, Appl
844	5	6.2	181	2	US-09-248-796A-23532	Sequence 23532, A	917	5	6.2	201	2	US-09-124-476-2	Sequence 2, Appli
845	5	6.2	182	2	US-09-107-532A-5187	Sequence 5187, Ap	918	5	6.2	201	2	US-09-577-796A-2	Sequence 2, Appli
846	5	6.2	182	2	US-09-270-767-60206	Sequence 60206, A	919	5	6.2	201	2	US-09-543-681A-4313	Sequence 4313, Ap
847	5	6.2	182	2	US-09-252-991A-20768	Sequence 20768, A	920	5	6.2	201	2	US-09-270-767-39567	Sequence 39567, A
848	5	6.2	183	2	US-09-621-976-3942	Sequence 3942, Ap	921	5	6.2	201	2	US-09-270-767-54784	Sequence 54784, A
849	5	6.2	183	2	US-09-248-796A-27774	Sequence 27774, A	922	5	6.2	201	2	US-09-270-767-312	Sequence 312, App
850	5	6.2	183	2	US-09-949-016-10537	Sequence 10537, A	923	5	6.2	201	2	US-09-710-279-2176	Sequence 2176, Ap
851	5	6.2	184	2	US-09-134-000C-5168	Sequence 5168, Ap	924	5	6.2	201	2	US-09-248-796A-17835	Sequence 17835, A
852	5	6.2	184	2	US-09-248-796A-19773	Sequence 19773, A	925	5	6.2	201	2	US-09-107-433-3237	Sequence 3237, Ap
853	5	6.2	184	2	US-09-248-796A-27001	Sequence 27001, A	926	5	6.2	201	2	US-09-902-540-16724	Sequence 16724, A
854	5	6.2	184	2	US-09-605-703B-2666	Sequence 2666, Ap	927	5	6.2	202	2	US-09-303-518D-540	Sequence 540, App
855	5	6.2	185	2	US-09-565-423-17	Sequence 17, Appl	928	5	6.2	202	2	US-09-252-991A-20714	Sequence 20714, A
856	5	6.2	185	2	US-09-270-767-61399	Sequence 61399, A	929	5	6.2	202	2	US-09-489-039A-8619	Sequence 8619, Ap
857	5	6.2	185	2	US-09-854-864-11	Sequence 11, Appl	930	5	6.2	202	2	US-09-248-796A-27997	Sequence 27997, A
858	5	6.2	185	2	US-09-107-433-3101	Sequence 3101, Ap	931	5	6.2	202	2	US-09-902-540-13660	Sequence 13660, A
859	5	6.2	186	2	US-09-252-991A-27076	Sequence 27076, A	932	5	6.2	202	2	US-09-605-703B-2356	Sequence 2356, Ap
860	5	6.2	186	2	US-09-540-236-2792	Sequence 2792, Ap	933	5	6.2	202	2	US-09-328-352-7727	Sequence 7727, Ap
861	5	6.2	186	2	US-09-902-540-11242	Sequence 11242, A	934	5	6.2	203	2	US-09-270-767-32925	Sequence 32925, A
862	5	6.2	187	2	US-08-493-071-19	Sequence 19, Appl	935	5	6.2	203	2	US-09-270-767-48142	Sequence 48142, A
863	5	6.2	187	2	US-09-125-619-23	Sequence 23, Appl	936	5	6.2	203	2	US-10-376-397B-14	Sequence 14, Appl
864	5	6.2	187	2	US-09-270-767-42688	Sequence 42688, A	937	5	6.2	204	2	US-09-149-476-429	Sequence 429, App
865	5	6.2	187	2	US-10-222-566-23	Sequence 23, Appl	938	5	6.2	204	2	US-09-252-991A-30644	Sequence 30644, A
866	5	6.2	187	2	US-10-143-024A-23	Sequence 23, Appl	939	5	6.2	204	2	US-09-540-236-2134	Sequence 2134, Ap
867	5	6.2	187	2	US-10-222-162-23	Sequence 23, Appl	940	5	6.2	204	2	US-09-270-767-60252	Sequence 60252, A
868	5	6.2	188	2	US-09-543-681A-7763	Sequence 7763, Ap	941	5	6.2	204	2	US-09-999-833A-36	Sequence 36, Appl
869	5	6.2	188	2	US-09-270-767-36000	Sequence 36000, Ap	942	5	6.2	204	2	US-10-020-445A-36	Sequence 36, Appl
870	5	6.2	188	2	US-09-270-767-52127	Sequence 52127, A	943	5	6.2	205	2	US-09-252-991A-24225	Sequence 24225, A
871	5	6.2	188	2	US-09-902-540-10761	Sequence 10761, A	944	5	6.2	205	2	US-09-252-991A-31579	Sequence 31579, A
872	5	6.2	188	2	US-09-712-363-277	Sequence 277, App	945	5	6.2	205	2	US-09-252-991A-32615	Sequence 32615, A
873	5	6.2	188	2	US-09-716-964B-91	Sequence 91, Appl	946	5	6.2	205	2	US-09-543-681A-8007	Sequence 8007, Ap
874	5	6.2	189	2	US-09-252-991A-17162	Sequence 17162, A	947	5	6.2	205	2	US-09-270-767-34421	Sequence 34421, A
875	5	6.2	190	2	US-08-858-207A-505	Sequence 505, App	948	5	6.2	205	2	US-09-270-767-47590	Sequence 47590, A
876	5	6.2	190	2	US-09-125-619-15	Sequence 15, Appl	949	5	6.2	205	2	US-09-270-767-49638	Sequence 49638, A
877	5	6.2	190	2	US-09-125-619-27	Sequence 27, Appl	950	5	6.2	206	2	US-09-248-796A-21349	Sequence 21349, A
878	5	6.2	190	2	US-09-125-619-29	Sequence 29, Appl	951	5	6.2	207	2	US-09-068-960-43	Sequence 43, App
879	5	6.2	190	2	US-10-222-566-15	Sequence 15, Appl	952	5	6.2	207	2	US-09-252-991A-26664	Sequence 26664, A
880	5	6.2	190	2	US-10-222-566-27	Sequence 27, Appl	953	5	6.2	208	2	US-08-961-083-214	Sequence 214, App
881	5	6.2	190	2	US-10-222-566-29	Sequence 29, Appl	954	5	6.2	208	2	US-09-125-619-47	Sequence 47, Appl
882	5	6.2	190	2	US-10-143-024A-15	Sequence 15, Appl	955	5	6.2	208	2	US-09-252-991A-26192	Sequence 26192, A
883	5	6.2	190	2	US-10-143-024A-27	Sequence 27, Appl	956	5	6.2	208	2	US-09-536-784-214	Sequence 214, App
884	5	6.2	190	2	US-10-143-024A-29	Sequence 29, Appl	957	5	6.2	208	2	US-10-222-566-47	Sequence 47, Appl
885	5	6.2	190	2	US-10-222-162-15	Sequence 15, Appl	958	5	6.2	208	2	US-10-143-024A-47	Sequence 47, Appl
886	5	6.2	190	2	US-10-222-162-27	Sequence 27, Appl	959	5	6.2	208	2	US-10-222-162-47	Sequence 47, Appl
887	5	6.2	190	2	US-10-222-162-29	Sequence 29, Appl	960	5	6.2	208	2	US-09-765-271-214	Sequence 214, App
888	5	6.2	191	2	US-09-252-991A-24515	Sequence 24515, A	961	5	6.2	208	2	US-09-765-272A-214	Sequence 214, App
889	5	6.2	191	2	US-09-543-681A-6682	Sequence 6682, Ap	962	5	6.2	209	2	US-09-125-619-33	Sequence 33, Appl
890	5	6.2	191	2	US-09-540-236-2229	Sequence 2229, Ap	963	5	6.2	209	2	US-09-125-619-42	Sequence 42, Appl
891	5	6.2	192	2	US-09-276-071-4	Sequence 4, Appli	964	5	6.2	209	2	US-09-125-619-45	Sequence 45, Appl
892	5	6.2	192	2	US-09-248-796A-17425	Sequence 17425, A	965	5	6.2	209	2	US-09-252-991A-32577	Sequence 32577, A
893	5	6.2	192	2	US-09-134-001C-4734	Sequence 4734, Ap	966	5	6.2	209	2	US-10-222-566-33	Sequence 33, Appl
894	5	6.2	193	2	US-09-270-767-33959	Sequence 33959, A	967	5	6.2	209	2	US-10-222-566-42	Sequence 42, Appl
895	5	6.2	193	2	US-09-270-767-51176	Sequence 51176, A	968	5	6.2	209	2	US-10-222-566-45	Sequence 45, Appl
896	5	6.2	193	2	US-09-489-039A-11929	Sequence 11929, A	969	5	6.2	209	2	US-10-143-024A-33	Sequence 33, Appl
897	5	6.2	194	2	US-09-134-000C-6648	Sequence 6648, Ap	970	5	6.2	209	2	US-10-143-024A-42	Sequence 42, Appl
898	5	6.2	194	2	US-09-270-767-59939	Sequence 59939, A	971	5	6.2	209	2	US-10-143-024A-45	Sequence 45, Appl
899	5	6.2	194	2	US-09-873-075A-1	Sequence 1, Appli	972	5	6.2	209	2	US-10-222-162-33	Sequence 33, Appl
900	5	6.2	195	2	US-09-252-991A-28846	Sequence 28846, A	973	5	6.2	209	2	US-10-222-162-42	Sequence 42, Appl
901	5	6.2	196	2	US-09-270-767-34969	Sequence 34969, A	974	5	6.2	209	2	US-10-222-162-45	Sequence 45, Appl
902	5	6.2	196	2	US-09-270-767-46267	Sequence 46267, A	975	5	6.2	209	2	US-10-222-162-45	Sequence 45, Appl
903	5	6.2	196	2	US-09-270-767-50186	Sequence 50186, A	976	5	6.2	210	2	US-09-270-767-31831	Sequence 31831, A

;; FILING DATE: 23 NOV 1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MANDRAGOURAS, AMY E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: RPI-002CPB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 227 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-253-751-6

Query Match 100.0%; Score 80; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQEFYKDTYNKLTKEPQRETAKAIHYALNCCGLAGGVEQFISDIPCKDV 60
Db 112 HKDEVKEVQEFYKDTYNKLTKEPQRETAKAIHYALNCCGLAGGVEQFISDIPCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 3
US-08-453-925-6
; Sequence 6, Application US/08453925
; Patent No. 5883223
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D., Freeman, Gordon J.
; TITLE OF INVENTION: METHODS FOR SELECTIVELY STIMULATING
; TITLE OF INVENTION: PROLIFERATION OF T-CELLS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,925
; FILING DATE: 30 MAY 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,751
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992

;; APPLICATION NUMBER: US 07/275,433
;; FILING DATE: 23 NOV 1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MANDRAGOURAS, AMY E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: RPI-002CPB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 227 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-453-925-6

Query Match 100.0%; Score 80; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQEFYKDTYNKLTKEPQRETAKAIHYALNCCGLAGGVEQFISDIPCKDV 60
Db 112 HKDEVKEVQEFYKDTYNKLTKEPQRETAKAIHYALNCCGLAGGVEQFISDIPCKDV 171

QY 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 4
US-08-403-253A-6
; Sequence 6, Application US/08403253A
; Patent No. 6352694
; GENERAL INFORMATION:
; APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
; APPLICANT: Gray, Gary S., Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,253A
; FILING DATE: March 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467

```
;
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-253A-6

Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVIKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 171

Qy 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 5
US-08-435-816A-6
; Sequence 6, Application US/08435816A
; Patent No. 6534055
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,816A
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10 MARCH 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
```

```
;
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-816A-6

Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVIKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 60
Db 112 HKDEVIKEVQEFYKDTYNTKLTQDEPQRETLKAIHYALNCCGLAGGVQFISDIPCCKDV 171

Qy 61 LETFTVKSCPDAIKEVFDNK 80
Db 172 LETFTVKSCPDAIKEVFDNK 191

RESULT 6
US-09-350-202-6
; Sequence 6, Application US/09350202
; Patent No. 6887466
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.; Thompson, Craig B.; Nabel, Gary J.
; APPLICANT: Gray, Gary S.; Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
```

APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-350-202-6

Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQEFYKDTYNKLTKEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 60
Db 112 HKDEVKEVQEFYKDTYNKLTKEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 171

QY 61 LETFTVKSCPDAIKEVFNK 80
Db 172 LETFTVKSCPDAIKEVFNK 191

RESULT 7
US-08-592-711-6
Sequence 6, Application US/08592711
Patent No. 6905680
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964

FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-711-6

Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVQEFYKDTYNKLTKEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 60
Db 112 HKDEVKEVQEFYKDTYNKLTKEPQRETLKAIHYALNCCGLAGGVEQFISDIPCKDV 171

QY 61 LETFTVKSCPDAIKEVFNK 80
Db 172 LETFTVKSCPDAIKEVFNK 191

RESULT 8
US-09-349-915B-6
Sequence 6, Application US/09349915B
Patent No. 6905681
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,915B
FILING DATE: 01-Aug-2000
CLASSIFICATION: <Unknown>

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 36119-125 (US10)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6564
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-349-915B-6

Query Match 100.0%; Score 80; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQFYKDYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKDQV 60
DB 112 HKDEVIKEVQFYKDYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKDQV 171

QY 61 LETFTVKSCPDAIKEVFNK 80
DB 172 LETFTVKSCPDAIKEVFNK 191
```

RESULT 9
US-08-408-222B-1
Sequence 1, Application US/08408222B
Patent No. 5776727
GENERAL INFORMATION:
APPLICANT: Ikeyama, Shuichi
APPLICANT: Koyama, Masaru
APPLICANT: Miyake, Masayuki
APPLICANT: Senoo, Masaharu
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```
;
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-408-222B-1

Query Match 100.0%; Score 80; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQFYKDYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKDQV 60
DB 113 HKDEVIKEVQFYKDYTNKLTQDEPQRETLKAIHYALNCCGLAGGVQFTSDICPKDQV 172

QY 61 LETFTVKSCPDAIKEVFNK 80
DB 173 LETFTVKSCPDAIKEVFNK 192
```

RESULT 10
US-08-630-172-8
Sequence 8, Application US/08630172
Patent No. 6060054
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-172-8

Query Match 58.8%; Score 47; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTQKDPQRETLKAIHYALNCCGLAGV 47
DB 1 HKDEVIKEVQEFYKDTYNNKLTQKDPQRETLKAIHYALNCCGLAGV 47

RESULT 11
US-09-375-419-8
Sequence 8, Application US/09375419
Patent No. 6264950
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/09/375,419
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-375-419-8

Query Match 58.8%; Score 47; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVIKEVQEFYKDTYNNKLTQKDPQRETLKAIHYALNCCGLAGV 47
DB 1 HKDEVIKEVQEFYKDTYNNKLTQKDPQRETLKAIHYALNCCGLAGV 47

RESULT 12
US-08-254-493-4
Sequence 4, Application US/08254493
Patent No. 5439886
GENERAL INFORMATION:
APPLICANT: IKEYAMA, SHUICHI
APPLICANT: KOYAMA, MASARU
APPLICANT: MIYAKE, MASAYUKI
APPLICANT: SENOO, MASAHARU
TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
TITLE OF INVENTION: PRODUCTION THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-493-4

Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVIKEVQEFYKDTYNNKLTQKDPQRETL 31
DB 1 KDEVIKEVQEFYKDTYNNKLTQKDPQRETL 30

RESULT 13

US-08-408-222B-4
; Sequence 4, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-6440
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-408-222B-4
Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KDEVIKEVQEFYKOTYNKLTDEPQRETL 31
Db 1 KDEVIKEVQEFYKOTYNKLTDEPQRETL 30
RESULT 14
US-08-254-493-5
; Sequence 5, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US

; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-5
Query Match 36.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 QRETLKAIHYALNCCGLAGVGEQFISDIC 55
Db 1 QRETLKAIHYALNCCGLAGVGEQFISDIC 29
RESULT 15
US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,493
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865552
FILING DATE: 09-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 079996-1991
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 085396-1991
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 022321-1992
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-493-6

Query Match 36.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 SDICPKQVLETFYVKSCPDAIKEVFDNK 80
|||||
Db 1 SDICPKQVLETFYVKSCPDAIKEVFDNK 29

Search completed: January 20, 2006, 17:45:25
Job time : 35.2308 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:44:47 ; Search time 76 Seconds
(without alignments)
462.504 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192

Perfect score: 80

Sequence: 1 HKDEVIKEQVEFYKDYNNKL.....LETFVTKSCPDAIKVFDPNK 80

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1293556

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Listing first 1000 summaries

Database :

A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	58.8	79	2	AAW35851 Human CD9
2	47	58.8	79	6	ABU05058 Human exp
3	38	47.5	38	8	ADJ57561 Human CD9
4	32	40.0	30	6	ABP76310 Human GEN
5	30	37.5	30	6	ABU05051 Human exp
6	25	31.2	25	8	ADJ57562 Human CD9
7	22	27.5	22	8	ADJ57564 Human CD9
8	22	27.5	24	8	ADJ57578 Human CD9
9	18	22.5	18	8	ADJ57563 Human CD9
10	10	12.5	10	6	ABU03385 Human exp
11	8	10.0	33	5	ABP43064 Human ova
12	7	8.8	58	5	ABU51670 Helicobac
13	6	7.5	16	6	ABR67406 Human pro
14	6	7.5	16	2	AAW31082 Human exp
15	6	7.5	18	9	ADJ67376 Amino aci
16	6	7.5	20	8	ADJ95249 OSPF-rela
17	6	7.5	20	8	ADJ95250 OSPF-rela
18	6	7.5	25	9	ADJ28634 Novel mod
19	6	7.5	25	9	ADJ28635 Novel mod
20	6	7.5	29	7	ADG14386 Cytochrom
21	6	7.5	31	7	ADJ49210 Human FMG
22	6	7.5	33	6	ABU18835 Human Bcl
23	6	7.5	37	7	ADJ13922 Human end
24	6	7.5	42	3	AAW55485 Arabidops

25	6	7.5	43	5	AAO15500 Porphyra
26	6	7.5	62	5	ABP26527 Streptoco
27	6	7.5	62	8	ABO58008 Human gen
28	6	7.5	66	5	AAO15501 Porphyra
29	6	7.5	68	2	AAW98521 H. pylori
30	6	7.5	69	2	AAY39395 Mutant Sh
31	6	7.5	69	2	AAY43002 Mutant Sh
32	6	7.5	71	7	ADF14031 Human end
33	6	7.5	72	4	AAW83932 Human imm
34	6	7.5	72	4	ABG07225 Novel hum
35	6	7.5	73	6	ABM73013 Staphyloc
36	6	7.5	74	4	AAW86173 Human imm
37	6	7.5	74	5	ABP00618 Human ORF
38	6	7.5	75	7	ADG66297 Klebsiell
39	6	7.5	76	7	ADC94793 E. faeciu
40	6	7.5	78	8	ADJ74566 Plant ful
41	6	7.5	78	8	ADJ74707 Plant ful
42	5	6.2	5	8	ADJ57560 Human CD9
43	5	6.2	6	2	AAW95026 Sorbitol
44	5	6.2	7	5	ABG77628 Targettin
45	5	6.2	7	5	ABG77629 Targettin
46	5	6.2	7	5	ABG77652 Targettin
47	5	6.2	7	8	ADJ95875 Human pro
48	5	6.2	7	8	ADJ95876 Human pro
49	5	6.2	7	8	ADJ30795 Brain tar
50	5	6.2	7	8	ADP84753 Organ/tis
51	5	6.2	8	2	AAV30138 Peptide t
52	5	6.2	9	4	ABP73167 Tumour an
53	5	6.2	9	4	ABP88282 Hep-65 pe
54	5	6.2	9	4	ABP88230 Hep-65 pe
55	5	6.2	9	4	ABP88235 Hep-65 pe
56	5	6.2	9	5	AAU95802 Immunogen
57	5	6.2	9	6	ABR26232 Human can
58	5	6.2	9	6	ABR25766 Human can
59	5	6.2	9	6	ABR26370 Human can
60	5	6.2	9	6	ABR26234 Human can
61	5	6.2	9	7	ABR25849 Human can
62	5	6.2	9	7	ADG67261 Human 161
63	5	6.2	9	7	ADG67532 Human 161
64	5	6.2	9	7	ADG68698 Human 161
65	5	6.2	9	7	ADG68173 Human 161
66	5	6.2	9	7	ADG69070 Human 161
67	5	6.2	9	7	ADG69088 Human 161
68	5	6.2	9	7	ADG67509 Human 161
69	5	6.2	9	7	ADG68274 Human 161
70	5	6.2	9	8	ADP30585 Arthrobac
71	5	6.2	9	8	ADT74782 Human RSV
72	5	6.2	9	8	ADT74776 Human RSV
73	5	6.2	10	2	AAV30139 Peptide t
74	5	6.2	10	3	AAW23173 Gluconoba
75	5	6.2	10	4	AAW93951 Human com
76	5	6.2	10	4	AAW94450 Human com
77	5	6.2	10	4	AAW96790 Human com
78	5	6.2	10	4	AAW97932 Human com
79	5	6.2	10	4	AAW96711 Human com
80	5	6.2	10	4	AAW97931 Human com
81	5	6.2	10	4	AAW96788 Human com
82	5	6.2	10	4	AAW88239 Hap-65 pe
83	5	6.2	10	4	AAW87987 Saccharom
84	5	6.2	10	4	AAW87986 Saccharom
85	5	6.2	10	5	ABJ15209 Immunogen
86	5	6.2	10	6	ABP97524 Amino aci
87	5	6.2	10	6	ABP97530 Amino aci
88	5	6.2	10	6	ABP97527 Amino aci
89	5	6.2	10	6	ABP97525 Amino aci
90	5	6.2	10	6	ABR26751 Human can
91	5	6.2	10	6	ABR26505 Human can
92	5	6.2	10	6	ABR26324 Human can
93	5	6.2	10	6	ABR26550 Human can
94	5	6.2	10	6	ABR26548 Human can
95	5	6.2	10	6	ABR25883 Human can
96	5	6.2	10	6	ABR26103 Human can
97	5	6.2	10	6	ABP75169 Proteome

98	5	6.2	10	6	ABP75115	Abp75115 Proteome	171	5	6.2	15	7	ADE70504	Adc70504 Human 161
99	5	6.2	10	7	AD223868	Ad223868 Breast ca	172	5	6.2	15	7	ADE70503	Adc70503 Human 161
100	5	6.2	10	7	AD66418	Ad66418 Human 161	173	5	6.2	15	7	ADE70820	Adc70820 Human 161
101	5	6.2	10	7	AD69278	Ad69278 Human 161	174	5	6.2	15	7	ADW33381	Adw33381 HLA bindi
102	5	6.2	10	7	AD69292	Ad69292 Human 161	175	5	6.2	15	7	ADW33381	Adw33381 HLA bindi
103	5	6.2	10	7	AD67636	Ad67636 Human 161	176	5	6.2	15	8	ADP26486	Adp26486 Plaemodiu
104	5	6.2	10	7	AD666384	Ad666384 Human 161	177	5	6.2	15	8	ADR19120	Adr19120 Type IV c
105	5	6.2	10	7	AD666679	Ad666679 Human 161	178	5	6.2	15	8	ADR19111	Adr19111 Type IV c
106	5	6.2	10	7	AD667382	Ad667382 Human 161	179	5	6.2	15	9	ADV21817	Adv21817 SIV pol p
107	5	6.2	10	7	ADW30960	Adw30960 HLA bindi	180	5	6.2	15	9	ADV21818	Adv21818 SIV pol p
108	5	6.2	10	8	ADG94770	Adg94770 Human JAM	181	5	6.2	15	9	ADV21819	Adv21819 SIV pol p
109	5	6.2	10	8	ADI47144	Adi47144 Human-der	182	5	6.2	15	9	ADW86218	Adw86218 Human mus
110	5	6.2	10	8	ADK05372	Adk05372 Hepatitis	183	5	6.2	15	9	ADZ88943	Adz88943 Human mus
111	5	6.2	10	8	ADK06991	Adk06991 Hepatitis	184	5	6.2	16	2	AAW38987	Aaw38987 Peptide r
112	5	6.2	10	8	ADP87345	Adp87345 Human cla	185	5	6.2	17	2	AAW54389	Aaw54389 RAE 29.1-
113	5	6.2	11	1	AAW33025	Aaw33025 Shiga tox	186	5	6.2	17	2	AAW02473	Aaw02473 RAE 29.1-
114	5	6.2	11	4	AAW88297	Aaw88297 Hsp-65 pe	187	5	6.2	17	4	AAW88288	Aaw88288 Hsp-65 pe
115	5	6.2	11	4	AAW88232	Aaw88232 Hsp-65 pe	188	5	6.2	17	4	AAW88288	Aaw88288 Hsp-65 pe
116	5	6.2	11	4	AAW88298	Aaw88298 Hsp-65 pe	189	5	6.2	17	8	ADM96816	Adm96816 Tissue fa
117	5	6.2	11	6	ABU36793	Abj36793 G protein	190	5	6.2	17	8	ADM96816	Adm96816 Tissue fa
118	5	6.2	11	8	ADT51214	Adt51214 G protein	191	5	6.2	18	2	AAW96915	Aaw96915 Tissue fa
119	5	6.2	12	7	ADW35524	Adw35524 HLA bindi	192	5	6.2	18	2	AAW43523	Aaw43523 Mycobacte
120	5	6.2	12	7	ADW34291	Adw34291 HLA bindi	193	5	6.2	18	4	AAW51354	Aaw51354 Mycobacte
121	5	6.2	12	8	ADT40727	Adt40727 hSARS vir	194	5	6.2	18	4	AAW88292	Aaw88292 Hsp-65 pe
122	5	6.2	12	8	ADW80143	Adw80143 SARS viru	195	5	6.2	18	4	AAW88292	Aaw88292 Hsp-65 pe
123	5	6.2	12	8	ADT38257	Adt38257 hSARS vir	196	5	6.2	18	4	AAW88287	Aaw88287 Hsp-65 pe
124	5	6.2	12	9	ADV25827	Adv25827 SARS coro	197	5	6.2	18	7	ADC17673	Adc17673 Type IV c
125	5	6.2	12	9	ADV12954	Adv12954 Human pho	198	5	6.2	18	8	ADR84049	Adr84049 S. pyogen
126	5	6.2	13	2	AAW50131	Aaw50131 Pan DR bi	199	5	6.2	19	4	AAW88286	Aaw88286 Hsp-65 pe
127	5	6.2	13	4	AAW88296	Aaw88296 Hsp-65 pe	200	5	6.2	19	4	AAW88291	Aaw88291 Hsp-65 pe
128	5	6.2	13	5	ADG66141	Adg66141 Human pro	201	5	6.2	19	5	AAU8289	Aau8289 Insulin/i
129	5	6.2	13	5	ADG66144	Adg66144 Human pro	202	5	6.2	19	6	ABU13493	Abu13493 Zona pell
130	5	6.2	13	5	ADG66142	Adg66142 Human pro	203	5	6.2	19	6	ABU13494	Abu13494 Zona pell
131	5	6.2	13	5	ADG66143	Adg66143 Human pro	204	5	6.2	19	7	ABM74372	Abm74372 DNA clone
132	5	6.2	13	5	ADG66140	Adg66140 Human pro	205	5	6.2	19	7	ADC17676	Adc17676 Type IV c
133	5	6.2	13	7	ADP23246	Adp23246 Breast ca	206	5	6.2	19	8	ADR19198	Adr19198 SRP plus
134	5	6.2	14	1	APB3024	Apb3024 Shiga tox	207	5	6.2	20	1	APB3023	Apb3023 Shiga Cox
135	5	6.2	14	2	AKW54390	Akw54390 RAE 29.1-	208	5	6.2	20	2	AAW54386	Aaw54386 RAE 29.1-
136	5	6.2	14	2	AAW02474	Aaw02474 RAE 29.1-	209	5	6.2	20	2	AAW54387	Aaw54387 RAE 29.1-
137	5	6.2	14	2	AAW02474	Aaw02474 RAE 29.1-	210	5	6.2	20	2	AAW13200	Aaw13200 Fragment
138	5	6.2	14	3	AAW99191	Aaw99191 HLA class	211	5	6.2	20	2	AAW02471	Aaw02471 RAE 29.1-
139	5	6.2	14	3	AAW30019	Aaw30019 Scaffold	212	5	6.2	20	2	AAW02470	Aaw02470 RAE 29.1-
140	5	6.2	14	4	AAW99099	Aaw99099 Vaccine r	213	5	6.2	20	2	AAW67520	Aaw67520 IGF-1/IGF
141	5	6.2	14	8	ADO40746	Ado40746 Human A6	214	5	6.2	20	2	AAW67521	Aaw67521 IGF-1/IGF
142	5	6.2	14	8	ADO40742	Ado40742 Human A6	215	5	6.2	20	2	AAW67521	Aaw67521 IGF-1/IGF
143	5	6.2	14	8	ADO40756	Ado40756 Human A6	216	5	6.2	20	3	AAW66841	Aaw66841 T cell an
144	5	6.2	14	8	ADO40754	Ado40754 Human A6	217	5	6.2	20	4	AAE12279	Aae12279 Mycobacte
145	5	6.2	14	8	ADO40736	Ado40736 Human A6	218	5	6.2	20	4	AAE12279	Aae12279 Mycobacte
146	5	6.2	14	8	ADO40744	Ado40744 Human A6	219	5	6.2	20	4	AAE12279	Aae12279 Mycobacte
147	5	6.2	15	2	AAW94846	Aaw94846 Peptide f	220	5	6.2	20	4	AAE12279	Aae12279 Mycobacte
148	5	6.2	15	2	AAW43524	Aaw43524 Mycobacte	221	5	6.2	20	4	AAE12279	Aae12279 Mycobacte
149	5	6.2	15	3	AAW03218	Aaw03218 Human epi	222	5	6.2	20	5	ABW73539	Abw73539 Vascular
150	5	6.2	15	3	AAW03318	Aaw03318 Human epi	223	5	6.2	20	5	ABW73539	Abw73539 Vascular
151	5	6.2	15	3	AAW03328	Aaw03328 Human epi	224	5	6.2	20	5	ABW73539	Abw73539 Vascular
152	5	6.2	15	4	AAW83346	Aaw83346 Dopamine	225	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
153	5	6.2	15	5	AAU73469	Aau73469 Vascular	226	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
154	5	6.2	15	5	AAU73469	Aau73469 Vascular	227	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
155	5	6.2	15	6	ABR38255	Abw38255 Human can	228	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
156	5	6.2	15	6	ABR38255	Abw38255 Human can	229	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
157	5	6.2	15	6	ABR38106	Abw38106 Human can	230	5	6.2	20	7	ADD12335	Add12335 PDZ ligan
158	5	6.2	15	6	ABR38056	Abw38056 Human can	231	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
159	5	6.2	15	6	ABR38064	Abw38064 Human can	232	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
160	5	6.2	15	6	ABR38091	Abw38091 Human can	233	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
161	5	6.2	15	6	ABR38158	Abw38158 G protein	234	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
162	5	6.2	15	7	ADC17598	Adc17598 Type IV c	235	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
163	5	6.2	15	7	ADC17598	Adc17598 Type IV c	236	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
164	5	6.2	15	7	ADW70454	Adw70454 Human 161	237	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
165	5	6.2	15	7	ADW70454	Adw70454 Human 161	238	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
166	5	6.2	15	7	ADW70643	Adw70643 Human 161	239	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
167	5	6.2	15	7	ADW70354	Adw70354 Human 161	240	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
168	5	6.2	15	7	ADW70728	Adw70728 Human 161	241	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
169	5	6.2	15	7	ADW70068	Adw70068 Human 161	242	5	6.2	20	8	ADP47645	Adp47645 Insulin-1
170	5	6.2	15	7	ADW70355	Adw70355 Human 161	243	5	6.2	20	8	ADP47645	Adp47645 Insulin-1

244	5	6.2	20	8	ADJ45156	Adj45156 Inhibitor	317	5	6.2	33	2	AAW29234	Aaw29234 Membrane
245	5	6.2	20	8	ADJ45155	Adj45155 Inhibitor	318	5	6.2	33	9	ADV13248	Adv13248 Human pho
246	5	6.2	20	8	ADM86651	Adm86651 E. coli p	319	5	6.2	34	9	Aaw29230	Aaw29230 Membrane
247	5	6.2	20	8	ADM76502	Adm76502 TGFBR-3 b	320	5	6.2	34	9	ADV56005	Adv56005 G protein
248	5	6.2	20	8	ADM76501	Adm76501 TGFBR-3 b	321	5	6.2	34	9	ADV55451	Adv55451 G protein
249	5	6.2	20	8	ADL08270	Adl08270 Inhibitor	322	5	6.2	34	9	ADV55963	Adv55963 G protein
250	5	6.2	20	8	ADL08269	Adl08269 Inhibitor	323	5	6.2	36	2	AAR54449	Aar54449 Amb A i.1
251	5	6.2	20	8	ADN32752	Adn32752 Insulin-1	324	5	6.2	36	2	AAW02504	Aaw02504 Peptide c
252	5	6.2	20	8	ADN32753	Adn32753 Insulin-1	325	5	6.2	36	2	AAV35985	Aav35985 Extended
253	5	6.2	20	8	ADU63739	Adu63739 SARS coro	326	5	6.2	36	2	AAW99616	Aaw99616 Human exc
254	5	6.2	21	4	AAB88285	Aab88285 Hsp-65 pe	327	5	6.2	36	4	AAW96738	Aaw96738 Human col
255	5	6.2	21	5	ABG69737	Abg69737 Polypepti	328	5	6.2	36	4	ABG26327	Abg26327 Novel hum
256	5	6.2	22	3	AAV98364	Aay98364 Alpha D p	329	5	6.2	36	4	AAW42431	Aam42431 Human kid
257	5	6.2	22	3	AAV98365	Aay98365 Alpha D p	330	5	6.2	36	4	ADP69608	Add69608 Human REM
258	5	6.2	22	5	ABP62321	Abp62321 Human inm	331	5	6.2	36	7	ADP19293	Adp19293 Human sec
259	5	6.2	22	5	ABP62322	Abp62322 Human inm	332	5	6.2	37	2	AAV20292	Aay20292 Human apo
260	5	6.2	22	5	ABP62320	Abp62320 Human inm	333	5	6.2	37	2	AAV20292	Aay20292 Human apo
261	5	6.2	22	5	ABP62319	Abp62319 Human inm	334	5	6.2	37	3	AAW07047	Aay07047 Breast ca
262	5	6.2	22	6	ABR54847	AbR54847 Human inm	335	5	6.2	37	3	AAW28204	Aab28204 Novel hum
263	5	6.2	22	9	AEB19163	Aeb19163 Igm heavy	336	5	6.2	37	6	ABU61207	Abu61207 Human A d
264	5	6.2	23	2	AAR54385	Aar54385 RAE 74.1-	337	5	6.2	37	8	ADP21429	Adp21429 Human LDL
265	5	6.2	23	2	AAW02469	Aaw02469 RAE 74.1-	338	5	6.2	38	4	AAW17291	Aam17291 Peptide #
266	5	6.2	23	4	AAB88295	Aab88295 Hsp-65 pe	339	5	6.2	38	4	ABB36296	Abb36296 Peptide #
267	5	6.2	23	5	ABG47126	Abg47126 Human pep	340	5	6.2	38	4	ABB42598	Abb42598 Peptide #
268	5	6.2	23	6	ABO12075	AbO12075 Human zin	341	5	6.2	38	4	AAW36414	Aam36414 Peptide #
269	5	6.2	24	4	AAB88284	Aab88284 Hsp-65 pe	342	5	6.2	38	4	AAW29790	Aam29790 Peptide #
270	5	6.2	24	9	ADV13017	Adv13017 Human pho	343	5	6.2	38	4	AAB64809	Aab64809 Human sec
271	5	6.2	25	2	AAW64578	Aaw64578 Human Fac	344	5	6.2	38	4	ABB31099	Abb31099 Peptide #
272	5	6.2	25	2	AAW00362	Aay00362 Fragment	345	5	6.2	38	4	ABB21657	Abb21657 Protein #
273	5	6.2	25	3	AAW44341	Aaw44341 Human sec	346	5	6.2	38	4	AAW69454	Aam69454 Human bon
274	5	6.2	25	4	AAW15499	Aam15499 Peptide #	347	5	6.2	38	4	AAW6304	Aam76304 Human bon
275	5	6.2	25	4	AAW34505	Abb34505 Peptide #	348	5	6.2	38	4	AAW57067	Aam57067 Human bra
276	5	6.2	25	4	AAW27987	Aam27987 Peptide #	349	5	6.2	38	4	AAW63489	Aam63489 Human bra
277	5	6.2	25	4	ABP29333	Abp29333 Peptide #	350	5	6.2	38	4	ABG51130	Abg51130 Human liv
278	5	6.2	25	4	ABR19216	AbR19216 Protein #	351	5	6.2	38	4	ABG58014	Abg58014 Human liv
279	5	6.2	25	4	AAW67690	Aam67690 Human bon	352	5	6.2	38	4	AAW04976	Aam04976 Peptide #
280	5	6.2	25	4	AAW55292	Aam55292 Human bra	353	5	6.2	38	5	ABG39078	Abg39078 Human pep
281	5	6.2	25	4	AAW64064	Aab64064 Human Cla	354	5	6.2	38	5	ABG45607	Abg45607 Human pep
282	5	6.2	25	4	AAW64063	Aab64063 Human Cla	355	5	6.2	39	7	ADD88693	Add88693 Malarial
283	5	6.2	25	4	ABG49323	Abg49323 Human liv	356	5	6.2	39	7	ADG18458	Adg18458 P. falcip
284	5	6.2	25	4	AAW03356	Aam03356 Peptide #	357	5	6.2	39	9	ADW92620	Adw92620 P. falcip
285	5	6.2	25	7	ADW90427	Adw90427 Novel hum	358	5	6.2	40	4	ABB41573	Abb41573 Peptide #
286	5	6.2	25	7	ADG90246	Adg90246 Human sec	359	5	6.2	40	4	ABB37513	Abb37513 Peptide #
287	5	6.2	25	9	ADY25586	Ady25586 Novel hum	360	5	6.2	40	4	AAW35365	Aam35365 Peptide #
288	5	6.2	26	2	AAR54435	Aar54435 AMB 4-9.1	361	5	6.2	40	4	AAW70626	Aam70626 Human bon
289	5	6.2	26	2	AAR54384	Aar54384 RAE 74.1.	362	5	6.2	40	4	AAW75253	Aam75253 Human bon
290	5	6.2	26	2	AAW02468	Aaw02468 RAE 74.1.	363	5	6.2	40	4	AAW05085	Aao05085 Human pol
291	5	6.2	26	2	AAW02416	Aaw02416 AMB 4-9.1	364	5	6.2	40	4	AAW58175	Aam58175 Human bra
292	5	6.2	26	2	AAW05595	Aaw05595 Membrane	365	5	6.2	40	4	AAW62444	Aam62444 Human bra
293	5	6.2	26	4	AAB88310	Aab88310 Hsp-65 pe	366	5	6.2	40	4	ABG57015	Abg57015 Human liv
294	5	6.2	26	6	ABR99526	AbR99526 Amino aci	367	5	6.2	40	4	AAW06061	Aam06061 Peptide #
295	5	6.2	27	4	AAW17891	Aam17891 Peptide #	368	5	6.2	40	5	ABG44901	Abg44901 Human pep
296	5	6.2	27	4	ABB36916	Abb36916 Peptide #	369	5	6.2	41	2	AAV49097	Aay49097 Amino aci
297	5	6.2	27	4	AAW30400	Aam30400 Peptide #	370	5	6.2	41	3	AAW53229	Aag53229 Protein c
298	5	6.2	27	4	ABB31700	Abb31700 Peptide #	371	5	6.2	41	3	AAW29580	Aag29580 Arabidops
299	5	6.2	27	4	ABB22241	Abb22241 Protein #	372	5	6.2	41	4	AAU29908	Aau29908 Novel hum
300	5	6.2	27	4	AAW70068	Aam70068 Human bon	373	5	6.2	41	7	ADL11747	Adel11747 Human sec
301	5	6.2	27	4	AAW57659	Aam57659 Human bra	374	5	6.2	42	2	AAW05617	Aaw05617 MVFlth-GG
302	5	6.2	27	4	ABG51759	AbG51759 Human liv	375	5	6.2	42	2	AAW05621	Aaw05621 HBSTH-GG-
303	5	6.2	27	4	AAW05544	Aam05544 Peptide #	376	5	6.2	42	3	AAV76125	Aay76125 Human sec
304	5	6.2	27	5	ABG39700	AbG39700 Human pep	377	5	6.2	43	2	AAW05618	Aaw05618 mIGR1-GG-
305	5	6.2	28	2	AAR54434	Aar54434 AMB 4-8.1	378	5	6.2	43	2	AAW05622	Aaw05622 mIGR1-GG-
306	5	6.2	28	4	AAW99100	Aam99100 Vaccine r	379	5	6.2	43	2	AAW91058	Aaw91058 Flanking
307	5	6.2	28	4	AAW07404	Aae07404 Synthetic	380	5	6.2	43	2	AAW49096	Aay49096 Amino aci
308	5	6.2	28	5	AAE15758	Aae15758 pda8 pep	381	5	6.2	43	3	AAW27072	Aab27072 Beta-cate
309	5	6.2	28	5	AAU76766	Aau76766 pda8 pep	382	5	6.2	43	3	AAW39250	Aab39250 Human sec
310	5	6.2	28	5	ABG75545	Abg75545 Opt.imised	383	5	6.2	43	4	AAU22457	Aau22457 Human car
311	5	6.2	29	2	AAW02415	Aaw02415 AMB 4-8.1	384	5	6.2	43	7	ABE46425	Ade46425 Human car
312	5	6.2	30	2	AAW54388	Aar54388 RAE 28+29	385	5	6.2	43	8	ADJ07843	Adj07843 Human car
313	5	6.2	30	2	AAW02472	Aaw02472 RAE 28+29	386	5	6.2	43	9	ADX25649	Adx25649 Potato pa
314	5	6.2	31	7	ADA07577	Ada07577 Human sec	387	5	6.2	44	4	AAW74910	Aag74910 Human col
315	5	6.2	31	8	ADN41386	Adn41386 Novel hum	388	5	6.2	44	4	AAW95874	Aam95874 Human rep
316	5	6.2	32	8	ADH18893	Adh18893 Human cel	389	5	6.2	44	6	ABB96405	Abb96405 Human tee
							389	5	6.2	44	6	ABB99525	Abb99525 Amino aci

390	5	6.2	45	4	ABB17677	Abb17677 Human ner	463	5	6.2	55	2	AAR13464	Aar13464 Membrane
391	5	6.2	45	5	ABR40588	AbR40588 Human sec	464	5	6.2	55	2	AAR43310	Aar43310 Human eps
392	45	6.2	45	8	ADH56328	Adh56328 Human S30	465	5	6.2	55	2	AAR60228	Aar60228 Human 1gE
393	5	6.2	45	8	ADS05162	AdS05162 Staphyloc	466	5	6.2	55	2	AAW90134	Aaw90134 Human 1gE
394	5	6.2	46	8	ADR84017	AdR84017 S. pyogen	467	5	6.2	55	4	AAM20074	Aam20074 Peptide #
395	5	6.2	46	2	AAW12809	Aaw12809 Hepatitis	468	5	6.2	55	4	ABB40231	Abb40231 Peptide #
396	5	6.2	46	4	AAM83497	Aam83497 Human imm	469	5	6.2	55	4	AAM33891	Aam33891 Peptide #
397	5	6.2	46	6	ABU06983	Abu06983 Maize Sta	470	5	6.2	55	4	AAM87877	Aam87877 Human imm
398	5	6.2	46	8	ADS14874	AdS14874 Pseudomon	471	5	6.2	55	4	AAW81203	Aaw81203 Human hae
399	5	6.2	47	2	AAW54445	Aaw54445 Amb a 1.1	472	5	6.2	55	4	ABB24663	Abb24663 Protein #
400	5	6.2	47	2	AAW02500	Aaw02500 Peptide c	473	5	6.2	55	4	AAW73705	Aam73705 Human bon
401	5	6.2	47	2	AAW71585	Aaw71585 Staphyloc	474	5	6.2	55	4	AAU67645	Aau67645 Propionib
402	5	6.2	47	3	AAV91367	Aay91367 Human sec	475	5	6.2	55	4	AAU61010	Aau61010 Human bra
403	5	6.2	47	4	AAW91285	Aam91285 Human imm	476	5	6.2	55	4	ABG55442	Abg55442 Human liv
404	5	6.2	47	4	AAW04542	Aao04542 Human pol	477	5	6.2	55	5	ABG43580	Abg43580 Human pep
405	5	6.2	47	5	ABU10245	Abj10245 Human lun	478	5	6.2	55	6	ABM64164	Abm64164 Propionib
406	5	6.2	47	5	AAW47160	Aam47160 Modular e	479	5	6.2	56	9	ADY65290	Ady65290 S. mansoni
407	5	6.2	47	6	ABW99527	Abw99527 Amino aci	480	5	6.2	58	2	ADH11263	Adh11263 Vertebrat
408	5	6.2	47	8	ADT40570	Adt40570 hSARS vir	481	5	6.2	58	4	AAW14808	Aam14808 Peptide #
409	5	6.2	47	8	ADS79987	AdS79987 SARS viru	482	5	6.2	58	4	AAW16867	Aam16867 Peptide #
410	5	6.2	47	8	ADT38100	Adt38100 hSARS vir	483	5	6.2	58	4	ABB33775	Abb33775 Peptide #
411	5	6.2	48	2	AAW19273	Aaw19273 Lactobin	484	5	6.2	58	4	ABB35850	Abb35850 Peptide #
412	5	6.2	48	4	ABG16211	Abg16211 Novel hum	485	5	6.2	58	4	AAW29352	Aam29352 Peptide #
413	5	6.2	48	5	ABW79289	Abw79289 Human pro	486	5	6.2	58	4	AAW27235	Aam27235 Peptide #
414	5	6.2	49	3	AAV97055	Aay97055 T helper	487	5	6.2	58	4	ABB28592	Abb28592 Peptide #
415	5	6.2	49	4	AAW18760	Aam18760 Peptide #	488	5	6.2	58	4	ABB21265	Abb21265 Protein #
416	5	6.2	49	4	ABB37858	Abb37858 Peptide #	489	5	6.2	58	4	ABB19219	Abb19219 Protein #
417	5	6.2	49	4	AAW31265	Aam31265 Peptide #	490	5	6.2	58	4	AAW69033	Aam69033 Human bon
418	5	6.2	49	4	ABB23118	Abb23118 Protein #	491	5	6.2	58	4	AAU56898	Aau56898 Propionib
419	5	6.2	49	4	AAW70989	Aam70989 Human bon	492	5	6.2	58	4	AAU5657	Aau5657 Human bra
420	5	6.2	49	4	AAW58489	Aam58489 Human bra	493	5	6.2	58	4	AAW54542	Aam54542 Human bra
421	5	6.2	49	4	ABG52706	Abg52706 Human liv	494	5	6.2	58	4	AAW56657	Aau56657 Human bra
422	5	6.2	49	5	ABG40508	Abg40508 Human pep	495	5	6.2	58	4	ABG50703	Abg50703 Human liv
423	5	6.2	49	5	ABG32776	Abg32776 Clone 161	496	5	6.2	58	4	ABG48612	Abg48612 Human liv
424	5	6.2	49	6	ABG73715	Abg73715 Murine TH	497	5	6.2	58	4	AAW02533	Aam02533 Peptide #
425	5	6.2	49	6	ABO01284	AbO01284 Growth de	498	5	6.2	58	5	ABP05921	Abp05921 Human ORF
426	5	6.2	49	8	ABH97009	Abh97009 S. pneumo	499	5	6.2	58	5	ABG36605	Abg36605 Human pep
427	5	6.2	49	9	ABG13364	Aec13364 Streptoco	500	5	6.2	58	5	ABG38630	Abg38630 Human pep
428	5	6.2	50	3	ABG15193	Aeg15193 Arabidops	501	5	6.2	58	6	ABW53417	Abw53417 Propionib
429	5	6.2	50	4	AAW90864	Aam90864 Human imm	502	5	6.2	59	4	AAW99721	Aam99721 Human exc
430	5	6.2	50	4	AAW83061	Aam83061 Human imm	503	5	6.2	59	4	AAW84823	Aam84823 Human imm
431	5	6.2	50	4	AAU43635	Aau43635 Propionib	504	5	6.2	59	4	AAW42536	Aam42536 Human kid
432	5	6.2	50	6	ABW40154	Abw40154 Propionib	505	5	6.2	59	5	ABP32508	Abp32508 Human ORF
433	5	6.2	50	9	ADY17142	Ady17142 PRO polyp	506	5	6.2	59	8	ADU69699	Adu69699 S agalact
434	5	6.2	50	9	ADZ98559	Adz98559 Human ami	507	5	6.2	60	4	ABW16085	Abw16085 Human ner
435	5	6.2	51	4	ABW38618	Abw38618 Peptide #	508	5	6.2	61	2	AAW58746	Aaw58746 Ragweed a
436	5	6.2	51	4	AAW32076	Aam32076 Peptide #	509	5	6.2	61	2	AAW58752	Aaw58752 Ragweed a
437	5	6.2	51	4	ABB23717	Abb23717 Protein #	510	5	6.2	61	2	AAW47457	Aau47457 Propionib
438	5	6.2	51	4	AAW71787	Aam71787 Human bon	511	5	6.2	61	4	AAU49699	Abp04969 Human ORF
439	5	6.2	51	4	AAU45988	Aau45988 Propionib	512	5	6.2	61	5	ABP04969	Abp04969 Human ORF
440	5	6.2	51	4	AAU64750	Aau64750 Propionib	513	5	6.2	61	5	ABW05858	Abw05858 UNC Clone
441	5	6.2	51	4	AAU49813	Aau49813 Propionib	514	5	6.2	61	5	ABW05856	Abw05856 UNC Clone
442	5	6.2	51	4	AAW59247	Aam59247 Human bra	515	5	6.2	61	5	ABW05930	Abw05930 UNC Clone
443	5	6.2	51	4	ABG53471	Abg53471 Human liv	516	5	6.2	61	5	ABW05928	Abw05928 UNC Clone
444	5	6.2	51	4	ABW15219	Abw15219 Human ner	517	5	6.2	61	6	ABW43976	Abw43976 Propionib
445	5	6.2	51	5	ABG41601	Abg41601 Human pep	518	5	6.2	62	4	AAU45594	Aau45594 Propionib
446	5	6.2	51	6	ABW46332	Abw46332 Propionib	519	5	6.2	62	5	ABP01694	Abp01694 Human ORF
447	5	6.2	51	6	ABW61269	Abw61269 Propionib	520	5	6.2	62	5	ABP30611	Abp30611 Streptoco
448	5	6.2	51	6	ABW42507	Abw42507 Propionib	521	5	6.2	62	5	ABG99606	Abg99606 Conus sp
449	5	6.2	52	2	AAW27803	Aaw27803 Amino aci	522	5	6.2	62	5	ABG99557	Abg99557 Conus sp
450	5	6.2	52	2	AAW93061	Aaw93061 Human Tan	523	5	6.2	62	5	ABG99589	Abg99589 Conus sp
451	5	6.2	52	4	AAO13321	Aao13321 Human pol	524	5	6.2	62	5	ABG99517	Abg99517 Conus sp
452	5	6.2	52	5	ABP02807	Abp02807 Human ORF	525	5	6.2	62	5	ABG99591	Abg99591 Conus sp
453	5	6.2	52	5	ABP34149	Abp34149 Human kin	526	5	6.2	62	5	ABG99604	Abg99604 Conus sp
454	5	6.2	53	2	AAW95647	Aar95647 Klebsiell	527	5	6.2	62	5	ABG99600	Abg99600 Conus sp
455	5	6.2	53	3	AAW12366	Aag12366 Zea mays	528	5	6.2	62	6	ABW42113	Abw42113 Propionib
456	5	6.2	53	4	ABG74472	Aag74472 Human col	529	5	6.2	62	6	ABU00317	Abu00317 Human nov
457	5	6.2	53	5	ABP06547	Abp06547 Human ORF	530	5	6.2	62	8	ADR50887	Adr50887 C. textil
458	5	6.2	54	3	ABG02662	Abg02662 Human sec	531	5	6.2	62	9	ABM90902	Abm90902 M. xanthu
459	5	6.2	54	5	ABP06309	Abp06309 Human ORF	532	5	6.2	62	9	ABW17626	Abw17626 Conus ban
460	5	6.2	54	8	ABO58532	AbO58532 Human gen	533	5	6.2	63	2	AAW55312	Aaw55312 H. pylori
461	5	6.2	54	8	ADV88816	Adv88816 Streptoco	534	5	6.2	63	2	AAW93058	Aaw93058 Human Tan
462	5	6.2	54	8	ADV80069	Adv80069 Streptoco	535	5	6.2	63	3	AAW97128	Aay97128 Tau conot

536	5	6.2	63	4	AAU46485	Aau46485	Propionib	609	5	6.2	69	2	AAV39396	Aav39396	Mutant Sh
537	5	6.2	63	6	ABM43004	Abm43004	Propionib	610	5	6.2	69	2	AAV43010	Aav43010	Mutant Sh
538	5	6.2	63	6	ABU61516	Abu61516	Novel fru	611	5	6.2	69	2	AAV43012	Aav43012	Mutant Sh
539	5	6.2	63	6	ABU30394	Abu30394	Protein e	612	5	6.2	69	2	AAV43015	Aav43015	Mutant Sh
540	5	6.2	63	8	ADK02076	Adk02076	Hepatitis	613	5	6.2	69	3	AAV68360	Aav68360	Verotoxin
541	5	6.2	63	8	ADK01365	Adk01365	Hepatitis	614	5	6.2	69	3	AAV66234	Aav66234	E coli he
542	5	6.2	64	3	AG26501	Aag26501	Arabidops	615	5	6.2	69	4	ADP39753	Adp39753	E. coli O
543	5	6.2	64	3	ABU00159	Abu00159	Human nov	616	5	6.2	69	8	ADP39753	Adp39753	E. coli O
544	5	6.2	64	7	ADCO0242	Adc00242	Enterohae	617	5	6.2	69	8	ADP39753	Adp39753	E. coli O
545	5	6.2	64	7	ADCO0547	Adc00547	Enterohae	618	5	6.2	69	9	ADP39753	Adp39753	E. coli O
546	5	6.2	65	2	AAV59677	Aay59677	Secreted	619	5	6.2	70	2	ADH11261	Adh11261	Shiga tox
547	5	6.2	65	3	AAV95754	Aay95754	Bacillus m	620	5	6.2	70	3	ADH11261	Adh11261	Shiga tox
548	5	6.2	65	3	AAV95754	Aay95754	Bacillus m	621	5	6.2	70	3	ADH11261	Adh11261	Shiga tox
549	5	6.2	65	4	AAU84262	Aam84262	Human imm	622	5	6.2	70	3	ADH11261	Adh11261	Shiga tox
550	5	6.2	65	4	AG90494	Aag90494	C glutami	623	5	6.2	70	4	AAU67594	Aau67594	Human pro
551	5	6.2	65	4	ABG08549	Abg08549	Novel hum	624	5	6.2	70	4	AAU67594	Aau67594	Human pro
552	5	6.2	65	5	ABP27246	Abp27246	Streptoco	625	5	6.2	70	6	ABM64113	Abm64113	Propionib
553	5	6.2	65	5	ABP27247	Abp27247	Streptoco	626	5	6.2	70	6	ABM64113	Abm64113	Propionib
554	5	6.2	65	5	AAQ22515	Aao22515	Small aci	627	5	6.2	70	6	ADA34659	Ada34659	Acinetoba
555	5	6.2	65	6	ABU46560	Abu46560	Protein e	628	5	6.2	70	7	ADP04299	Adp04299	Bacterial
556	5	6.2	65	7	ABU63673	Abu63673	Bacillus	629	5	6.2	70	7	ADP04299	Adp04299	Bacterial
557	5	6.2	65	7	ADP77827	Adm77827	Human pro	630	5	6.2	70	9	ADP04299	Adp04299	Bacterial
558	5	6.2	65	8	ADV88463	Adv88463	Human sec	631	5	6.2	71	2	AAW27924	Aaw27924	Human nep
559	5	6.2	65	8	ADV88463	Adv88463	Human sec	632	5	6.2	71	2	AAW27924	Aaw27924	Human nep
560	5	6.2	65	8	ADV79716	Adv79716	Streptoco	633	5	6.2	71	2	AAW27924	Aaw27924	Human nep
561	5	6.2	65	9	ADH86763	Adh86763	Alpha/bet	634	5	6.2	71	2	AAW27924	Aaw27924	Human nep
562	5	6.2	65	9	ADH86763	Adh86763	Alpha/bet	635	5	6.2	71	2	AAW27924	Aaw27924	Human nep
563	5	6.2	66	2	AAV60391	Aay60391	Human nor	636	5	6.2	71	4	ABM15829	Abm15829	Human ner
564	5	6.2	66	2	AAV60391	Aay60391	Human nor	637	5	6.2	71	4	ABM15829	Abm15829	Human ner
565	5	6.2	66	4	ABM15462	Aam15462	Peptide #	638	5	6.2	71	4	ABM15462	Aam15462	Peptide #
566	5	6.2	66	4	ABM15462	Aam15462	Peptide #	639	5	6.2	71	4	ABM15462	Aam15462	Peptide #
567	5	6.2	66	4	ABM15462	Aam15462	Peptide #	640	5	6.2	71	4	ABM15462	Aam15462	Peptide #
568	5	6.2	66	4	ABM15462	Aam15462	Peptide #	641	5	6.2	71	4	ABM15462	Aam15462	Peptide #
569	5	6.2	66	4	ABM15462	Aam15462	Peptide #	642	5	6.2	71	4	ABM15462	Aam15462	Peptide #
570	5	6.2	66	4	ABM15462	Aam15462	Peptide #	643	5	6.2	71	4	ABM15462	Aam15462	Peptide #
571	5	6.2	66	4	ABM15462	Aam15462	Peptide #	644	5	6.2	71	4	ABM15462	Aam15462	Peptide #
572	5	6.2	66	4	ABM15462	Aam15462	Peptide #	645	5	6.2	71	4	ABM15462	Aam15462	Peptide #
573	5	6.2	66	4	ABM15462	Aam15462	Peptide #	646	5	6.2	71	4	ABM15462	Aam15462	Peptide #
574	5	6.2	66	4	ABM15462	Aam15462	Peptide #	647	5	6.2	71	4	ABM15462	Aam15462	Peptide #
575	5	6.2	66	4	ABM15462	Aam15462	Peptide #	648	5	6.2	71	4	ABM15462	Aam15462	Peptide #
576	5	6.2	66	4	ABM15462	Aam15462	Peptide #	649	5	6.2	71	4	ABM15462	Aam15462	Peptide #
577	5	6.2	66	4	ABM15462	Aam15462	Peptide #	650	5	6.2	71	4	ABM15462	Aam15462	Peptide #
578	5	6.2	66	4	ABM15462	Aam15462	Peptide #	651	5	6.2	71	4	ABM15462	Aam15462	Peptide #
579	5	6.2	66	4	ABM15462	Aam15462	Peptide #	652	5	6.2	71	4	ABM15462	Aam15462	Peptide #
580	5	6.2	66	4	ABM15462	Aam15462	Peptide #	653	5	6.2	71	4	ABM15462	Aam15462	Peptide #
581	5	6.2	66	4	ABM15462	Aam15462	Peptide #	654	5	6.2	71	4	ABM15462	Aam15462	Peptide #
582	5	6.2	66	4	ABM15462	Aam15462	Peptide #	655	5	6.2	71	4	ABM15462	Aam15462	Peptide #
583	5	6.2	66	4	ABM15462	Aam15462	Peptide #	656	5	6.2	71	4	ABM15462	Aam15462	Peptide #
584	5	6.2	66	4	ABM15462	Aam15462	Peptide #	657	5	6.2	71	4	ABM15462	Aam15462	Peptide #
585	5	6.2	66	4	ABM15462	Aam15462	Peptide #	658	5	6.2	71	4	ABM15462	Aam15462	Peptide #
586	5	6.2	66	4	ABM15462	Aam15462	Peptide #	659	5	6.2	71	4	ABM15462	Aam15462	Peptide #
587	5	6.2	66	4	ABM15462	Aam15462	Peptide #	660	5	6.2	71	4	ABM15462	Aam15462	Peptide #
588	5	6.2	66	4	ABM15462	Aam15462	Peptide #	661	5	6.2	71	4	ABM15462	Aam15462	Peptide #
589	5	6.2	66	4	ABM15462	Aam15462	Peptide #	662	5	6.2	71	4	ABM15462	Aam15462	Peptide #
590	5	6.2	66	4	ABM15462	Aam15462	Peptide #	663	5	6.2	71	4	ABM15462	Aam15462	Peptide #
591	5	6.2	66	4	ABM15462	Aam15462	Peptide #	664	5	6.2	71	4	ABM15462	Aam15462	Peptide #
592	5	6.2	66	4	ABM15462	Aam15462	Peptide #	665	5	6.2	71	4	ABM15462	Aam15462	Peptide #
593	5	6.2	66	4	ABM15462	Aam15462	Peptide #	666	5	6.2	71	4	ABM15462	Aam15462	Peptide #
594	5	6.2	66	4	ABM15462	Aam15462	Peptide #	667	5	6.2	71	4	ABM15462	Aam15462	Peptide #
595	5	6.2	66	4	ABM15462	Aam15462	Peptide #	668	5	6.2	71	4	ABM15462	Aam15462	Peptide #
596	5	6.2	66	4	ABM15462	Aam15462	Peptide #	669	5	6.2	71	4	ABM15462	Aam15462	Peptide #
597	5	6.2	66	4	ABM15462	Aam15462	Peptide #	670	5	6.2	71	4	ABM15462	Aam15462	Peptide #
598	5	6.2	66	4	ABM15462	Aam15462	Peptide #	671	5	6.2	71	4	ABM15462	Aam15462	Peptide #
599	5	6.2	66	4	ABM15462	Aam15462	Peptide #	672	5	6.2	71	4	ABM15462	Aam15462	Peptide #
600	5	6.2	66	4	ABM15462	Aam15462	Peptide #	673	5	6.2	71	4	ABM15462	Aam15462	Peptide #
601	5	6.2	66	4	ABM15462	Aam15462	Peptide #	674	5	6.2	71	4	ABM15462	Aam15462	Peptide #
602	5	6.2	66	4	ABM15462	Aam15462	Peptide #	675	5	6.2	71	4	ABM15462	Aam15462	Peptide #
603	5	6.2	66	4	ABM15462	Aam15462	Peptide #	676	5	6.2	71	4	ABM15462	Aam15462	Peptide #
604	5	6.2	66	4	ABM15462	Aam15462	Peptide #	677	5	6.2	71	4	ABM15462	Aam15462	Peptide #
605	5	6.2	66	4	ABM15462	Aam15462	Peptide #	678	5	6.2	71	4	ABM15462	Aam15462	Peptide #
606	5	6.2	66	4	ABM15462	Aam15462	Peptide #	679	5	6.2	71	4	ABM15462	Aam15462	Peptide #
607	5	6.2	66	4	ABM15462	Aam15462	Peptide #	680	5	6.2	71	4	ABM15462	Aam15462	Peptide #
608	5	6.2	66	4	ABM15462	Aam15462	Peptide #	681	5	6.2	71	4	ABM15462	Aam15462	Peptide #

682	5	6.2	77	5	ABP38541	Abp38541	Staphyloc	755	4	5.0	5	9	ADX19158	Adx19158	Human	PSC
683	5	6.2	77	8	ADS06192	Ads06192	Staphyloc	756	4	5.0	5	9	AEb87868	Aeb87868	L. starke	
684	5	6.2	77	8	ADZ64429	Adz64429	Human can	757	4	5.0	5	9	AEb87888	Aeb87888	Lipomyces	
685	5	6.2	78	3	AGS1222	Agss1222	Arabidops	758	4	5.0	6	1	AAP40807	Aap40807	Sequence	
686	5	6.2	78	4	AM13898	Aam13898	Peptide #	759	4	5.0	6	2	AAR53677	Aar53677	Fragment	
687	5	6.2	78	4	ABB32843	Abb32843	Peptide #	760	4	5.0	6	2	AAR86350	Aar86350	Cyclic HI	
688	5	6.2	78	4	AM26304	Aam26304	Peptide #	761	4	5.0	6	2	AAR91817	Aar91817	Mab-425-C	
689	5	6.2	78	4	ABB27673	Abb27673	Human pep	762	4	5.0	6	2	AAR97589	Aar97589	Mab PK39H	
690	5	6.2	78	4	ABB18325	Abb18325	Protein #	763	4	5.0	6	2	AAR97581	Aar97581	Mab PK39H	
691	5	6.2	78	4	AM66029	Aam66029	Human bon	764	4	5.0	6	2	AAR97576	Aar97576	Mab PK39H	
692	5	6.2	78	4	AAU57775	Aau57775	Propionib	765	4	5.0	6	2	AAR97558	Aar97558	Mab PK39H	
693	5	6.2	78	4	AM53648	Aam53648	Human bra	766	4	5.0	6	2	AAW45020	Aaw45020	Immunomod	
694	5	6.2	78	4	ABG47695	Abg47695	Human liv	767	4	5.0	6	2	AAW45020	Aaw45020	Immunomod	
695	5	6.2	78	4	AM01641	Aam01641	Peptide #	768	4	5.0	6	2	AAW17510	Aaw17510	Protein k	
696	5	6.2	78	4	AAU33101	Aau33101	Novel hum	769	4	5.0	6	2	AAW51172	Aaw51172	Cysteine	
697	5	6.2	78	5	ABB94260	Abb94260	Chlamydia	770	4	5.0	6	2	AAW87273	Aaw87273	Peptide d	
698	5	6.2	78	5	ABG35677	Abg35677	Human pep	771	4	5.0	6	2	AAW87357	Aaw87357	Peptide d	
699	5	6.2	78	6	ABM54294	Abm54294	Propionib	772	4	5.0	6	2	AAW87290	Aaw87290	Peptide d	
700	5	6.2	78	6	ABR38910	Abr38910	pBAL ORF	773	4	5.0	6	2	AAW87266	Aaw87266	Peptide d	
701	5	6.2	78	6	ABU24462	Abu24462	Protein e	774	4	5.0	6	2	AAW23488	Aaw23488	V beta 6	
702	5	6.2	78	6	ABU26766	Abu26766	Protein e	775	4	5.0	6	2	AAW93518	Aaw93518	Bacterial	
703	5	6.2	78	8	ADR99395	Adr99395	Chlamydia	776	4	5.0	6	2	AAW09434	Aaw09434	Immunoad	
704	5	6.2	79	3	AAZ29579	Aaz29579	Arabidops	777	4	5.0	6	2	AAW28776	Aaw28776	Human hep	
705	5	6.2	79	3	AAZ28083	Aaz28083	Arabidops	778	4	5.0	6	2	AAW49058	Aaw49058	Membrane	
706	5	6.2	79	4	AM87265	Aam87265	Human imm	779	4	5.0	6	3	AAW99849	Aaw99849	Human t-p	
707	5	6.2	79	4	AAU52736	Aau52736	Propionib	780	4	5.0	6	3	AAW97482	Aaw97482	Hepatitis	
708	5	6.2	79	4	AAU18598	Aau18598	Human lun	781	4	5.0	6	3	AAW12865	Aaw12865	STAT3 DNA	
709	5	6.2	79	5	ABP06081	Abp06081	Human ORF	782	4	5.0	6	3	AAW12856	Aaw12856	STAT3 DNA	
710	5	6.2	79	5	ABP04941	Abp04941	Human ORF	783	4	5.0	6	3	AAW12857	Aaw12857	STAT3 DNA	
711	5	6.2	79	5	ABP64060	Abp64060	Human ORF	784	4	5.0	6	3	AAW01556	Aaw01556	Collagena	
712	5	6.2	79	5	ABB48090	Abb48090	Listeria	785	4	5.0	6	4	AAW01559	Aaw01559	Collagena	
713	5	6.2	79	6	ABM49255	Abm49255	Propionib	786	4	5.0	6	4	AAW49843	Aaw49843	Human end	
714	5	6.2	79	7	ABZ32222	Abz32222	Human nov	787	4	5.0	6	5	ABW46173	Abw46173	Desmoglei	
715	5	6.2	79	7	ADT59578	Adt59578	Human pol	788	4	5.0	6	5	AAU75031	Aau75031	4070A amp	
716	5	6.2	79	8	ADT56514	Adt56514	Plant pol	789	4	5.0	6	5	AAU85688	Aau85688	Collagena	
717	5	6.2	80	2	AAW74978	Aaw74978	Human sec	790	4	5.0	6	5	AAU81468	Aau81468	Collagena	
718	5	6.2	80	3	AAW44577	Aaw44577	Virulence	791	4	5.0	6	5	AAU81467	Aau81467	VapA prot	
719	5	6.2	80	4	AAE01366	Aae01366	Human gen	792	4	5.0	6	5	ABP95994	Abp95994	Microtetr	
720	5	6.2	80	4	AAQ01628	Aaq01628	Human pol	793	4	5.0	6	6	ADG17720	Adg17720	Human pro	
721	5	6.2	80	4	AAU64258	Aau64258	Propionib	794	4	5.0	6	7	ADH78397	Adh78397	JNK/SAPK-	
722	5	6.2	80	5	ABP54529	Abp54529	Actinobac	795	4	5.0	6	8	ADO37784	Ado37784	Binding p	
723	5	6.2	80	5	ABG64098	Abg64098	Human alb	796	4	5.0	6	8	ADO28306	Ado28306	Capture s	
724	5	6.2	80	5	ABP33468	Abp33468	Human ORF	797	4	5.0	6	8	ADQ94498	Adq94498	Novel dru	
725	5	6.2	80	5	ABG95438	Abg95438	Human nov	798	4	5.0	6	8	ADR50483	Adr50483	6-mer pep	
726	5	6.2	80	6	ABM60777	Abm60777	Propionib	799	4	5.0	6	8	ADR40513	Adr40513	Peptide o	
727	5	6.2	80	6	ABO34632	Ab034632	Region of	800	4	5.0	6	8	ADR87143	Adr87143	Anti-Stat	
728	5	6.2	80	7	ADI23293	Adi23293	Novel hum	801	4	5.0	6	8	ADR87144	Adr87144	Stat3 con	
729	5	6.2	80	7	ABO76130	Ab076130	Pseudomon	802	4	5.0	6	8	ADS96129	Ads96129	Tagged po	
730	5	6.2	80	8	ADH74295	Adh74295	Human sec	803	4	5.0	6	9	ADM86814	Adm86814	Protein 1	
731	5	6.2	80	8	ADL77363	Adl77363	Albumin f	804	4	5.0	6	9	ADX39149	Adx39149	STAT3ip p	
732	4	5.0	4	2	AAW53727	Aaw53727	Tetrapept	805	4	5.0	6	9	ADZ46489	Adz46489	Antigenic	
733	4	5.0	4	4	AAE02264	Aae02264	Human 36P	806	4	5.0	6	9	AEA01814	Aea01814	Cleavable	
734	4	5.0	4	4	AAW51331	Aaw51331	Angiotens	807	4	5.0	6	9	AEA41781	Aea41781	GAG-bindi	
735	4	5.0	4	6	ABU10294	Abu10294	Undaria p	808	4	5.0	6	9	AEA41260	Aea41260	GAG-bindi	
736	4	5.0	4	9	AEA13862	Aea13862	VEGF rela	809	4	5.0	6	9	AEA41258	Aea41258	GAG-bindi	
737	4	5.0	4	9	AEA39593	Aea39593	Caspase s	810	4	5.0	6	9	AEA41774	Aea41774	GAG-bindi	
738	4	5.0	5	2	AAZ23469	Aaz23469	V beta 6	811	4	5.0	6	9	ABE30599	Ab30599	Therapeut	
739	4	5.0	5	2	AAZ01537	Aaz01537	Peptide d	812	4	5.0	7	2	AAW24662	Aaw24662	Immunomod	
740	4	5.0	5	5	ABJ11489	Abj11489	Human 125	813	4	5.0	7	2	AAW60922	Aaw60922	Enterotox	
741	4	5.0	5	5	AAU81483	Aau81483	VapA prot	814	4	5.0	7	2	AAW60923	Aaw60923	Enterotox	
742	4	5.0	5	5	AAU81482	Aau81482	VapA prot	815	4	5.0	7	2	AAW64889	Aaw64889	C7 peptid	
743	4	5.0	5	6	ABU72728	Abu72728	Novel pro	816	4	5.0	7	2	AAW83024	Aaw83024	Calcium-i	
744	4	5.0	5	6	ABU12234	Abu12234	Streptoco	817	4	5.0	7	2	AAW01485	Aaw01485	Calcium-i	
745	4	5.0	5	6	ABU12233	Abu12233	Streptoco	818	4	5.0	7	2	AAW86702	Aaw86702	Pilin der	
746	4	5.0	5	6	ABP75024	Abp75024	Proteome	819	4	5.0	7	2	AAW13169	Aaw13169	Ca-indepe	
747	4	5.0	5	6	ABT57034	Abt57034	184P1E2-r	820	4	5.0	7	2	AAW17840	Aaw17840	Cytosolic	
748	4	5.0	5	7	ADC17578	Adc17578	Type IV c	821	4	5.0	7	2	ABB76924	Abb76924	Cyclodext	
749	4	5.0	5	7	ADL17474	Adl17474	Type IV c	822	4	5.0	7	2	AAW23406	Aaw23406	V beta 6	
750	4	5.0	5	8	ADO63973	Ado63973	Human 213	823	4	5.0	7	2	AAW93504	Aaw93504	Bacterial	
751	4	5.0	5	8	ADR19100	Adr19100	Type IV c	824	4	5.0	7	2	AAW17020	Aaw17020	Heat choc	
752	4	5.0	5	8	ADR18996	Adr18996	Human typ	825	4	5.0	7	2	AAW49020	Aaw49020	Membrane	
753	4	5.0	5	8	ADR90638	Adr90638	Human mon	826	4	5.0	7	2	AAW49015	Aaw49015	Membrane	
754	4	5.0	5	8	ADU73684	Adu73684	Control c	827	4	5.0	7	2	AAW48624	Aaw48624	Membrane	

828	4	5.0	7	2	AAW81831	901	4	5.0	7	9	AEA27966	Aea27966 Transform
829	4	5.0	7	3	AAW78302	902	4	5.0	7	9	AEb11125	Neurotrop
830	4	5.0	7	3	AAy84969	903	4	5.0	7	9	AEb52362	Chymosin
831	4	5.0	7	3	AAy52584	904	4	5.0	7	9	AEb52363	Atlantic
832	4	5.0	7	3	AAy52582	905	4	5.0	7	9	AEb52364	Human pep
833	4	5.0	7	4	AAU04419	906	4	5.0	7	9	AEb52365	Porcine p
834	4	5.0	7	4	AAU72162	907	4	5.0	8	2	AAr43485	Ro/SSA ep
835	4	5.0	7	4	AAAB49848	908	4	5.0	8	2	AAr43460	Ro/SSA ep
836	4	5.0	7	4	AAAB49847	909	4	5.0	8	2	AAr60632	Human PC
837	4	5.0	7	5	AAE21386	910	4	5.0	8	2	AAr66349	Cyclic HI
838	4	5.0	7	5	AAU80712	911	4	5.0	8	2	AAr67973	EII loop
839	4	5.0	7	5	ABB46180	912	4	5.0	8	2	AAr95061	Multidoma
840	4	5.0	7	5	AAU81557	913	4	5.0	8	2	AAW17688	Substrate
841	4	5.0	7	5	ABG96779	914	4	5.0	8	2	AAy21397	Human HUP
842	4	5.0	7	5	ABP49525	915	4	5.0	8	2	AAy23401	V beta 6
843	4	5.0	7	5	ABJ11431	916	4	5.0	8	2	AAy10407	T cell ep
844	4	5.0	7	5	ABJ11433	917	4	5.0	8	2	AAy16849	Heat choc
845	4	5.0	7	5	ABB80641	918	4	5.0	8	2	AAW86117	Streptoki
846	4	5.0	7	5	AAU81453	919	4	5.0	8	3	AAb01334	MHC Class
847	4	5.0	7	5	AAU81455	920	4	5.0	8	3	AAb12056	GI GTPase
848	4	5.0	7	5	AAU81454	921	4	5.0	8	3	AAy61863	Cadherin-
849	4	5.0	7	5	AAU81456	922	4	5.0	8	3	AAm98727	Human pep
850	4	5.0	7	5	ABP52983	923	4	5.0	8	4	AAU04422	Neisseria
851	4	5.0	7	5	AAE28528	924	4	5.0	8	4	AAU04422	Neisseria
852	4	5.0	7	5	ABG77640	925	4	5.0	8	4	AAg79237	Peptide o
853	4	5.0	7	5	ABG77666	926	4	5.0	8	4	ABP24008	HIV A11 m
854	4	5.0	7	5	ABG77639	927	4	5.0	8	4	ABP22232	HIV A03 m
855	4	5.0	7	5	ABG77627	928	4	5.0	8	4	AAJ02617	Hepatitis
856	4	5.0	7	5	ABG77631	929	4	5.0	8	4	AAJ02930	Hepatitis
857	4	5.0	7	5	ABG68028	930	4	5.0	8	4	AAJ00830	Hepatitis
858	4	5.0	7	5	AAE20564	931	4	5.0	8	4	AAe08157	Peptide #
859	4	5.0	7	5	ABB82221	932	4	5.0	8	4	ABb78120	Amino aci
860	4	5.0	7	6	ABU72676	933	4	5.0	8	5	ABb78121	Amino aci
861	4	5.0	7	6	ABU72664	934	4	5.0	8	5	ABB46465	Desmoglei
862	4	5.0	7	6	ABU79839	935	4	5.0	8	5	ABB46187	Desmoglei
863	4	5.0	7	6	ABJ39341	936	4	5.0	8	5	ABB46194	Desmoglei
864	4	5.0	7	6	ABJ39334	937	4	5.0	8	5	ABG69774	Polypepti
865	4	5.0	7	6	ABU61532	938	4	5.0	8	5	AAU11508	PAIV-5 pV
866	4	5.0	7	6	AAO19862	939	4	5.0	8	5	AAU11507	PAIV-5 pV
867	4	5.0	7	6	ABP75033	940	4	5.0	8	5	AAU73285	Human pro
868	4	5.0	7	6	ABP75098	941	4	5.0	8	5	ABB83320	Ras prote
869	4	5.0	7	6	ABP75148	942	4	5.0	8	5	ABP62250	Human inm
870	4	5.0	7	6	ABU61908	943	4	5.0	8	5	ABP62249	Human inm
871	4	5.0	7	6	ADA24183	944	4	5.0	8	5	AAU81439	Vapa prot
872	4	5.0	7	7	ADA63881	945	4	5.0	8	5	AAU81442	Vapa prot
873	4	5.0	7	7	ADP379619	946	4	5.0	8	5	AAU81440	Vapa prot
874	4	5.0	7	7	ADC44273	947	4	5.0	8	5	AAU81443	Vapa prot
875	4	5.0	7	7	ADD69528	948	4	5.0	8	5	ABP52982	Cellular
876	4	5.0	7	7	ADP70698	949	4	5.0	8	5	ABP52982	Cellular
877	4	5.0	7	7	ADG72830	950	4	5.0	8	5	AAU97758	Mycobacte
878	4	5.0	7	7	ADG72830	951	4	5.0	8	5	AAU98641	Mycobacte
879	4	5.0	7	7	ADW21836	952	4	5.0	8	5	ABG80089	MHC class
880	4	5.0	7	7	ADJ98596	953	4	5.0	8	5	AAU80832	Rat Rb-in
881	4	5.0	7	8	ADH73690	954	4	5.0	8	6	ABJ19914	MHC bindi
882	4	5.0	7	8	ADH73690	955	4	5.0	8	6	ABP72180	Carcinoma
883	4	5.0	7	8	ADL95987	956	4	5.0	8	6	ABP72180	Carcinoma
884	4	5.0	7	8	ADL95874	957	4	5.0	8	7	ADA07599	Human sec
885	4	5.0	7	8	ADL95878	958	4	5.0	8	7	ADC98779	Staphyloc
886	4	5.0	7	8	ADJ95886	959	4	5.0	8	7	ADH84707	Mammalian
887	4	5.0	7	8	ADO63915	960	4	5.0	8	7	ADG72954	Heat choc
888	4	5.0	7	8	ADO63915	961	4	5.0	8	7	ADL17630	Human AP6
889	4	5.0	7	8	ADN08577	962	4	5.0	8	7	ADW31889	HLA bindi
890	4	5.0	7	8	ADN08697	963	4	5.0	8	7	ADW31888	HLA bindi
891	4	5.0	7	8	ADP75021	964	4	5.0	8	8	ADG94462	Human JAM
892	4	5.0	7	8	ADQ94503	965	4	5.0	8	8	ADG94466	Human JAM
893	4	5.0	7	8	ADU08796	966	4	5.0	8	8	ADG94489	Human JAM
894	4	5.0	7	8	ADT78253	967	4	5.0	8	8	ADG94621	Human JAM
895	4	5.0	7	8	ADU64144	968	4	5.0	8	8	ADH89860	Cell pene
896	4	5.0	7	9	ADV86454	969	4	5.0	8	8	ADK63028	Epicope 1
897	4	5.0	7	9	ADW39229	970	4	5.0	8	8	ADI46865	Permeabil
898	4	5.0	7	9	ADY59630	971	4	5.0	8	8	ADI46860	Permeabil
899	4	5.0	7	9	ADZ17658	972	4	5.0	8	8	ADI46887	Permeabil
900	4	5.0	7	9	ADZ04432	973	4	5.0	8	8	ADI47020	Permeabil

CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 79 AA;

Query Match 58.8%; Score 47; DB 6; Length 79;
 Best Local Similarity 100.0%; Pred. No. 3.1e-40;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKDEVKEVOEYKTYNKLTKDPEQRETLKAIHYALNCCGLAGV 47
 DB 1 HKDEVKEVOEYKTYNKLTKDPEQRETLKAIHYALNCCGLAGV 47

RESULT 3
 ADJ57561
 ID ADJ57561 standard; protein; 38 AA.

AC ADJ57561;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Human CD9 fibronectin-binding domain polypeptide fragment.
 DE
 XX Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
 KW haemostatic; antiangiogenic; cytostatic.
 XX
 XX Homo sapiens.

OS
 XX WO2004007685-A2.
 PN
 XX 22-JAN-2004.
 PD
 XX 14-JUL-2003; 2003WO-US022050.
 PF
 XX 12-JUL-2002; 2002US-0395864P.
 PR
 XX (UYTE-) UNIV TENNESSEE RES FOUND.

PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MW;
 PI Crossno JT, Lu Y;
 XX WPI; 2004-122924/12.
 DR
 XX Interfering with CD9 binding to fibronectin by binding a fibronectin-
 PT binding domain of the CD9 protein or polypeptide, useful in treating
 PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
 PT and cancers.

PS Claim 7; SEQ ID NO 4; 126pp; English.
 XX
 XX The present sequence is that of a polypeptide fragment from the
 CC fibronectin-binding domain of human CD9 ADJ57558. The peptide, or an
 CC antibody that binds to it, is used in claimed methods for: interfering
 CC with CD9 binding to fibronectin; modifying adhesion, motility or
 CC spreading of a CD9-expressing cell on fibronectin; inhibiting
 CC proliferation or survival of CD9-expressing cells; modifying pericellular
 CC fibronectin matrix assembly; modifying invasiveness of a cell through a
 CC collagen and/or laminin matrix; and modifying cell-to-cell interaction.
 CC The methods are based on the finding that increased CD9 expression is

CC implicated in (i) decreased adhesiveness of cells to extracellular matrix
 CC (via alpha5-beta1 integrin) and/or decreased cell invasiveness and/or
 CC decreased pericellular fibronectin matrix assembly, and/or (ii) increased
 CC cell motility, spreading, proliferation, cell survival against apoptosis,
 CC and/or cell-to-cell contacts. Conditions or disease states involving
 CC proliferation or survival of CD9-expressing cells can be treated, e.g.
 CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplanted
 CC arteriopathy, bleeding disorders, angiogenesis, and primary and
 CC metastatic cancers including breast cancer, prostate cancer, colon
 CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.

XX Sequence 38 AA;

Query Match 47.5%; Score 38; DB 8; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.8e-31;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICPKDV 60
 DB 1 KDEPQRETLKAIHYALNCCGLAGVGEQFISDICPKDV 38

RESULT 4
 ABP76310
 ID ABP76310 standard; protein; 80 AA.

XX AC ABP76310;
 XX
 XX 21-FEB-2003 (first entry)
 DT
 XX Human GENSET protein SEQ ID 860.
 DE
 XX Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;
 KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;
 KW inflammatory disease; immune disorder; neuromuscular; toxicity;
 KW central nervous system; cardiovascular; gastrointestinal.

XX Homo sapiens.

XX WO200283898-A1.

XX 24-OCT-2002.

XX 18-APR-2001; 2001WO-IB000914.

XX 18-APR-2001; 2001WO-IB000914.

XX (GEST) GENSET.

XX Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;

XX WPI; 2003-075548/07.

XX New GENSET polynucleotides and polypeptides, useful for treating heavy
 PT metal toxicity, cancer, inflammatory diseases, immune disorders, and the
 PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
 PT toxicity.

PS Claim 14; Page 710; 735pp; English.

XX The present invention relates to novel GENSET polynucleotides (AB236404-
 CC AB236911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides
 CC and polypeptides are useful in screening and diagnostic assays for
 CC abnormal GENSET expression and/or biological activity. They are also
 CC useful for screening of compounds for treating or preventing GENSET-
 CC related disorders, such as heavy metal toxicity, cancer, inflammatory
 CC diseases, immune disorders, and the neuromuscular, central nervous system
 CC (CNS), cardiovascular or gastrointestinal effects of the toxicity

XX Sequence 80 AA;

Query Match 40.0%; Score 32; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 8.3e-25;

```
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQSEYKDYTNKLTQKDEPQRETLK 32
Db 44 HKDEVKEVQSEYKDYTNKLTQKDEPQRETLK 75

RESULT 5
ABU05051
ID ABU05051 standard; protein; 30 AA.
XX AC ABU05051;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (BPT) #1717.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCO INC.
XX FI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX PS Example 2; SEQ ID NO 1717; 134pp; English.
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 30 AA;

Query Match 37.5%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.8e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQSEYKDYTNKLTQKDEPQRETLK 32
Db 44 HKDEVKEVQSEYKDYTNKLTQKDEPQRETLK 75

RESULT 6
ADJ57562
ID ADJ57562 standard; peptide; 25 AA.
XX AC ADJ57562;
XX DT 06-MAY-2004 (first entry)
XX DE Human CD9 fibronectin-binding domain peptide fragment.
XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
KW haemostatic; antiangiogenic; cytostatic.
XX OS Homo sapiens.
XX PN WO2004007685-A2.
XX PD 22-JAN-2004.
XX PF 14-JUL-2003; 2003WO-US022050.
XX PR 12-JUL-2002; 2002US-0395864P.
XX PA (UYTE-) UNIV TENNESSEE RES FOUND.
XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
XX PI Croesno JT, Lu Y;
XX DR WPI; 2004-122924/12.
XX PT Interfering with CD9 binding to fibronectin by binding a fibronectin-
PT binding domain of the CD9 protein or polypeptide, useful in treating
PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
PT and cancers.
XX PS Claim 7; SEQ ID NO 5; 126pp; English.
CC The present sequence is that of a peptide fragment from the fibronectin-
CC binding domain of human CD9 ADJ57562. The peptide, or an antibody that
CC binds to it, is used in claimed methods for: interfering with CD9 binding
CC to fibronectin; modifying adhesion, motility or spreading of a CD9-
CC expressing cell on fibronectin; inhibiting proliferation or survival of
CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
CC modifying invasiveness of a cell through a collagen and/or laminin matrix
CC ; and modifying cell-to-cell interaction. The methods are based on the
CC finding that increased CD9 expression is implicated in (i) decreased
CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1
CC integrin) and/or decreased cell invasiveness and/or decreased
CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
CC motility, spreading, proliferation, cell survival against apoptosis,
CC and/or cell-to-cell contacts. Conditions or disease states involving
CC proliferation or survival of CD9-expressing cells can be treated, e.g.
CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
CC arteriopathy, bleeding disorders, angiogenesis, and primary and
CC metastatic cancers including breast cancer, prostate cancer, colon
CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
XX Sequence 25 AA;

Query Match 31.2%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 PKDVLFTFTVKSCFDAIKEVFDNK 80
Db 1 PKDVLFTFTVKSCFDAIKEVFDNK 25
```

```
RESULT 7
ADJ57564
ID ADJ57564 standard; peptide; 22 AA.
XX
XX AC ADJ57564;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human CD9 fibronectin-binding domain peptide fragment.
XX
XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
XX KW haemostatic; antiangiogenic; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN WO2004007685-A2.
XX
XX PD 22-JAN-2004.
XX
XX PF 14-JUL-2003; 2003WO-US022050.
XX
XX PR 12-JUL-2002; 2002US-0395864P.
XX
XX PA (UYTE-) UNIV TENNESSEE RES FOUND.
XX
XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
XX PI Crossno JT, Lu Y;
XX
XX DR WPI; 2004-122924/12.
XX
XX PT Interfering with CD9 binding to fibronectin by binding a fibronectin-
XX PT binding domain of the CD9 protein or polypeptide, useful in treating
XX PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
XX PT and cancers.
XX
XX PS Example 1; SEQ ID NO 7; 126pp; English.
XX
XX CC The present sequence is that of a peptide fragment from the extracellular
XX CC domain (amino acids 125-146) of human CD9 ADJ57558. The peptide was used
XX CC in an example from the invention to investigate the interaction between
XX CC CD9 and fibronectin. Peptide fragments ADJ57560-ADJ57563 of human CD9 are
XX CC used in claimed methods for: interfering with CD9 binding to fibronectin;
XX CC modifying adhesion, motility or spreading of a CD9-expressing cell on
XX CC fibronectin; inhibiting proliferation or survival of CD9-expressing cells
XX CC ; modifying pericellular fibronectin matrix assembly; modifying
XX CC invasiveness of a cell through a collagen and/or laminin matrix; and
XX CC modifying cell-to-cell interaction. The methods are based on the finding
XX CC that increased CD9 expression is implicated in (i) decreased adhesiveness
XX CC of cells to extracellular matrix (via alpha5-beta1 integrin) and/or
XX CC decreased cell invasiveness and/or decreased pericellular fibronectin
XX CC matrix assembly, and/or (ii) increased cell motility, spreading,
XX CC proliferation, cell survival against apoptosis, and/or cell-to-cell
XX CC contacts. Conditions or disease states involving proliferation or
XX CC survival of CD9-expressing cells can be treated, e.g. thrombosis,
XX CC atherosclerosis, vein graft failure, restenosis, transplant arteriopathy,
XX CC bleeding disorders, angiogenesis, and primary and metastatic cancers
XX CC including breast cancer, prostate cancer, colon cancer, melanoma, ovarian
XX CC cancer, neuroblastoma, glioma and glioblastoma.
XX
XX SQ Sequence 22 AA;
XX
XX Query Match 27.5%; Score 22; DB 8; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-15;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 YKDTYNKLTQDEPQRETLKAI 34
XX | | | | | | | | | | | | | | | |
XX Db 1 YKDTYNKLTQDEPQRETLKAI 22
XX
XX RESULT 8
ADJ57563
ID ADJ57563 standard; peptide; 18 AA.
```

```
ADJ57578
ID ADJ57578 standard; peptide; 24 AA.
XX
XX AC ADJ57578;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human CD9 extracellular domain 2 peptide fragment.
XX
XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
XX KW haemostatic; antiangiogenic; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN WO2004007685-A2.
XX
XX PD 22-JAN-2004.
XX
XX PF 14-JUL-2003; 2003WO-US022050.
XX
XX PR 12-JUL-2002; 2002US-0395864P.
XX
XX PA (UYTE-) UNIV TENNESSEE RES FOUND.
XX
XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
XX PI Crossno JT, Lu Y;
XX
XX DR WPI; 2004-122924/12.
XX
XX PT Interfering with CD9 binding to fibronectin by binding a fibronectin-
XX PT binding domain of the CD9 protein or polypeptide, useful in treating
XX PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
XX PT and cancers.
XX
XX PS Example 5; SEQ ID NO 21; 126pp; English.
XX
XX CC The present sequence is that of a peptide fragment from the second
XX CC extracellular domain (EC2) of human CD9 ADJ57558. The peptide was used in
XX CC an example from the invention which demonstrated that EC2 of CD9 contains
XX CC functional domains important in CHO cell adhesion and pericellular
XX CC fibronectin matrix assembly. Peptide fragments ADJ57560-ADJ57563 of human
XX CC CD9 are used in claimed methods for: interfering with CD9 binding to
XX CC fibronectin; modifying adhesion, motility or spreading of a CD9-
XX CC expressing cell on fibronectin; inhibiting proliferation or survival of
XX CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
XX CC modifying invasiveness of a cell through a collagen and/or laminin matrix
XX CC ; and modifying cell-to-cell interaction. The methods are based on the
XX CC finding that increased CD9 expression is implicated in (i) decreased
XX CC adhesiveness of cells to extracellular matrix (via alpha5-beta1
XX CC integrin) and/or decreased cell invasiveness and/or decreased cell
XX CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
XX CC motility, spreading, proliferation, cell survival against apoptosis,
XX CC and/or cell-to-cell contacts. Conditions or disease states involving
XX CC proliferation or survival of CD9-expressing cells can be treated, e.g.
XX CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
XX CC arteriopathy, bleeding disorders, angiogenesis, and primary and
XX CC metastatic cancers including breast cancer, prostate cancer, colon
XX CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
XX
XX SQ Sequence 24 AA;
XX
XX Query Match 27.5%; Score 22; DB 8; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-15;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HKDEVIKVQBFYKDTYNKLT 22
XX | | | | | | | | | | | | | | | |
XX Db 3 HKDEVIKVQBFYKDTYNKLT 24
XX
XX RESULT 9
ADJ57563
ID ADJ57563 standard; peptide; 18 AA.
```

XX AC ADJ57563;
XX DT 06-MAY-2004 (first entry)
XX DE Human CD9 fibronectin-binding domain peptide fragment.
XX KW Human; CD9; antithrombotic; antiarteriosclerotic; vasotropic;
KW KW haemostatic; antiangiogenic; cytostatic.
XX OS Homo sapiens.
XX PN WO2004007585-A2.
XX PD 22-JAN-2004.
XX PF 14-JUL-2003; 2003WO-US022050.
XX PR 12-JUL-2002; 2002US-0395864P.
XX PA (UYTE-) UNIV TENNESSEE RES FOUND.
XX PI Jennings LK, Longhurst CM, Cook GA, Bao J, Zhang C, White MM;
PI Crossno JT, Lu Y;
XX WPI; 2004-122924/12.
DR Interfering with CD9 binding to fibronectin by binding a fibronectin-
PT binding domain of the CD9 protein or polypeptide, useful in treating
PT thrombosis, atherosclerosis, restenosis, bleeding disorders, angiogenesis
PT and cancers.
XX Claim 7; SEQ ID NO 6; 126pp; English.
XX PS The present sequence is that of a peptide fragment from the fibronectin-
CC binding domain of human CD9 ADJ57558. The peptide, or an antibody that
CC binds to it, is used in claimed methods for: interfering with CD9 binding
CC to fibronectin; modifying adhesion, motility or spreading of a CD9-
CC expressing cell on fibronectin; inhibiting proliferation or survival of
CC CD9-expressing cells; modifying pericellular fibronectin matrix assembly;
CC modifying invasiveness of a cell through a collagen and/or laminin matrix
CC ; and modifying cell-to-cell interaction. The methods are based on the
CC finding that increased CD9 expression is implicated in (i) decreased
CC adhesiveness of cells to extracellular matrix (via alpha5-beta-1
CC integrin) and/or decreased cell invasiveness and/or decreased
CC pericellular fibronectin matrix assembly, and/or (ii) increased cell
CC motility, spreading, proliferation, cell survival against apoptosis,
CC and/or cell-to-cell contacts. Conditions or disease states involving
CC proliferation or survival of CD9-expressing cells can be treated, e.g.
CC thrombosis, atherosclerosis, vein graft failure, restenosis, transplant
CC arteriopathy, bleeding disorders, angiogenesis, and primary and
CC metastatic cancers including breast cancer, prostate cancer, colon
CC cancer, melanoma, ovarian cancer, neuroblastoma, glioma and glioblastoma.
XX SQ Sequence 18 AA;
Query Match 22.5%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 PKQVLEFTVKSCPDAI 73
Db 1 PKQVLEFTVKSCPDAI 18
RESULT 10
ABU03385
ID ABU03385 standard; protein; 10 AA.
XX AC ABU03385;
XX DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #165.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCO INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Claim 10; SEQ ID NO 165; 134pp; English.
XX PS The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 10 AA;
Query Match 12.5%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 58 KDVLETFVK 67
Db 1 KDVLETFVK 10
RESULT 11
ABP43064
ID ABP43064 standard; protein; 33 AA.
XX AC ABP43064;
XX DT 22-AUG-2002 (first entry)
XX

DE Human ovarian antigen HVCAC42, SEQ ID NO:4196.
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
XX
PD 03-JAN-2002.
XX
XX
PF 07-JUN-2001; 2001WO-US018569.
XX
XX
PR 07-JUN-2000; 2000US-0209467P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Birse CE, Rosen CA;
XX
XX
DR WPI: 2002-147878/19.
DR N-PSDB; ABQ56141.
XX
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX
XX
PS Claim 11; SEQ ID NO 4196; 2922pp; English.
XX
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 33 AA;

Query Match 10.0%; Score 8; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YKDTYNKL 20
Db ||||| 29
22 YKDTYNKL 29
RESULT 12
ABU51670
ID ABU51670 standard; protein; 58 AA.
XX
AC ABU51670;
XX
DT 07-MAY-2003 (first entry)
XX
DE Helicobacter pylori selected interacting domain (SID) protein #1014.
XX
KW Protein-protein interaction; ulcer; selected interacting domain; SID.
XX
OS Helicobacter pylori.
XX
PN WO200266501-A2.
XX
PD 29-AUG-2002.
XX
PF 28-DEC-2001; 2001WO-EP015428.
XX
PR 02-JAN-2001; 2001US-0259302P.
XX
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
XX
PI Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX
XX
DR WPI: 2002-674910/72.
DR N-PSDB; ABX66415.
XX
XX
PT New complexes of protein-protein interactions in Helicobacter pylori,
PT useful for identifying modulating compounds for treating or preventing
PT ulcers in mammals.
XX
PS Claim 6; Page 334; 642pp; English.
XX
CC The invention describes a complex of protein-protein interactions in
CC Helicobacter pylori selected from 421 complexes given in the
CC specification. The complex of protein-protein interactions are useful for
CC screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This is the
CC amino acid sequence of a selected interacting domain (SID), identified
CC via protein-protein interactions. Note: Where the patent number printed
CC at the top of the pages in the specification has obscured areas of
CC protein sequence, the indexer has replaced the residue with an X to
CC represent an illegible residue
XX
SQ Sequence 58 AA;
Query Match 8.8%; Score 7; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 IKEVFDN 79
Db ||||| 44
38 IKEVFDN 44
RESULT 13
ABR67406
ID ABR67406 standard; peptide; 9 AA.
XX
XX
AC ABR67406;
XX
DT 07-AUG-2003 (first entry)
XX
DE Human protein disulfide isomerase peptide residues 539-547.

XX human; human leukocyte antigen-E; HLA-E; CD94/NGK2 cell receptor;
KW cycostatic; antirheumatic; antiarthritic; antitumor; antineoplastic;
KW neuroprotective; antidiabetic; dermatological; immunosuppressive;
KW thymic; antianaemic; antiatherosclerotic; hypotensive; virucide;
tumour.
XX Homo sapiens.
OS WO2003011895-A2.
XX PN 13-FEB-2003.
XX PD 31-JUL-2002; 2002WO-US024311.
XX PF 31-JUL-2001; 2001US-0308598P.
XX PR (SOED/) SOEDERSTROEM K P.
XX PA Soederstroem KP;
PI WPI; 2003-256432/25.
XX DR Novel human leukocyte antigen-E binding peptide, useful in medicine for
XX modulating the effect of CD94/NGK2 cell receptors and in tumor treatment.
PT Disclosure; Page 26; 140pp; English.
XX PS The invention relates to a novel human leukocyte antigen (HLA)-E binding
XX peptide that modulates the effect of CD94/NGK2 cell receptors. A peptide
CC of the invention has cytostatic, antirheumatic, antiarthritic, antitumor,
CC antineoplastic, neuroprotective, antidiabetic, dermatological,
CC immunosuppressive, thymic, antianaemic, antiatherosclerotic,
CC hypotensive, and virucide activity. A peptide of the invention is useful
CC in medicine and for modulating the effect of CD94/NGK2 cell receptors.
CC The peptide is also useful in tumor treatment. The peptides shown in
CC ABR67357-ABR67464, and also in ABR67466-ABR67467 represent peptides of
CC the invention
XX
XX Sequence 9 AA;
SQ
Query Match 7.5%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 PKKQVL 61
Db 4 PKKQVL 9
RESULT 14
AAW31082
ID AAW31082 standard; peptide; 16 AA.
XX AC AAW31082;
XX DT 09-JAN-1998 (first entry)
XX DE Mugwort pollen allergen T cell epitope.
XX KW Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW conserved.
XX Artemisia vulgaris.
OS WO9705258-A2.
XX PN 13-FEB-1997.
XX PD 02-AUG-1996; 96WO-AT000141.
XX PF
XX

PR 02-AUG-1995; 95AT-00001320.
XX (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX Ferreira F, Richter K, Engel E, Ebner C, Jilek A, Rheinberger H;
PI Kraft D, Breitenbach M;
XX WPI; 1997-145695/13.
XX DR New recombinant DNA encoding plant phosphoglycerate mutase or its
XX antigenic epitope(s) - useful for diagnosis or treatment of allergies to
PT pollen and plant-derived foods.
PT Disclosure; Fig 12a; 160pp; German.
XX PS AAW31041-W31050 are T cell epitopes of mugwort pollen co-factor-
XX independent phosphoglycerate mutase (PGM-i) isoform Art6. PGM-i is a
CC highly conserved plant allergen (panallergen) which can cause cross-
CC reactivity in patients allergic to pollen and plant-derived foods. PGM-i
CC and it's B cell and T cell epitopes can be used for the in vitro
CC detection of allergy against PGM-i, by measuring serum IgE or a cellular
CC reaction. They can also be used in immunotherapy and will not cause an
CC autoimmune response because PGM-i is significantly different from the
CC human enzyme, which is co-factor dependent
XX Sequence 16 AA;
SQ
Query Match 7.5%; Score 6; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 DAIKEV 76
Db 9 DAIKEV 14
RESULT 15
ADV67376
ID ADV67376 standard; peptide; 18 AA.
XX AC ADV67376;
XX DT 10-MAR-2005 (first entry)
XX DE Amino acid sequence of antimicrobial peptide Gen2 variant #9.
XX KW antimicrobial; microbial infection; bacterial infection;
KW fungal infection; lung disease; sexually transmitted disease;
KW food additive; cosmetics; preservation; cleaning; disinfection; paint;
KW water line; water; Gen2.
XX OS Synthetic.
XX OS WO2004108757-A2.
XX PN 16-DEC-2004.
XX PD 10-JUN-2004; 2004WO-DK000399.
XX PF 11-JUN-2003; 2003DK-00000865.
XX PR 20-JUN-2003; 2003DK-00000924.
XX KW (NOVO) NOVOZYMES AS.
XX PA (UETR-) UNIV TRIESTE.
XX PI Segura DR, Mygind PH, Hoegenhaug HK, Tossi A;
XX WPI; 2005-031659/03.
XX Novel antimicrobial polypeptide, useful for killing or inhibiting growth
PT of microbial cells and as medicament, antimicrobial veterinarian or human
PT therapeutic or prophylactic agent.
XX

PS Claim 3; SEQ ID NO 11; 62pp; English.

XX
CC ADV67367-ADV67411 represent synthetic antimicrobial peptides, based on a
CC formula given in the specification. Antimicrobial peptides of the
CC invention are useful for killing, or inhibiting the growth of, microbial
CC cells. They are useful as a medicament, antimicrobial veterinarian or
CC human therapeutic or prophylactic agent, and for preparing veterinarian
CC or human therapeutic agents for treating microbial infections, such as
CC bacterial or fungal infections, preferably gram positive bacterial
CC infections (the infections may be associated with lung diseases and
CC sexually transmitted diseases). Antimicrobial peptides of the invention
CC are for preserving foods, beverages and cosmetics. They are also useful
CC for cleaning surfaces and cooking utensils in food processing plants and
CC in any area in which food is prepared or served such as hospitals,
CC nursing homes, restaurants, especially fast food restaurants etc. . The
CC antimicrobial peptides are useful as a preservation agent or disinfection
CC agent in water based paints, and for microbial control of water lines,
CC for disinfection of water.

XX
SQ Sequence 18 AA;

Query Match 7.5%; Score 6; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. NO. 1.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NKLKTK 23

Db |||||

4 NKLKTK 9

Search completed: January 20, 2006, 17:49:37

Job time : 108 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:47:48 ; Search time 23 Seconds
(without alignments)
287.568 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192
Perfect score: 80
Sequence: 1 HKDEVIKEVQEPFYKDYNNKL.....LEFTVKSCPDAIKVFNDK 80

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0
Total number of hits satisfying chosen parameters: 345832

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/1/aaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/aaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/aaa/H COMB.pep.*
4: /cgn2_6/prodata/1/aaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/aaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	58.8	79	2	US-08-630-172-8
2	47	58.8	79	2	US-09-375-419-8
3	30	37.5	30	1	US-08-254-493-4
4	30	37.5	30	1	US-08-408-222B-4
5	29	36.2	29	1	US-08-254-493-5
6	29	36.2	29	1	US-08-254-493-6
7	29	36.2	29	1	US-08-408-222B-5
8	29	36.2	29	1	US-08-408-222B-6
9	6	7.5	62	2	US-09-621-976-5649
10	6	7.5	75	2	US-09-489-039A-12814
11	6	7.5	76	2	US-09-107-532A-4420
12	5	6.2	6	2	US-09-136-251-9
13	5	6.2	6	2	US-09-634-496-9
14	5	6.2	6	2	US-09-635-145A-9
15	5	6.2	8	2	US-09-200-757-1
16	5	6.2	8	2	US-09-200-757-2
17	5	6.2	8	2	US-09-200-757-3
18	5	6.2	10	2	US-09-200-757-4
19	5	6.2	10	2	US-09-526-163B-18
20	5	6.2	10	2	US-10-394-980-398
21	5	6.2	10	2	US-10-394-980-452
22	5	6.2	11	6	5204097-5
23	5	6.2	13	1	US-08-305-871A-28
24	5	6.2	14	6	5204097-4
25	5	6.2	15	2	US-09-490-702B-15
26	5	6.2	15	2	US-09-767-460-15
27	5	6.2	16	2	US-08-602-999A-384
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 5, Appli
					Sequence 12814, A
					Sequence 4420, Ap
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 4, Appli
					Sequence 18, Appl
					Sequence 398, App
					Sequence 452, App
					Patent No. 5204097
					Sequence 28, Appl
					Patent No. 5204097
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 384, App

28	5	6.2	16	2	US-09-500-124-384	Sequence 384, App
29	5	6.2	17	2	US-09-479-479-23	Sequence 23, Appl
30	5	6.2	17	2	US-09-297-851-23	Sequence 23, Appl
31	5	6.2	19	2	US-09-441-502B-90	Sequence 90, Appl
32	5	6.2	19	2	US-09-441-502B-91	Sequence 91, Appl
33	5	6.2	20	1	US-08-399-696-87	Sequence 87, Appl
34	5	6.2	20	2	US-08-825-852-63	Sequence 63, Appl
35	5	6.2	20	2	US-08-825-852-64	Sequence 64, Appl
36	5	6.2	20	2	US-09-052-888-64	Sequence 64, Appl
37	5	6.2	20	2	US-09-052-888-65	Sequence 65, Appl
38	5	6.2	20	2	US-09-723-890-64	Sequence 64, Appl
39	5	6.2	20	2	US-09-723-890-65	Sequence 65, Appl
40	5	6.2	20	2	US-09-723-901-64	Sequence 64, Appl
41	5	6.2	20	2	US-09-723-901-65	Sequence 65, Appl
42	5	6.2	20	2	US-09-723-547-64	Sequence 64, Appl
43	5	6.2	20	2	US-09-723-547-65	Sequence 65, Appl
44	5	6.2	20	2	US-09-724-127-64	Sequence 64, Appl
45	5	6.2	20	2	US-09-724-127-65	Sequence 65, Appl
46	5	6.2	20	2	US-09-723-931-64	Sequence 64, Appl
47	5	6.2	20	2	US-09-723-931-65	Sequence 65, Appl
48	5	6.2	20	2	US-09-723-873-64	Sequence 64, Appl
49	5	6.2	20	2	US-09-723-873-65	Sequence 65, Appl
50	5	6.2	20	2	US-09-724-114-64	Sequence 64, Appl
51	5	6.2	20	2	US-09-724-114-65	Sequence 65, Appl
52	5	6.2	20	2	US-09-723-913-64	Sequence 64, Appl
53	5	6.2	20	2	US-09-723-913-65	Sequence 65, Appl
54	5	6.2	20	2	US-09-723-912-64	Sequence 64, Appl
55	5	6.2	20	2	US-09-723-912-65	Sequence 65, Appl
56	5	6.2	20	2	US-09-724-095-64	Sequence 64, Appl
57	5	6.2	20	2	US-09-724-095-65	Sequence 65, Appl
58	5	6.2	20	2	US-09-724-157-64	Sequence 64, Appl
59	5	6.2	20	2	US-09-724-157-65	Sequence 65, Appl
60	5	6.2	20	2	US-09-724-062-64	Sequence 64, Appl
61	5	6.2	20	2	US-09-724-062-65	Sequence 65, Appl
62	5	6.2	20	2	US-09-724-065-64	Sequence 64, Appl
63	5	6.2	20	2	US-09-724-065-65	Sequence 65, Appl
64	5	6.2	20	2	US-09-724-481-64	Sequence 64, Appl
65	5	6.2	20	2	US-09-724-481-65	Sequence 65, Appl
66	5	6.2	20	6	5204097-3	Patent No. 5204097
67	5	6.2	22	2	US-10-038-612-79	Sequence 79, Appl
68	5	6.2	22	2	US-10-038-612-80	Sequence 80, Appl
69	5	6.2	23	2	US-09-479-479-29	Sequence 29, Appl
70	5	6.2	23	2	US-09-297-851-29	Sequence 29, Appl
71	5	6.2	25	2	US-09-200-757-5	Sequence 5, Appli
72	5	6.2	26	4	PCT-US95-13841-1	Sequence 1, Appli
73	5	6.2	28	2	US-09-058-459-2	Sequence 2, Appli
74	5	6.2	28	2	US-09-127-926-2	Sequence 2, Appli
75	5	6.2	28	2	US-09-714-357-2	Sequence 2, Appli
76	5	6.2	28	2	US-10-057-552-2	Sequence 2, Appli
77	5	6.2	28	2	US-09-827-960-2	Sequence 2, Appli
78	5	6.2	28	2	US-09-837-886-2	Sequence 2, Appli
79	5	6.2	28	2	US-09-812-034-2	Sequence 2, Appli
80	5	6.2	30	1	US-08-287-959-14	Sequence 14, Appl
81	5	6.2	31	2	US-09-227-357-398	Sequence 398, App
82	5	6.2	31	2	US-09-973-278-508	Sequence 508, App
83	5	6.2	39	2	US-09-270-767-58213	Sequence 58213, A
84	5	6.2	42	4	PCT-US95-13841-25	Sequence 25, Appl
85	5	6.2	42	4	PCT-US95-13841-29	Sequence 29, Appl
86	5	6.2	43	2	US-09-057-363C-59	Sequence 59, Appl
87	5	6.2	43	2	US-09-265-107-59	Sequence 59, Appl
88	5	6.2	43	2	US-09-270-767-62022	Sequence 62022, A
89	5	6.2	43	4	PCT-US95-13841-26	Sequence 26, Appl
90	5	6.2	43	4	PCT-US95-13841-30	Sequence 30, Appl
91	5	6.2	46	1	US-08-639-857-30	Sequence 30, Appl
92	5	6.2	46	2	US-09-270-767-56973	Sequence 56973, A
93	5	6.2	47	2	US-08-936-165A-345	Sequence 345, App
94	5	6.2	47	2	US-09-904-615-88	Sequence 88, Appl
95	5	6.2	47	2	US-10-002-344A-178	Sequence 178, App
96	5	6.2	47	2	US-10-054-988-88	Sequence 88, Appl
97	5	6.2	49	2	US-08-398-633-18	Sequence 18, Appl
98	5	6.2	49	2	US-08-480-070C-24	Sequence 24, Appl
99	5	6.2	49	2	US-08-829-525-38	Sequence 38, Appl
100	5	6.2	49	2	US-09-310-367-38	Sequence 38, Appl

101	5	6.2	51	6	5274075-11	Patent No. 5274075	174	5	6.2	80	2	US-09-149-476-578	Sequence 578, App
102	5	6.2	52	2	US-09-128-155-8	Sequence 8, Appli	175	5	6.2	80	2	US-09-252-991A-24876	Sequence 24876, A
103	5	6.2	53	2	US-08-836-500A-8	Sequence 8, Appli	176	5	6.2	80	2	US-09-270-767-44007	Sequence 44007, A
104	5	6.2	54	2	US-09-679-750-8	Sequence 8, Appli	177	5	6.2	80	2	US-09-270-767-59415	Sequence 59415, A
105	5	6.2	55	2	US-09-270-767-36652	Sequence 36652, A	178	5	6.2	80	2	US-09-809-665A-129	Sequence 129, App
106	5	6.2	56	2	US-09-270-767-51869	Sequence 51869, A	179	4	5.0	4	1	US-08-456-424-138	Sequence 138, App
107	5	6.2	57	2	US-09-513-999C-6743	Sequence 6743, Ap	180	4	5.0	4	2	US-09-258-754-430	Sequence 430, App
108	5	6.2	58	1	US-08-290-448A-57	Sequence 57, Appl	181	4	5.0	4	2	US-09-042-107-430	Sequence 430, App
109	5	6.2	59	1	US-08-290-448A-51	Sequence 61, Appl	182	4	5.0	4	2	US-09-722-250D-430	Sequence 430, App
110	5	6.2	60	1	US-08-290-448A-57	Sequence 57, Appl	183	4	5.0	4	2	US-09-676-475A-430	Sequence 430, App
111	5	6.2	61	1	US-08-290-448A-61	Sequence 61, Appl	184	4	5.0	4	2	US-09-698-781-10	Sequence 10, Appl
112	5	6.2	62	1	US-08-175-069A-57	Sequence 57, Appl	185	4	5.0	4	2	US-10-607-595-430	Sequence 430, App
113	5	6.2	63	1	US-08-175-069A-61	Sequence 61, Appl	186	4	5.0	4	1	US-07-778-156-11	Sequence 11, Appl
114	5	6.2	64	2	US-08-446-137B-12	Sequence 12, Appl	187	4	5.0	5	1	US-08-335-138-41	Sequence 41, Appl
115	5	6.2	65	2	US-08-461-939B-57	Sequence 57, Appl	188	4	5.0	5	1	US-08-422-166-11	Sequence 11, Appl
116	5	6.2	66	2	US-08-461-939B-61	Sequence 61, Appl	189	4	5.0	5	2	US-09-012-669F-52	Sequence 52, Appl
117	5	6.2	67	2	US-08-464-000-57	Sequence 57, Appl	190	4	5.0	5	2	US-09-133-521-10	Sequence 10, Appl
118	5	6.2	68	2	US-08-464-000-61	Sequence 61, Appl	191	4	5.0	5	2	US-09-621-377B-30	Sequence 30, Appl
119	5	6.2	69	2	US-09-248-796A-21602	Sequence 21602, A	192	4	5.0	5	2	US-10-031-893-30	Sequence 30, Appl
120	5	6.2	70	2	US-09-580-201A-16	Sequence 16, Appl	193	4	5.0	5	2	US-09-788-006-106	Sequence 106, App
121	5	6.2	71	2	US-09-902-540-10101	Sequence 10101, A	194	4	5.0	5	2	US-09-788-006-107	Sequence 107, App
122	5	6.2	72	2	US-09-128-155-4	Sequence 4, Appli	195	4	5.0	5	2	US-10-353-174-30	Sequence 30, Appl
123	5	6.2	73	2	US-09-497-491-47	Sequence 47, Appl	196	4	5.0	5	2	US-10-394-980-307	Sequence 307, App
124	5	6.2	74	2	US-09-248-796A-21203	Sequence 21203, A	197	4	5.0	6	1	US-08-180-209B-52	Sequence 52, Appl
125	5	6.2	75	2	US-09-248-796A-22702	Sequence 22702, A	198	4	5.0	6	1	US-08-260-199A-3	Sequence 3, Appli
126	5	6.2	76	2	US-09-248-796A-25412	Sequence 25412, A	199	4	5.0	6	1	US-08-260-199A-8	Sequence 8, Appli
127	5	6.2	77	2	US-09-898-659-38	Sequence 38, Appl	200	4	5.0	6	1	US-08-260-199A-13	Sequence 13, Appl
128	5	6.2	78	2	US-09-248-796A-24891	Sequence 24891, A	201	4	5.0	6	1	US-08-260-199A-24	Sequence 24, Appl
129	5	6.2	79	2	US-09-981-012A-11	Sequence 11, Appl	202	4	5.0	6	1	US-08-260-199A-25	Sequence 25, Appl
130	5	6.2	80	2	US-09-247-155-108	Sequence 108, App	203	4	5.0	6	1	US-08-594-447-69	Sequence 69, Appl
131	5	6.2	81	2	US-09-337-501-10	Sequence 10, Appl	204	4	5.0	6	1	US-08-541-964-68	Sequence 68, Appl
132	5	6.2	82	2	US-09-621-976-4513	Sequence 4513, Ap	205	4	5.0	6	1	US-08-528-523-4	Sequence 4, Appli
133	5	6.2	83	2	US-09-479-040-29	Sequence 29, Appl	206	4	5.0	6	1	US-08-665-647-83	Sequence 83, Appl
134	5	6.2	84	2	US-09-903-190-108	Sequence 108, App	207	4	5.0	6	2	US-08-474-853-52	Sequence 52, Appl
135	5	6.2	85	2	US-08-437-607A-44	Sequence 44, Appl	208	4	5.0	6	2	US-09-166-205B-52	Sequence 52, Appl
136	5	6.2	86	2	US-08-446-137B-10	Sequence 10, Appl	209	4	5.0	6	2	US-08-877-605-166	Sequence 166, App
137	5	6.2	87	2	US-09-540-236-2981	Sequence 2981, Ap	210	4	5.0	6	2	US-08-877-605-173	Sequence 173, App
138	5	6.2	88	2	US-09-621-976-3994	Sequence 3994, Ap	211	4	5.0	6	2	US-08-877-605-190	Sequence 190, App
139	5	6.2	89	2	US-09-465-559-22	Sequence 22, Appl	212	4	5.0	6	2	US-08-877-605-257	Sequence 257, App
140	5	6.2	90	2	US-09-248-796A-22622	Sequence 22622, A	213	4	5.0	6	2	US-09-535-852-917	Sequence 917, App
141	5	6.2	91	2	US-08-180-761B-3	Sequence 3, Appli	214	4	5.0	6	2	US-09-881-572A-6	Sequence 6, Appli
142	5	6.2	92	2	US-09-248-796A-26169	Sequence 26169, A	215	4	5.0	6	2	US-09-586-937-28	Sequence 28, Appl
143	5	6.2	93	1	US-08-292-968-21	Sequence 21, Appl	216	4	5.0	6	4	US-09-586-937-31	Sequence 31, Appl
144	5	6.2	94	1	US-08-467-974-21	Sequence 21, Appl	217	4	5.0	6	4	PCT-US94-02629-52	Sequence 52, Appl
145	5	6.2	95	1	US-08-467-536-21	Sequence 21, Appl	218	4	5.0	7	1	US-08-281-133-8	Sequence 8, Appli
146	5	6.2	96	2	US-08-467-976-21	Sequence 21, Appl	219	4	5.0	7	1	US-08-084-739-4	Sequence 4, Appli
147	5	6.2	97	2	US-09-082-514-21	Sequence 21, Appl	220	4	5.0	7	1	US-07-638-492-11	Sequence 11, Appl
148	5	6.2	98	2	US-09-270-767-41728	Sequence 41728, A	221	4	5.0	7	1	US-08-422-106-8	Sequence 8, Appli
149	5	6.2	99	2	US-09-328-352-5946	Sequence 5946, Ap	222	4	5.0	7	1	US-08-260-199A-2	Sequence 2, Appli
150	5	6.2	100	2	US-09-543-681A-4584	Sequence 4584, Ap	223	4	5.0	7	1	US-08-735-716-8	Sequence 8, Appli
151	5	6.2	101	6	5204097-1	Patent No. 5204097	224	4	5.0	7	1	US-08-555-568B-8	Sequence 8, Appli
152	5	6.2	102	2	US-09-621-976-4752	Sequence 4752, Ap	225	4	5.0	7	2	US-08-916-443A-8	Sequence 8, Appli
153	5	6.2	103	2	US-08-836-500A-6	Sequence 6, Appli	226	4	5.0	7	2	US-09-258-754-389	Sequence 389, App
154	5	6.2	104	2	US-09-679-750-6	Sequence 6, Appli	227	4	5.0	7	2	US-09-258-754-404	Sequence 404, App
155	5	6.2	105	2	US-09-366-887A-24	Sequence 24, Appl	228	4	5.0	7	2	US-09-042-107-389	Sequence 389, App
156	5	6.2	106	2	US-09-248-796A-24220	Sequence 24220, A	229	4	5.0	7	2	US-09-042-107-404	Sequence 404, App
157	5	6.2	107	2	US-09-517-204-24	Sequence 24, Appl	230	4	5.0	7	2	US-09-519-223-8	Sequence 8, Appli
158	5	6.2	108	2	US-09-134-000C-5163	Sequence 5163, Ap	231	4	5.0	7	2	US-09-187-859-1700	Sequence 1700, Ap
159	5	6.2	109	2	US-09-540-236-3737	Sequence 3737, Ap	232	4	5.0	7	2	US-08-897-843A-8	Sequence 8, Appli
160	5	6.2	110	2	US-09-248-796A-25808	Sequence 25808, A	233	4	5.0	7	2	US-09-839-542B-1700	Sequence 1700, Ap
161	5	6.2	111	2	US-09-513-999C-5127	Sequence 5127, Ap	234	4	5.0	7	2	US-08-753-750B-16	Sequence 16, Appl
162	5	6.2	112	2	US-09-180-827-3	Sequence 3, Appli	235	4	5.0	7	2	US-09-722-250D-389	Sequence 389, App
163	5	6.2	113	2	US-09-252-991A-32156	Sequence 32156, A	236	4	5.0	7	2	US-09-722-250D-404	Sequence 404, App
164	5	6.2	114	2	US-09-583-110-3419	Sequence 3419, Ap	237	4	5.0	7	2	US-09-535-852-924	Sequence 924, App
165	5	6.2	115	2	US-09-248-796A-24296	Sequence 24296, A	238	4	5.0	7	2	US-09-927-180-8	Sequence 8, Appli
166	5	6.2	116	2	US-08-858-207A-285	Sequence 285, App	239	4	5.0	7	2	US-09-676-475A-389	Sequence 389, App
167	5	6.2	117	2	US-09-134-001C-3386	Sequence 3386, Ap	240	4	5.0	7	2	US-09-676-475A-404	Sequence 404, App
168	5	6.2	118	2	US-09-248-796A-23767	Sequence 23767, A	241	4	5.0	7	2	US-09-620-840C-7	Sequence 7, Appli
169	5	6.2	119	2	US-09-248-796A-23996	Sequence 23996, A	242	4	5.0	7	2	US-09-884-767A-24	Sequence 24, Appl
170	5	6.2	120	2	US-09-248-796A-27345	Sequence 27345, A	243	4	5.0	7	2	US-10-394-980-316	Sequence 316, App
171	5	6.2	121	2	US-09-621-976-4746	Sequence 4746, Ap	244	4	5.0	7	2	US-10-394-980-381	Sequence 381, App
172	5	6.2	122	2	US-09-270-767-44291	Sequence 44291, A	245	4	5.0	7	2	US-10-394-980-431	Sequence 431, App
173	5	6.2	123	2	US-09-248-796A-24174	Sequence 24174, A	246	4	5.0	7	2	US-10-607-595-389	Sequence 389, App

247	4	5.0	7	2	US-10-607-595-404	Sequence 404, App	320	4	5.0	10	2	US-08-475-955-69	Sequence 69, Appl
248	4	5.0	7	2	US-10-006-869-1700	Sequence 1700, Ap	321	4	5.0	10	2	US-09-504-262D-15	Sequence 15, Appl
249	4	5.0	7	4	PCT-US95-08069-8	Sequence 8, Appli	322	4	5.0	10	2	US-09-620-091-17	Sequence 17, Appl
250	4	5.0	7	6	5169835-27	Patent No. 5169835	323	4	5.0	10	2	US-09-211-715-202	Sequence 202, App
251	4	5.0	8	1	US-08-213-897A-2	Sequence 2, Appli	324	4	5.0	10	2	US-09-935-430-94	Sequence 94, Appl
252	4	5.0	8	1	US-08-032-846-36	Sequence 36, Appl	325	4	5.0	10	2	US-09-935-430-632	Sequence 632, App
253	4	5.0	8	1	US-08-024-253-13	Sequence 13, Appl	326	4	5.0	10	2	US-09-767-460-45	Sequence 45, Appl
254	4	5.0	8	1	US-08-059-568-42	Sequence 42, Appl	327	4	5.0	10	2	US-10-102-283-189	Sequence 189, App
255	4	5.0	8	1	US-08-399-411-42	Sequence 42, Appl	328	4	5.0	10	2	US-07-867-819D-18	Sequence 18, Appl
256	4	5.0	8	2	US-08-516-859A-42	Sequence 42, Appl	329	4	5.0	10	2	US-07-867-819D-69	Sequence 69, Appl
257	4	5.0	8	2	US-08-160-604-61	Sequence 61, Appl	330	4	5.0	11	1	US-08-424-957-40	Sequence 40, Appl
258	4	5.0	8	2	US-08-584-008A-6	Sequence 6, Appli	331	4	5.0	11	1	US-08-746-283-21	Sequence 21, Appl
259	4	5.0	8	2	US-08-474-636-36	Sequence 36, Appl	332	4	5.0	11	1	US-08-916-443A-1	Sequence 1, Appli
260	4	5.0	8	2	US-09-586-472-42	Sequence 42, Appl	333	4	5.0	11	2	US-09-215-966-5	Sequence 5, Appli
261	4	5.0	8	2	US-09-227-377-420	Sequence 420, App	334	4	5.0	11	2	US-09-215-966-20	Sequence 20, Appl
262	4	5.0	8	2	US-09-187-859-1701	Sequence 1701, Ap	335	4	5.0	11	2	US-09-035-686-40	Sequence 40, Appl
263	4	5.0	8	2	US-09-528-706-42	Sequence 42, Appl	336	4	5.0	11	2	US-08-160-604-57	Sequence 57, Appl
264	4	5.0	8	2	US-09-839-542B-1701	Sequence 1701, Ap	337	4	5.0	11	2	US-09-133-521-20	Sequence 20, Appl
265	4	5.0	8	2	US-09-535-852-931	Sequence 931, App	338	4	5.0	11	2	US-09-268-347-14	Sequence 14, Appl
266	4	5.0	8	2	US-09-535-852-938	Sequence 938, App	339	4	5.0	11	2	US-09-576-824A-490	Sequence 490, App
267	4	5.0	8	2	US-09-535-852-1209	Sequence 1209, Ap	340	4	5.0	11	2	US-09-756-983-7	Sequence 7, Appli
268	4	5.0	8	2	US-08-475-955-156	Sequence 156, App	341	4	5.0	11	2	US-09-419-788-129	Sequence 129, App
269	4	5.0	8	2	US-08-475-955-166	Sequence 166, App	342	4	5.0	11	2	US-09-419-788-155	Sequence 155, App
270	4	5.0	8	2	US-09-865-548A-79	Sequence 79, Appl	343	4	5.0	11	2	US-09-555-115A-20	Sequence 20, Appl
271	4	5.0	8	2	US-09-973-278-647	Sequence 647, App	344	4	5.0	11	2	US-09-555-115A-21	Sequence 21, Appl
272	4	5.0	8	2	US-09-756-283A-30	Sequence 30, Appl	345	4	5.0	11	2	US-09-555-115A-22	Sequence 22, Appl
273	4	5.0	8	2	US-10-006-869-1701	Sequence 1701, Ap	346	4	5.0	11	6	5187155-25	Patent No. 5187155
274	4	5.0	9	1	US-08-215-805A-39	Sequence 39, Appl	347	4	5.0	12	1	US-08-212-433A-10	Sequence 10, Appl
275	4	5.0	9	1	US-08-032-846-11	Sequence 11, Appl	348	4	5.0	12	1	US-08-166-930-5	Sequence 5, Appli
276	4	5.0	9	1	US-08-292-968-18	Sequence 18, Appl	349	4	5.0	12	1	US-08-190-788A-158	Sequence 158, App
277	4	5.0	9	1	US-08-637-899-8	Sequence 8, Appli	350	4	5.0	12	1	US-08-383-474B-161	Sequence 161, App
278	4	5.0	9	1	US-08-467-974-18	Sequence 18, Appl	351	4	5.0	12	1	US-08-465-391A-158	Sequence 158, App
279	4	5.0	9	1	US-08-467-536-18	Sequence 18, Appl	352	4	5.0	12	1	US-08-406-330-34	Sequence 34, Appl
280	4	5.0	9	2	US-08-467-976-18	Sequence 18, Appl	353	4	5.0	12	1	US-08-464-538B-158	Sequence 158, App
281	4	5.0	9	2	US-09-082-514-18	Sequence 18, Appl	354	4	5.0	12	1	US-08-556-597-34	Sequence 34, Appl
282	4	5.0	9	2	US-08-474-636-11	Sequence 11, Appl	355	4	5.0	12	1	US-08-463-076B-210	Sequence 210, App
283	4	5.0	9	2	US-09-187-859-1702	Sequence 1702, Ap	356	4	5.0	12	1	US-08-874-678-7	Sequence 7, Appli
284	4	5.0	9	2	US-09-297-269-38	Sequence 26, Appl	357	4	5.0	12	1	US-08-993-581B-33	Sequence 33, Appl
285	4	5.0	9	2	US-09-297-269-38	Sequence 38, Appl	358	4	5.0	12	1	US-08-727-045A-5	Sequence 5, Appli
286	4	5.0	9	2	US-09-244-583-16	Sequence 16, Appl	359	4	5.0	12	2	US-08-716-256-10	Sequence 10, Appl
287	4	5.0	9	2	US-09-481-620A-117	Sequence 117, App	360	4	5.0	12	2	US-08-742-243-3	Sequence 3, Appli
288	4	5.0	9	2	US-09-341-982-73	Sequence 73, Appl	361	4	5.0	12	2	US-08-742-243-65	Sequence 65, Appl
289	4	5.0	9	2	US-09-839-542B-1702	Sequence 1702, Ap	362	4	5.0	12	2	US-08-742-243-66	Sequence 66, Appl
290	4	5.0	9	2	US-09-535-852-1216	Sequence 1216, Ap	363	4	5.0	12	2	US-08-742-243-67	Sequence 67, Appl
291	4	5.0	9	2	US-08-765-837-6	Sequence 6, Appli	364	4	5.0	12	2	US-08-643-839-7	Sequence 68, Appl
292	4	5.0	9	2	US-09-865-548A-56	Sequence 56, Appl	365	4	5.0	12	2	US-09-238-448-2	Sequence 2, Appli
293	4	5.0	9	2	US-09-865-548A-176	Sequence 176, App	366	4	5.0	12	2	US-09-133-521-22	Sequence 22, Appl
294	4	5.0	9	2	US-09-680-514-26	Sequence 26, Appl	367	4	5.0	12	2	US-09-308-175A-20	Sequence 20, Appl
295	4	5.0	9	2	US-09-065-903-17	Sequence 17, Appl	368	4	5.0	12	2	US-09-348-886-7	Sequence 7, Appli
296	4	5.0	9	2	US-10-006-869-1702	Sequence 1702, Ap	369	4	5.0	12	2	US-09-408-172-5	Sequence 12, Appl
297	4	5.0	10	1	US-08-424-682A-2	Sequence 2, Appli	370	4	5.0	12	2	US-09-999-689A-12	Sequence 12, Appl
298	4	5.0	10	1	US-08-214-650-36	Sequence 36, Appl	371	4	5.0	12	2	US-09-341-982-79	Sequence 79, Appl
299	4	5.0	10	1	US-08-468-543-21	Sequence 21, Appl	372	4	5.0	12	2	US-10-053-485-22	Sequence 22, Appl
300	4	5.0	10	1	US-08-469-692-21	Sequence 21, Appl	373	4	5.0	12	2	US-09-403-752A-111	Sequence 111, App
301	4	5.0	10	1	US-08-482-228-121	Sequence 121, App	374	4	5.0	12	2	US-09-748-578-1	Sequence 1, Appli
302	4	5.0	10	1	US-08-398-046-21	Sequence 21, Appl	375	4	5.0	12	2	US-09-385-219A-82	Sequence 82, Appl
303	4	5.0	10	2	US-09-139-762A-45	Sequence 45, Appl	376	4	5.0	12	2	US-09-551-151A-111	Sequence 111, App
304	4	5.0	10	2	US-09-139-762A-89	Sequence 89, Appl	377	4	5.0	12	2	US-08-167-608-5	Sequence 5, Appli
305	4	5.0	10	2	US-09-139-762A-105	Sequence 105, App	378	4	5.0	12	2	US-10-105-901A-7	Sequence 7, Appli
306	4	5.0	10	2	US-08-482-528-121	Sequence 121, App	379	4	5.0	12	2	US-09-381-903-57	Sequence 57, Appl
307	4	5.0	10	2	US-09-184-658-15	Sequence 15, Appl	380	4	5.0	12	2	US-09-381-903-58	Sequence 58, Appl
308	4	5.0	10	2	US-08-159-339A-487	Sequence 487, App	381	4	5.0	12	2	PCT-US94-02191-5	Sequence 5, Appli
309	4	5.0	10	2	US-08-159-339A-500	Sequence 500, App	382	4	5.0	12	2	PCT-US95-03239-10	Sequence 10, Appl
310	4	5.0	10	2	US-08-159-339A-627	Sequence 627, App	383	4	5.0	12	2	5252328-15	Patent No. 5252328
311	4	5.0	10	2	US-08-159-339A-834	Sequence 834, App	384	4	5.0	12	2		
312	4	5.0	10	2	US-08-159-339A-836	Sequence 836, App	385	4	5.0	12	2		
313	4	5.0	10	2	US-09-042-353-364	Sequence 364, App	386	4	5.0	12	2		
314	4	5.0	10	2	US-08-758-417A-212	Sequence 212, App	387	4	5.0	12	2		
315	4	5.0	10	2	US-09-311-784A-269	Sequence 269, App	388	4	5.0	12	2		
316	4	5.0	10	2	US-09-311-784A-288	Sequence 288, App	389	4	5.0	12	4		
317	4	5.0	10	2	US-09-490-702B-45	Sequence 45, Appl	390	4	5.0	12	4		
318	4	5.0	10	2	US-09-784-642-11	Sequence 11, Appl	391	4	5.0	12	4		
319	4	5.0	10	2	US-08-475-955-18	Sequence 18, Appl	392	4	5.0	12	6		

393	4	5.0	13	1	US-07-732-114A-4	Sequence 4, Appl	466	4	5.0	13	2	US-10-090-185-35	Sequence 35, Appl
394	4	5.0	13	1	US-08-336-087-5	Sequence 5, Appl	467	4	5.0	13	2	US-10-090-185-39	Sequence 39, Appl
395	4	5.0	13	1	US-08-186-266-10	Sequence 10, Appl	468	4	5.0	13	4	PCT-US95-04121-13	Sequence 13, Appl
396	4	5.0	13	1	US-08-479-400-5	Sequence 5, Appl	469	4	5.0	14	1	US-08-084-739-3	Sequence 3, Appl
397	4	5.0	13	1	US-08-305-871A-19	Sequence 19, Appl	470	4	5.0	14	1	US-07-961-837-7	Sequence 7, Appl
398	4	5.0	13	1	US-08-305-871A-20	Sequence 20, Appl	471	4	5.0	14	1	US-08-325-071-17	Sequence 17, Appl
399	4	5.0	13	1	US-08-305-871A-21	Sequence 21, Appl	472	4	5.0	14	1	US-08-232-453A-68	Sequence 68, Appl
400	4	5.0	13	1	US-08-305-871A-22	Sequence 22, Appl	473	4	5.0	14	1	US-08-463-620-6	Sequence 6, Appl
401	4	5.0	13	1	US-08-305-871A-23	Sequence 23, Appl	474	4	5.0	14	1	US-08-463-620-7	Sequence 7, Appl
402	4	5.0	13	1	US-08-305-871A-24	Sequence 24, Appl	475	4	5.0	14	1	US-08-480-190-189	Sequence 189, App
403	4	5.0	13	1	US-08-305-871A-25	Sequence 25, Appl	476	4	5.0	14	1	US-08-764-640-95	Sequence 95, Appl
404	4	5.0	13	1	US-08-305-871A-26	Sequence 26, Appl	477	4	5.0	14	1	US-08-764-640-96	Sequence 96, Appl
405	4	5.0	13	1	US-08-305-871A-27	Sequence 27, Appl	478	4	5.0	14	1	US-08-488-379-189	Sequence 189, App
406	4	5.0	13	1	US-08-305-871A-29	Sequence 29, Appl	479	4	5.0	14	1	US-08-480-793-1	Sequence 1, Appl
407	4	5.0	13	1	US-08-170-114A-4	Sequence 4, Appl	480	4	5.0	14	1	US-08-224-917-6	Sequence 6, Appl
408	4	5.0	13	1	US-08-188-583-33	Sequence 33, Appl	481	4	5.0	14	1	US-08-224-917-7	Sequence 7, Appl
409	4	5.0	13	1	US-08-397-286-3	Sequence 3, Appl	482	4	5.0	14	1	US-08-484-905-56	Sequence 56, Appl
410	4	5.0	13	1	US-08-395-204-5	Sequence 5, Appl	483	4	5.0	14	1	US-08-914-853-6	Sequence 6, Appl
411	4	5.0	13	2	US-09-076-646-3	Sequence 3, Appl	484	4	5.0	14	1	US-08-914-853-7	Sequence 7, Appl
412	4	5.0	13	2	US-08-913-805A-13	Sequence 13, Appl	485	4	5.0	14	2	US-08-481-985B-56	Sequence 56, Appl
413	4	5.0	13	2	US-08-526-136-23	Sequence 23, Appl	486	4	5.0	14	2	US-08-807-952B-9	Sequence 9, Appl
414	4	5.0	13	2	US-08-751-359-20	Sequence 20, Appl	487	4	5.0	14	2	US-08-807-952B-12	Sequence 12, Appl
415	4	5.0	13	2	US-09-442-629-13	Sequence 13, Appl	488	4	5.0	14	2	US-08-973-225-95	Sequence 95, Appl
416	4	5.0	13	2	US-08-907-146-20	Sequence 20, Appl	489	4	5.0	14	2	US-08-973-225-96	Sequence 96, Appl
417	4	5.0	13	2	US-09-387-418A-35	Sequence 35, Appl	490	4	5.0	14	2	US-08-973-225-218	Sequence 218, App
418	4	5.0	13	2	US-09-387-418A-39	Sequence 39, Appl	491	4	5.0	14	2	US-09-244-238A-95	Sequence 95, Appl
419	4	5.0	13	2	US-08-788-822A-23	Sequence 23, Appl	492	4	5.0	14	2	US-09-244-238A-96	Sequence 96, Appl
420	4	5.0	13	2	US-08-788-822A-24	Sequence 24, Appl	493	4	5.0	14	2	US-08-370-476-56	Sequence 56, Appl
421	4	5.0	13	2	US-08-788-822A-25	Sequence 25, Appl	494	4	5.0	14	2	US-09-385-442-31	Sequence 31, Appl
422	4	5.0	13	2	US-08-788-822A-26	Sequence 26, Appl	495	4	5.0	14	2	US-08-461-004A-17	Sequence 17, Appl
423	4	5.0	13	2	US-08-788-822A-27	Sequence 27, Appl	496	4	5.0	14	2	US-09-516-704-95	Sequence 95, Appl
424	4	5.0	13	2	US-08-469-260A-445	Sequence 445, App	497	4	5.0	14	2	US-09-516-704-96	Sequence 96, Appl
425	4	5.0	13	2	US-08-488-446-445	Sequence 445, App	498	4	5.0	14	2	US-09-025-596-100	Sequence 100, App
426	4	5.0	13	2	US-09-692-170C-29	Sequence 29, Appl	499	4	5.0	14	2	US-09-549-090-95	Sequence 95, Appl
427	4	5.0	13	2	US-08-467-344A-445	Sequence 445, App	500	4	5.0	14	2	US-09-549-090-96	Sequence 96, Appl
428	4	5.0	13	2	US-09-543-608A-26	Sequence 26, Appl	501	4	5.0	14	2	US-09-549-090-218	Sequence 218, App
429	4	5.0	13	2	US-09-543-608A-27	Sequence 27, Appl	502	4	5.0	14	2	US-09-675-922-12	Sequence 12, Appl
430	4	5.0	13	2	US-09-543-608A-28	Sequence 28, Appl	503	4	5.0	14	2	US-09-832-230A-95	Sequence 95, Appl
431	4	5.0	13	2	US-09-543-608A-29	Sequence 29, Appl	504	4	5.0	14	2	US-09-832-230A-96	Sequence 96, Appl
432	4	5.0	13	2	US-09-543-608A-30	Sequence 30, Appl	505	4	5.0	14	2	US-08-475-399A-189	Sequence 189, App
433	4	5.0	13	2	US-09-543-608A-31	Sequence 31, Appl	506	4	5.0	14	2	US-09-394-455-30	Sequence 30, Appl
434	4	5.0	13	2	US-09-543-608A-32	Sequence 32, Appl	507	4	5.0	14	2	US-09-202-077-14	Sequence 14, Appl
435	4	5.0	13	2	US-09-543-608A-33	Sequence 33, Appl	508	4	5.0	14	2	US-09-073-661-100	Sequence 100, App
436	4	5.0	13	2	US-09-543-608A-34	Sequence 34, Appl	509	4	5.0	14	2	US-09-428-082B-52	Sequence 52, Appl
437	4	5.0	13	2	US-09-543-608A-35	Sequence 35, Appl	510	4	5.0	14	2	US-10-100-785-100	Sequence 100, App
438	4	5.0	13	2	US-09-543-608A-36	Sequence 36, Appl	511	4	5.0	14	2	US-09-443-199C-1239	Sequence 1239, Ap
439	4	5.0	13	2	US-09-543-608A-37	Sequence 37, Appl	512	4	5.0	14	2	US-09-405-986A-21	Sequence 21, Appl
440	4	5.0	13	2	US-09-543-608A-41	Sequence 41, Appl	513	4	5.0	14	2	US-08-077-255A-189	Sequence 189, App
441	4	5.0	13	2	US-08-475-955-54	Sequence 54, Appl	514	4	5.0	14	2	US-09-848-664A-3	Sequence 3, Appl
442	4	5.0	13	2	US-09-060-450-8	Sequence 8, Appl	515	4	5.0	14	2	US-10-101-279-100	Sequence 100, App
443	4	5.0	13	2	US-09-405-986A-4	Sequence 4, Appl	516	4	5.0	14	2	US-09-388-316C-30	Sequence 30, Appl
444	4	5.0	13	2	US-09-405-986A-6	Sequence 6, Appl	517	4	5.0	14	2	US-09-709-201B-100	Sequence 100, App
445	4	5.0	13	2	US-09-239-043D-2575	Sequence 2575, App	518	4	5.0	14	2	US-09-623-548A-1410	Sequence 1410, Ap
446	4	5.0	13	2	US-08-424-550B-445	Sequence 445, App	519	4	5.0	14	2	US-10-100-759-100	Sequence 100, App
447	4	5.0	13	2	US-10-405-231A-29	Sequence 29, Appl	520	4	5.0	14	2	US-09-657-276-1410	Sequence 1410, Ap
448	4	5.0	13	2	US-10-238-607-29	Sequence 29, Appl	521	4	5.0	14	2	US-09-563-760A-12	Sequence 12, Appl
449	4	5.0	13	2	US-09-984-365-29	Sequence 29, Appl	522	4	5.0	14	2	US-09-586-937-56	Sequence 56, Appl
450	4	5.0	13	2	US-09-724-961-44	Sequence 44, Appl	523	4	5.0	14	2	US-09-798-338B-3	Sequence 3, Appl
451	4	5.0	13	2	US-09-556-818-65	Sequence 65, Appl	524	4	5.0	14	4	PCT-US92-05825A-1	Sequence 1, Appl
452	4	5.0	13	2	US-09-580-018-44	Sequence 44, Appl	525	4	5.0	14	4	PCT-US93-07545-189	Sequence 189, App
453	4	5.0	13	2	US-09-724-951-44	Sequence 44, Appl	526	4	5.0	14	4	PCT-US95-03934A-6	Sequence 6, Appl
454	4	5.0	13	2	US-10-697-055-29	Sequence 29, Appl	527	4	5.0	14	4	PCT-US95-03934A-7	Sequence 7, Appl
455	4	5.0	13	2	US-09-935-430-654	Sequence 654, App	528	4	5.0	14	4	PCT-US95-11127-20	Sequence 20, Appl
456	4	5.0	13	2	US-09-724-953-2	Sequence 2, Appl	529	4	5.0	14	6	5178861-2	Patent No. 5178861
457	4	5.0	13	2	US-09-724-567-2	Sequence 2, Appl	530	4	5.0	14	6	5178861-11	Patent No. 5178861
458	4	5.0	13	2	US-07-867-819D-54	Sequence 54, Appl	531	4	5.0	14	6	5405952-6	Patent No. 5405952
459	4	5.0	13	2	US-09-724-940-44	Sequence 44, Appl	532	4	5.0	14	6	5445818-2	Patent No. 5445818
460	4	5.0	13	2	US-09-979-952-2	Sequence 2, Appl	533	4	5.0	15	1	US-07-859-291C-27	Sequence 27, Appl
461	4	5.0	13	2	US-09-585-817-2	Sequence 2, Appl	534	4	5.0	15	1	US-07-768-286B-16	Sequence 16, Appl
462	4	5.0	13	2	US-10-153-469A-41	Sequence 41, Appl	535	4	5.0	15	1	US-07-768-286B-18	Sequence 18, Appl
463	4	5.0	13	2	US-10-153-469A-42	Sequence 42, Appl	536	4	5.0	15	1	US-08-127-351-26	Sequence 26, Appl
464	4	5.0	13	2	US-10-104-889-41	Sequence 41, Appl	537	4	5.0	15	1	US-08-030-077-9	Sequence 9, Appl
465	4	5.0	13	2	US-10-104-889-42	Sequence 42, Appl	538	4	5.0	15	1	US-08-245-853-2	Sequence 2, Appl

539	4	5.0	15	1	US-08-480-367B-26	Sequence 26, Appl	612	4	5.0	16	2	US-08-959-206A-23	Sequence 23, Appl
540	4	5.0	15	1	US-08-487-221A-26	Sequence 26, Appl	613	4	5.0	16	2	US-09-315-304B-1192	Sequence 1192, Ap
541	4	5.0	15	1	US-08-480-370-26	Sequence 26, Appl	614	4	5.0	16	2	US-09-598-784-5	Sequence 5, Appli
542	4	5.0	15	1	US-08-299-636-5	Sequence 5, Appli	615	4	5.0	16	2	US-08-788-822A-10	Sequence 10, Appl
543	4	5.0	15	1	US-08-279-155-6	Sequence 5, Appli	616	4	5.0	16	2	US-08-413-233-3	Sequence 3, Appli
544	4	5.0	15	1	US-08-464-456-5	Sequence 5, Appli	617	4	5.0	16	2	US-09-834-784-1192	Sequence 1192, Ap
545	4	5.0	15	1	US-08-573-673-2	Sequence 2, Appli	618	4	5.0	16	2	US-09-515-965A-1192	Sequence 1192, Ap
546	4	5.0	15	1	US-08-703-988A-6	Sequence 6, Appli	619	4	5.0	16	2	US-09-532-709G-6	Sequence 6, Appli
547	4	5.0	15	1	US-08-463-052-5	Sequence 5, Appli	620	4	5.0	16	2	US-09-350-641C-1192	Sequence 1192, Ap
548	4	5.0	15	1	US-08-477-108A-11	Sequence 11, Appl	621	4	5.0	16	2	US-09-405-986A-22	Sequence 22, Appl
549	4	5.0	15	1	US-08-480-551-5	Sequence 5, Appli	622	4	5.0	16	2	US-09-405-986A-23	Sequence 23, Appl
550	4	5.0	15	1	US-08-195-874-2	Sequence 2, Appli	623	4	5.0	16	2	US-09-925-715-23	Sequence 23, Appl
551	4	5.0	15	1	US-08-616-844-51	Sequence 51, Appl	624	4	5.0	16	2	US-09-910-009A-27	Sequence 27, Appl
552	4	5.0	15	1	US-08-750-856A-8	Sequence 8, Appli	625	4	5.0	16	2	US-09-910-009A-388	Sequence 388, App
553	4	5.0	15	1	US-08-400-796-9	Sequence 9, Appli	626	4	5.0	16	2	US-09-709-103-62	Sequence 62, Appl
554	4	5.0	15	1	US-08-637-759B-239	Sequence 239, App	627	4	5.0	16	2	US-09-439-410A-62	Sequence 62, Appl
555	4	5.0	15	1	US-08-599-654-51	Sequence 51, Appl	628	4	5.0	16	2	US-09-350-841A-1192	Sequence 1192, Ap
556	4	5.0	15	1	US-08-612-842-6	Sequence 6, Appli	629	4	5.0	16	2	US-09-674-973A-35	Sequence 35, Appl
557	4	5.0	15	1	US-08-484-905-26	Sequence 26, Appl	630	4	5.0	16	2	US-09-541-345-67	Sequence 67, Appl
558	4	5.0	15	2	US-08-481-985B-26	Sequence 26, Appl	631	4	5.0	16	2	US-09-541-345-93	Sequence 93, Appl
559	4	5.0	15	2	US-08-871-355A-239	Sequence 239, App	632	4	5.0	16	2	US-09-908-322-32	Sequence 32, Appl
560	4	5.0	15	2	US-08-944-868A-51	Sequence 51, Appl	633	4	5.0	16	2	US-09-208-658-231	Sequence 231, App
561	4	5.0	15	2	US-08-944-423A-51	Sequence 51, Appl	634	4	5.0	16	2	US-10-226-877A-51	Sequence 51, Appl
562	4	5.0	15	2	US-08-946-026-45	Sequence 45, Appl	635	4	5.0	16	2	US-09-836-770A-4	Sequence 4, Appli
563	4	5.0	15	2	US-08-834-314-3	Sequence 3, Appli	636	4	5.0	16	2	US-09-825-517A-67	Sequence 67, Appl
564	4	5.0	15	2	US-08-944-496-51	Sequence 51, Appl	637	4	5.0	16	2	US-10-680-670-6	Sequence 6, Appli
565	4	5.0	15	2	US-08-370-476-26	Sequence 26, Appl	638	4	5.0	16	2	US-10-680-670-6	Sequence 6, Appli
566	4	5.0	15	2	US-09-201-945-239	Sequence 239, App	639	4	5.0	16	4	PCT-US96-01314-28	Sequence 28, Appl
567	4	5.0	15	2	US-09-310-187A-3	Sequence 3, Appli	640	4	5.0	16	6	5445818-10	Patent No. 5445818
568	4	5.0	15	2	US-08-475-955-5	Sequence 5, Appli	641	4	5.0	17	1	US-08-084-739-5	Sequence 5, Appli
569	4	5.0	15	2	US-09-671-089-50	Sequence 50, Appl	642	4	5.0	17	1	US-07-638-492-1	Sequence 1, Appli
570	4	5.0	15	2	US-09-160-076-2	Sequence 2, Appli	643	4	5.0	17	1	US-07-638-492-2	Sequence 2, Appli
571	4	5.0	15	2	US-09-819-308-17	Sequence 17, Appl	644	4	5.0	17	1	US-08-194-290-8	Sequence 8, Appli
572	4	5.0	15	2	US-07-867-819D-5	Sequence 5, Appli	645	4	5.0	17	1	US-08-325-553-38	Sequence 38, Appl
573	4	5.0	15	4	PCT-US93-08699-1	Sequence 1, Appli	646	4	5.0	17	1	US-08-318-200-22	Sequence 22, Appl
574	4	5.0	15	4	PCT-US95-01671-2	Sequence 2, Appli	647	4	5.0	17	1	US-08-388-756-5	Sequence 5, Appli
575	4	5.0	15	4	PCT-US95-11127-21	Sequence 21, Appl	648	4	5.0	17	1	US-08-015-770B-1	Sequence 1, Appli
576	4	5.0	15	6	517843-11	Patent No. 517843	649	4	5.0	17	1	US-08-486-135-11	Sequence 11, Appl
577	4	5.0	15	6	5443956-1	Patent No. 5443956	650	4	5.0	17	1	US-08-260-199A-1	Sequence 1, Appli
578	4	5.0	15	6	5470825-2	Patent No. 5470825	651	4	5.0	17	1	US-08-468-975-8	Sequence 8, Appli
579	4	5.0	16	1	US-08-127-351-25	Sequence 25, Appl	652	4	5.0	17	1	US-08-470-152-11	Sequence 11, Appl
580	4	5.0	16	1	US-08-480-367B-25	Sequence 25, Appl	653	4	5.0	17	1	US-08-460-502-6	Sequence 6, Appli
581	4	5.0	16	1	US-08-107-235-5	Sequence 5, Appli	654	4	5.0	17	1	US-08-748-428-5	Sequence 5, Appli
582	4	5.0	16	1	US-08-487-221A-25	Sequence 25, Appl	655	4	5.0	17	1	US-08-500-860A-25	Sequence 25, Appl
583	4	5.0	16	1	US-08-480-370-25	Sequence 25, Appl	656	4	5.0	17	1	US-08-468-964B-9	Sequence 9, Appli
584	4	5.0	16	1	US-08-299-636-4	Sequence 4, Appli	657	4	5.0	17	1	US-08-394-152A-38	Sequence 38, Appl
585	4	5.0	16	1	US-08-279-153-5	Sequence 5, Appli	658	4	5.0	17	1	US-08-475-634D-1	Sequence 1, Appli
586	4	5.0	16	1	US-08-464-456-4	Sequence 4, Appli	659	4	5.0	17	1	US-07-871-282A-9	Sequence 9, Appli
587	4	5.0	16	1	US-08-468-543-6	Sequence 6, Appli	660	4	5.0	17	1	US-08-363-276B-9	Sequence 9, Appli
588	4	5.0	16	1	US-08-305-871A-9	Sequence 9, Appli	661	4	5.0	17	1	US-08-614-377A-8	Sequence 8, Appli
589	4	5.0	16	1	US-08-703-988A-5	Sequence 5, Appli	662	4	5.0	17	1	US-08-253-678A-9	Sequence 9, Appli
590	4	5.0	16	1	US-08-463-052-4	Sequence 4, Appli	663	4	5.0	17	2	US-08-785-247-10	Sequence 10, Appl
591	4	5.0	16	1	US-08-178-268-39	Sequence 39, Appl	664	4	5.0	17	2	US-08-582-134B-9	Sequence 9, Appli
592	4	5.0	16	1	US-08-631-427A-5	Sequence 5, Appli	665	4	5.0	17	2	US-08-722-240-19	Sequence 19, Appl
593	4	5.0	16	1	US-08-480-551-4	Sequence 4, Appli	666	4	5.0	17	2	US-08-170-299-9	Sequence 9, Appli
594	4	5.0	16	1	US-08-476-062A-28	Sequence 28, Appl	667	4	5.0	17	2	US-08-467-791-8	Sequence 8, Appli
595	4	5.0	16	1	US-08-469-692-6	Sequence 6, Appli	668	4	5.0	17	2	US-09-215-966-4	Sequence 4, Appli
596	4	5.0	16	1	US-08-433-133-1	Sequence 1, Appli	669	4	5.0	17	2	US-08-974-549A-100	Sequence 100, App
597	4	5.0	16	1	US-09-133-774-4	Sequence 4, Appli	670	4	5.0	17	2	US-08-996-679-63	Sequence 63, Appl
598	4	5.0	16	1	US-09-133-774-5	Sequence 5, Appli	671	4	5.0	17	2	US-08-061-376-8	Sequence 8, Appli
599	4	5.0	16	1	US-09-133-774-6	Sequence 6, Appli	672	4	5.0	17	2	US-08-933-853A-14	Sequence 14, Appl
600	4	5.0	16	1	US-08-398-046-6	Sequence 6, Appli	673	4	5.0	17	2	US-08-755-034-9	Sequence 9, Appli
601	4	5.0	16	1	US-08-612-842-5	Sequence 5, Appli	674	4	5.0	17	2	US-09-115-395-23	Sequence 23, Appl
602	4	5.0	16	2	US-09-303-862-4	Sequence 4, Appli	675	4	5.0	17	2	US-09-142-648B-8	Sequence 8, Appli
603	4	5.0	16	2	US-09-303-862-5	Sequence 5, Appli	676	4	5.0	17	2	US-08-990-823-86	Sequence 86, Appl
604	4	5.0	16	2	US-09-303-862-6	Sequence 6, Appli	677	4	5.0	17	2	US-08-990-823-87	Sequence 87, Appl
605	4	5.0	16	2	US-08-714-960B-5	Sequence 5, Appli	678	4	5.0	17	2	US-08-990-823-88	Sequence 88, Appl
606	4	5.0	16	2	US-09-284-625-25	Sequence 25, Appl	679	4	5.0	17	2	US-09-113-977C-68	Sequence 68, Appl
607	4	5.0	16	2	US-08-975-040-11	Sequence 11, Appl	680	4	5.0	17	2	US-08-860-904-11	Sequence 11, Appl
608	4	5.0	16	2	US-09-082-279B-1192	Sequence 1192, Ap	681	4	5.0	17	2	US-09-055-075C-10	Sequence 10, Appl
609	4	5.0	16	2	US-08-960-054A-27	Sequence 27, Appl	682	4	5.0	17	2	US-09-055-075C-12	Sequence 12, Appl
610	4	5.0	16	2	US-08-981-392-32	Sequence 32, Appl	683	4	5.0	17	2	US-09-250-059-54	Sequence 54, Appl
611	4	5.0	16	2	US-08-958-993A-27	Sequence 27, Appl	684	4	5.0	17	2	US-09-248-074-54	Sequence 54, Appl

685	4	5.0	17	2	US-09-187-859-50	Sequence 50, Appl	758	4	5.0	18	2	US-10-283-599-196	Sequence 196, App
686	4	5.0	17	2	US-09-148-711A-6	Sequence 6, Appli	759	4	5.0	18	2	US-09-465-718-196	Sequence 196, App
687	4	5.0	17	2	US-09-458-870-54	Sequence 54, Appl	760	4	5.0	18	2	US-10-615-599-32	Sequence 32, Appl
688	4	5.0	17	2	US-09-351-048A-68	Sequence 68, Appl	761	4	5.0	18	2	US-09-973-278-658	Sequence 658, App
689	4	5.0	17	2	US-08-912-951-100	Sequence 100, App	762	4	5.0	18	6	5459046-9	Patent No. 5459046
690	4	5.0	17	2	US-09-345-624A-1	Sequence 1, Appli	763	4	5.0	18	6	5523089-34	Patent No. 5523089
691	4	5.0	17	2	US-09-919-124-10	Sequence 10, Appl	764	4	5.0	19	1	US-08-101-041A-5	Sequence 5, Appli
692	4	5.0	17	2	US-09-919-124-12	Sequence 12, Appl	765	4	5.0	19	1	US-08-392-646-18	Sequence 18, Appl
693	4	5.0	17	2	US-08-705-477E-38	Sequence 38, Appl	766	4	5.0	19	1	US-08-503-062-1	Sequence 1, Appli
694	4	5.0	17	2	US-09-839-542B-50	Sequence 50, Appl	767	4	5.0	19	1	US-08-503-062-21	Sequence 21, Appl
695	4	5.0	17	2	US-09-477-135A-86	Sequence 86, Appl	768	4	5.0	19	2	US-09-010-999-8	Sequence 8, Appli
696	4	5.0	17	2	US-09-477-135A-87	Sequence 87, Appl	769	4	5.0	19	2	US-08-604-365-11	Sequence 11, Appl
697	4	5.0	17	2	US-09-477-135A-88	Sequence 88, Appl	770	4	5.0	19	2	US-08-975-040-11	Sequence 2, Appli
698	4	5.0	17	2	US-09-402-181B-100	Sequence 100, App	771	4	5.0	19	2	US-08-975-040-8	Sequence 8, Appli
699	4	5.0	17	2	US-09-721-456-100	Sequence 100, App	772	4	5.0	19	2	US-08-975-040-19	Sequence 19, Appl
700	4	5.0	17	2	US-09-567-003C-3	Sequence 3, Appli	773	4	5.0	19	2	US-09-082-279B-1190	Sequence 1190, Ap
701	4	5.0	17	2	US-09-535-852-1935	Sequence 1935, Ap	774	4	5.0	19	2	US-09-027-998A-34	Sequence 34, Appl
702	4	5.0	17	2	US-09-662-052-7	Sequence 7, Appli	775	4	5.0	19	2	US-09-101-927-17	Sequence 17, Appl
703	4	5.0	17	2	US-09-383-062-47	Sequence 47, Appl	776	4	5.0	19	2	US-09-101-927-19	Sequence 19, Appl
704	4	5.0	17	2	US-09-674-973A-36	Sequence 36, Appl	777	4	5.0	19	2	US-09-315-304B-1190	Sequence 1190, Ap
705	4	5.0	17	2	US-09-839-884-47	Sequence 68, Appl	778	4	5.0	19	2	US-09-149-476-569	Sequence 569, App
706	4	5.0	17	2	US-09-839-884-47	Sequence 47, Appl	779	4	5.0	19	2	US-09-082-358B-75	Sequence 75, Appl
707	4	5.0	17	2	US-09-937-126-20	Sequence 20, Appl	780	4	5.0	19	2	US-09-486-072-18	Sequence 18, Appl
708	4	5.0	17	2	US-08-466-381C-38	Sequence 38, Appl	781	4	5.0	19	2	US-09-834-784-1190	Sequence 1190, Ap
709	4	5.0	17	2	US-10-006-869-50	Sequence 50, Appl	782	4	5.0	19	2	US-09-689-678-11	Sequence 11, Appl
710	4	5.0	17	4	PCT-US95-16718-9	Sequence 9, Appli	783	4	5.0	19	2	US-09-829-855-214	Sequence 214, App
711	4	5.0	17	4	PCT-US96-08995-9	Sequence 9, Appli	784	4	5.0	19	2	US-09-515-965A-1190	Sequence 1190, Ap
712	4	5.0	18	1	US-07-920-597-7	Sequence 2, Appli	785	4	5.0	19	2	US-09-350-641C-1190	Sequence 1190, Ap
713	4	5.0	18	1	US-08-288-568-2	Sequence 2, Appli	786	4	5.0	19	2	US-09-302-626B-153	Sequence 153, App
714	4	5.0	18	1	US-08-487-461-2	Sequence 2, Appli	787	4	5.0	19	2	US-09-302-626B-154	Sequence 154, App
715	4	5.0	18	1	US-08-487-461-2	Sequence 2, Appli	788	4	5.0	19	2	US-09-302-626B-155	Sequence 155, App
716	4	5.0	18	1	US-08-432-691-2	Sequence 2, Appli	789	4	5.0	19	2	US-10-038-612-33	Sequence 33, Appl
717	4	5.0	18	1	US-08-327-709-2	Sequence 2, Appli	790	4	5.0	19	2	US-10-038-612-34	Sequence 34, Appl
718	4	5.0	18	1	US-08-423-399B-15	Sequence 15, Appl	791	4	5.0	19	2	US-09-525-269A-22	Sequence 22, Appl
719	4	5.0	18	1	US-08-487-459-2	Sequence 2, Appli	792	4	5.0	19	2	US-09-350-841A-1190	Sequence 1190, Ap
720	4	5.0	18	1	US-08-190-687B-26	Sequence 26, Appl	793	4	5.0	19	2	US-09-471-276-1251	Sequence 1251, Ap
721	4	5.0	18	1	US-08-652-369A-1	Sequence 1, Appli	794	4	5.0	19	2	US-09-762-767B-13	Sequence 13, Appl
722	4	5.0	18	1	US-08-464-956-2	Sequence 2, Appli	795	4	5.0	19	2	US-09-962-756-1197	Sequence 1197, Ap
723	4	5.0	18	1	US-07-876-941A-29	Sequence 29, Appl	796	4	5.0	19	2	US-09-962-756-1552	Sequence 1552, Ap
724	4	5.0	18	1	US-08-031-538-37	Sequence 37, Appl	797	4	5.0	19	2	US-09-943-692-34	Sequence 34, Appl
725	4	5.0	18	2	US-08-940-095-196	Sequence 196, App	798	4	5.0	19	4	PCT-US96-11495-1	Sequence 1, Appli
726	4	5.0	18	2	US-08-807-992B-6	Sequence 6, Appli	799	4	5.0	19	4	PCT-US96-11495-21	Sequence 21, Appl
727	4	5.0	18	2	US-08-807-992B-15	Sequence 15, Appl	800	4	5.0	20	1	US-07-851-976B-2	Sequence 2, Appli
728	4	5.0	18	2	US-08-807-992B-19	Sequence 19, Appl	801	4	5.0	20	1	US-08-082-844-1	Sequence 1, Appli
729	4	5.0	18	2	US-08-807-992B-26	Sequence 26, Appl	802	4	5.0	20	1	US-07-864-475A-5	Sequence 5, Appli
730	4	5.0	18	2	US-08-940-093-196	Sequence 196, App	803	4	5.0	20	1	US-08-442-884-4	Sequence 4, Appli
731	4	5.0	18	2	US-08-940-096-196	Sequence 196, App	804	4	5.0	20	1	US-08-291-609-2	Sequence 2, Appli
732	4	5.0	18	2	US-09-109-957-10	Sequence 10, Appl	805	4	5.0	20	1	US-08-401-136-7	Sequence 7, Appli
733	4	5.0	18	2	US-07-861-458C-119	Sequence 119, App	806	4	5.0	20	1	US-08-416-950-7	Sequence 7, Appli
734	4	5.0	18	2	US-09-465-719-196	Sequence 196, App	807	4	5.0	20	1	US-08-464-235-18	Sequence 18, Appl
735	4	5.0	18	2	US-09-453-605-196	Sequence 196, App	808	4	5.0	20	1	US-08-480-130-190	Sequence 190, App
736	4	5.0	18	2	US-09-227-357-431	Sequence 431, App	809	4	5.0	20	1	US-08-468-279-35	Sequence 35, Appl
737	4	5.0	18	2	US-09-453-838-196	Sequence 196, App	810	4	5.0	20	1	US-08-564-972-16	Sequence 16, Appl
738	4	5.0	18	2	US-08-469-260A-571	Sequence 571, App	811	4	5.0	20	1	US-08-564-972-17	Sequence 17, Appl
739	4	5.0	18	2	US-09-140-749-60	Sequence 60, Appl	812	4	5.0	20	1	US-08-394-600B-19	Sequence 19, Appl
740	4	5.0	18	2	US-09-840-009-22	Sequence 22, Appl	813	4	5.0	20	1	US-08-657-884-2	Sequence 2, Appli
741	4	5.0	18	2	US-08-940-136-196	Sequence 196, App	814	4	5.0	20	1	US-08-714-677-17	Sequence 17, Appl
742	4	5.0	18	2	US-08-488-446-571	Sequence 571, App	815	4	5.0	20	1	US-08-393-540-17	Sequence 17, Appl
743	4	5.0	18	2	US-09-453-841-196	Sequence 196, App	816	4	5.0	20	1	US-08-714-537-17	Sequence 17, Appl
744	4	5.0	18	2	US-10-053-485-62	Sequence 62, Appl	817	4	5.0	20	1	US-08-637-759B-395	Sequence 395, App
745	4	5.0	18	2	US-08-467-344A-571	Sequence 571, App	818	4	5.0	20	1	US-08-637-759B-458	Sequence 458, App
746	4	5.0	18	2	US-08-442-001C-83	Sequence 83, Appl	819	4	5.0	20	1	US-08-488-379-190	Sequence 190, App
747	4	5.0	18	2	US-09-453-833-196	Sequence 196, App	820	4	5.0	20	1	US-08-468-249A-5	Sequence 5, Appli
748	4	5.0	18	2	US-10-009-999A-32	Sequence 32, Appl	821	4	5.0	20	1	US-08-469-830-7	Sequence 7, Appli
749	4	5.0	18	2	US-09-453-826-196	Sequence 196, App	822	4	5.0	20	1	US-08-385-540A-4	Sequence 4, Appli
750	4	5.0	18	2	US-09-453-840-196	Sequence 196, App	823	4	5.0	20	1	US-08-600-273A-4	Sequence 4, Appli
751	4	5.0	18	2	US-08-424-550B-571	Sequence 571, App	824	4	5.0	20	1	US-08-726-306A-31	Sequence 31, Appl
752	4	5.0	18	2	US-09-865-989-196	Sequence 196, App	825	4	5.0	20	2	US-08-850-554-2	Sequence 2, Appli
753	4	5.0	18	2	US-09-525-269A-10	Sequence 10, Appl	826	4	5.0	20	2	US-08-871-355A-395	Sequence 395, App
754	4	5.0	18	2	US-09-453-834-196	Sequence 196, App	827	4	5.0	20	2	US-08-871-355A-458	Sequence 458, App
755	4	5.0	18	2	US-10-079-478-32	Sequence 32, Appl	828	4	5.0	20	2	US-08-115-753-12	Sequence 12, Appl
756	4	5.0	18	2	US-10-079-478-33	Sequence 33, Appl	829	4	5.0	20	2	US-08-486-820-4	Sequence 4, Appli
757	4	5.0	18	2	US-09-763-397A-17	Sequence 17, Appl	830	4	5.0	20	2	US-08-908-643C-69	Sequence 69, Appl

977 4 5.0 22 2 US-10-238-607-18 Sequence 18, Appl
978 4 5.0 22 2 US-10-238-607-20 Sequence 20, Appl
979 4 5.0 22 2 US-10-238-607-21 Sequence 21, Appl
980 4 5.0 22 2 US-10-238-607-22 Sequence 22, Appl
981 4 5.0 22 2 US-10-238-607-23 Sequence 23, Appl
982 4 5.0 22 2 US-10-238-607-24 Sequence 24, Appl
983 4 5.0 22 2 US-09-984-365-17 Sequence 17, Appl
984 4 5.0 22 2 US-09-984-365-18 Sequence 18, Appl
985 4 5.0 22 2 US-09-984-365-20 Sequence 20, Appl
986 4 5.0 22 2 US-09-984-365-21 Sequence 21, Appl
987 4 5.0 22 2 US-09-984-365-22 Sequence 22, Appl
988 4 5.0 22 2 US-09-984-365-23 Sequence 23, Appl
989 4 5.0 22 2 US-09-984-365-24 Sequence 24, Appl
990 4 5.0 22 2 US-09-865-989-189 Sequence 189, App
991 4 5.0 22 2 US-09-453-834-189 Sequence 189, App
992 4 5.0 22 2 US-09-293-769A-75 Sequence 75, Appl
993 4 5.0 22 2 US-09-093-450-2 Sequence 2, Appl
994 4 5.0 22 2 US-10-697-055-17 Sequence 17, Appl
995 4 5.0 22 2 US-10-697-055-18 Sequence 18, Appl
996 4 5.0 22 2 US-10-697-055-20 Sequence 20, Appl
997 4 5.0 22 2 US-10-697-055-21 Sequence 21, Appl
998 4 5.0 22 2 US-10-697-055-22 Sequence 22, Appl
999 4 5.0 22 2 US-10-697-055-23 Sequence 23, Appl
1000 4 5.0 22 2 US-10-697-055-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-630-172-8
; Sequence 8, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,172
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-172-8

Query Match 58.8%; Score 47; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGV 47
Db 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGV 47

RESULT 2

US-09-375-419-8
; Sequence 8, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-375-419-8

Query Match 58.8%; Score 47; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGV 47
Db 1 HKDEVKEVQBFYKDTYNKLTQDEPQRETLKAIHYALNCCGLAGV 47

RESULT 3

US-08-254-493-4
; Sequence 4, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON

Query Match 58.8%; Score 47; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-254-493-4
Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVIKEVQEFYKDTYNKLTQDEPQRETL 31
Db 1 KDEVIKEVQEFYKDTYNKLTQDEPQRETL 30

RESULT 4
US-08-408-222B-4
; Sequence 4, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

US-08-254-493-5
Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVIKEVQEFYKDTYNKLTQDEPQRETL 31
Db 1 KDEVIKEVQEFYKDTYNKLTQDEPQRETL 30

RESULT 5
US-08-254-493-5
; Sequence 5, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 0799996-1991
; FILING DATE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-0799996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-408-222B-4
Query Match 37.5%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDEVIKEVQEFYKDTYNKLTQDEPQRETL 31
Db 1 KDEVIKEVQEFYKDTYNKLTQDEPQRETL 30
```

; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-5

Query Match 36.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 QRETLKAIHYALNCCGLAGGVQEQFISDIC 55
Db 1 QRETLKAIHYALNCCGLAGGVQEQFISDIC 29

RESULT 6
US-08-254-493-6
; Sequence 6, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-254-493-6
Query Match 36.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 SDICPKDVLFTFTVKSCPDAIKEVFDNK 80
Db 1 SDICPKDVLFTFTVKSCPDAIKEVFDNK 29
RESULT 7
US-08-408-222B-5
; Sequence 5, Application US/08408222B
; Patent No. 576727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masauyuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-408-222B-5

Query Match 36.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 QRETLKAIHYALNCCGLAGGVQFISDIC 55
Db 1 QRETLKAIHYALNCCGLAGGVQFISDIC 29

RESULT 8
US-08-408-222B-6
; Sequence 6, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41777-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-408-222B-6

Query Match 36.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 SDICPKQDVLETFIVKSCPDALKEVFDNK 80
Db 1 SDICPKQDVLETFIVKSCPDALKEVFDNK 29

RESULT 9
US-09-621-976-5649
; Sequence 5649, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5649
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
; NAME/KEY: UNSURE
; LOCATION: -3
; OTHER INFORMATION: Xaa = Ser,Thr
US-09-621-976-5649

Query Match 7.5%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 LAGGVE 48
Db 15 LAGGVE 20

RESULT 10
US-09-489-039A-12814
; Sequence 12814, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12814
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12814

Query Match 7.5%; Score 6; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY .66 VKSCPD 71
Db 6 VKSCPD 11

RESULT 11
US-09-107-532A-4420
; Sequence 4420, Application US/09107532A

; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4420:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...76
; SEQUENCE DESCRIPTION: SEQ ID NO: 4420:
US-09-107-532A-4420

Query Match 7.5%; Score 6; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YNKLKT 22
Db 4 YNKLKT 9

RESULT 12
US-09-136-251-9
; Sequence 9, Application US/09136251A
; Patent No. 6127156
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 6127156ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
; CURRENT APPLICATION NUMBER: US/09/136,251A
; CURRENT FILING DATE: 1998-08-19
; EARLIER APPLICATION NUMBER: EP 97114432.4
; EARLIER FILING DATE: 1997-08-21

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-136-251-9

Query Match 6.2%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIK 74
Db 1 PDAIK 5

RESULT 13
US-09-634-496-9
; Sequence 9, Application US/09634496
; Patent No. 644449
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 644449ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
; CURRENT APPLICATION NUMBER: US/09/634,496
; CURRENT FILING DATE: 2000-08-08
; EARLIER APPLICATION NUMBER: US/09/136,251
; EARLIER FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-634-496-9

Query Match 6.2%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIK 74
Db 1 PDAIK 5

RESULT 14
US-09-635-145A-9
; Sequence 9, Application US/09635145A
; Patent No. 6653115
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 6653115ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: C38435/118291
; CURRENT APPLICATION NUMBER: US/09/635,145A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: EP 97114432.4
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-635-145A-9

Query Match 6.2%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PDAIK 74
Db 1 PDAIK 5

RESULT 15

US-09-200-757-1
; Sequence 1, Application US/09200757
; Patent No. 6277958
; GENERAL INFORMATION:
; APPLICANT: Ajimoto, Saburho
; TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE THIOL ESTER
; FILE REFERENCE: 31763-138092
; CURRENT APPLICATION NUMBER: US/09/200,757
; CURRENT FILING DATE: 1998-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Asp(OBut)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Thr(But)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: Thr(But)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Lys(Boc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Gly(S-CH2CH2-CO)
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated C-terminus
US-09-200-757-1

Query Match 6.2%; Score 5; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TPTVK 67
Db 2 TPTVK 6

Search completed: January 20, 2006, 17:51:31
Job time : 31 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:45:33 ; Search time 16 Seconds
(without alignments)
481.084 Million cell updates/sec

Title: US-10-619-323-1_COPY_113_192

Perfect score: 80

Sequence: 1 HKDEVIKEVQEFYKDTYNKL.....LETFVKSQPDIAKEVFDNK 80

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 26016

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Listing first 1000 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	7.5	15	2 S03353	plastocyanin - Mic
2	6	7.5	57	2 H35057	MHC class II histo
3	6	7.5	60	2 H82927	hypothetical prote
4	6	7.5	66	2 PQ0469	cysteine proteinas
5	6	7.5	68	2 D64538	hypothetical prote
6	5	6.2	33	2 S42781	relaxin - oranguta
7	5	6.2	39	2 A61232	pregnancy-associat
8	5	6.2	39	2 S23804	homeotic protein 1
9	5	6.2	39	2 S23803	homeotic protein 1
10	5	6.2	39	2 C37264	E2 glycoprotein -
11	5	6.2	40	2 H81591	hypothetical prote
12	5	6.2	41	2 PQ0560	nonstructural prot
13	5	6.2	41	2 PQ0563	nonstructural prot
14	5	6.2	41	2 PQ0564	nonstructural prot
15	5	6.2	41	2 PQ0562	nonstructural prot
16	5	6.2	41	2 PQ0565	nonstructural prot
17	5	6.2	46	2 C83437	hypothetical prote
18	5	6.2	49	2 T37008	hypothetical prote
19	5	6.2	48	2 B46485	Ig epsilon chain C
20	5	6.2	55	2 B89903	hypothetical prote
21	5	6.2	57	2 G35057	MHC class II histo
22	5	6.2	57	2 C35058	MHC class II histo
23	5	6.2	58	2 B43928	probable collagen
24	5	6.2	59	1 RS9PL5	integrase - Staphy
25	5	6.2	60	2 T34737	probable gas vesic
26	5	6.2	61	2 D97920	hypothetical prote
27	5	6.2	63	1 H64095	carbon storage reg
28	5	6.2	63	1 FECLC	ferredoxin [4Fe-4S
29	5	6.2	63	2 C59147	conotoxin Gms.1 pr

30	5	6.2	64	2 H91000	hypothetical prote
31	5	6.2	64	2 B90779	hypothetical prote
32	5	6.2	65	2 D22810	small acid-soluble
33	5	6.2	66	2 B87379	ribosomal protein
34	5	6.2	66	2 S14932	homeotic protein H
35	5	6.2	67	2 B71666	ribosomal protein
36	5	6.2	68	1 IABY3	proteinase A inhib
37	5	6.2	68	1 QOHSNB	proteinase A inhib
38	5	6.2	68	2 B84267	hypothetical prote
39	5	6.2	68	2 C71970	hypothetical prote
40	5	6.2	69	2 S14074	hypothetical prote
41	5	6.2	69	2 T48461	hypothetical prote
42	5	6.2	70	2 S34217	hypothetical prote
43	5	6.2	71	2 T03353	acclimation protei
44	5	6.2	71	2 D82686	gene e14 protein -
45	5	6.2	73	2 G89307	hypothetical prote
46	5	6.2	75	1 BVBCRY	protein T01C3.2 [i
47	5	6.2	75	2 A13305	tray protein - Esc
48	5	6.2	76	2 S65527	hypothetical prote
49	5	6.2	76	2 B69472	H+-exporting ATPas
50	5	6.2	76	2 S69162	conserved hypothet
51	5	6.2	76	2 S69162	serine proteinase
52	5	6.2	77	2 H96955	serine proteinase
53	5	6.2	78	2 E86580	hypothetical prote
54	5	6.2	78	2 H72043	CT659 hypothetical
55	5	6.2	78	2 B75193	conserved hypothet
56	5	6.2	78	2 J07625	hypothetical prote
57	5	6.2	79	2 AB1238	proteinase A inhib
58	5	6.2	79	2 AG1600	B. subtilis yneF p
59	5	6.2	79	2 F72354	B. subtilis yneF p
60	5	6.2	79	2 B69874	hypothetical prote
61	5	6.2	79	2 T02461	hypothetical prote
62	5	6.2	79	2 T04983	hypothetical prote
63	5	6.2	80	2 F75598	hypothetical prote
64	5	5.0	9	2 S02617	hypothetical prote
65	4	5.0	9	2 S66636	alcohol dehydrogen
66	4	5.0	10	2 E49033	alpha-2-macroglobu
67	4	5.0	10	2 P70213	T-cell receptor ga
68	4	5.0	10	2 A61354	T-cell receptor al
69	4	5.0	11	2 S23364	T-cell receptor al
70	4	5.0	12	2 S65626	carnitine medium/1
71	4	5.0	13	2 PC1149	T-cell receptor al
72	4	5.0	14	1 QMVHMM	phosphorylase b -
73	4	5.0	14	1 JN0389	equinotoxin 1A - s
74	4	5.0	14	2 I56388	mastoparan M - hor
75	4	5.0	15	2 I52734	histamine-releasein
76	4	5.0	15	2 I29501	Km(r) protein - Es
77	4	5.0	16	2 PH1770	gene c-Ki-ras prot
78	4	5.0	16	2 S51733	fibrinopeptide A -
79	4	5.0	16	2 PH0791	T cell receptor al
80	4	5.0	16	2 PH0791	T cell receptor al
81	4	5.0	17	2 PH1789	T-cell receptor al
82	4	5.0	18	2 I73024	T cell receptor be
83	4	5.0	18	2 A32220	T-cell receptor de
84	4	5.0	18	2 S21669	1H-4-oxoquinoline
85	4	5.0	18	2 B48408	21K high mobility
86	4	5.0	18	2 PH1794	T cell receptor al
87	4	5.0	18	2 B32220	T-cell receptor de
88	4	5.0	18	2 S27141	hypothetical prote
89	4	5.0	19	2 S38895	kmR protein - Yeas
90	4	5.0	19	2 PH0793	T-cell receptor al
91	4	5.0	19	2 A48408	21K high mobility
92	4	5.0	20	2 B53875	creatine kinase (E
93	4	5.0	20	2 A56900	chymotrypsin I (EC
94	4	5.0	20	2 S71601	recombination prot
95	4	5.0	20	2 A20569	C-reactive protein
96	4	5.0	20	2 F56046	urinary tract ston
97	4	5.0	21	2 A35646	mast cell proteina
98	4	5.0	21	2 D42762	proteasome endopep
99	4	5.0	21	2 A21590	hyaluronidase (EC 3
100	4	5.0	21	2 B33600	glutamate-ammonia
101	4	5.0	22	2 PH1325	Ig heavy chain DJ
102	4	5.0	23	2 C27262	nicotinic acetylch

103	4	5.0	25	2	PC4445	L-ascorbate peroxi	176	4	5.0	40	2	S58853	homeotic protein u
104	4	5.0	26	1	SREPT4	stp protein - phag	177	4	5.0	41	2	P0561	nonstructural prot
105	4	5.0	26	2	S04376	hypothetical prote	178	4	5.0	41	2	G72312	hypothetical prote
106	4	5.0	26	2	S55799	stp protein - phag	179	4	5.0	41	2	D82130	hypothetical prote
107	4	5.0	26	2	S55798	stp protein - phag	180	4	5.0	41	2	A97948	hypothetical prote
108	4	5.0	26	2	S55797	stp protein - phag	181	4	5.0	41	2	B47752	RNA recognition mo
109	4	5.0	26	2	S55800	stp protein (varia	182	4	5.0	41	2	GIBO	gastric inhibitory
110	4	5.0	26	2	H44589	hypothetical prote	183	4	5.0	42	1	GIPG	gastric inhibitory
111	4	5.0	26	2	S00579	hypothetical prote	184	4	5.0	42	1	G56271	lpfA 5'-region hyp
112	4	5.0	27	2	I40764	hypothetical prote	185	4	5.0	42	2	T07320	hypothetical prote
113	4	5.0	27	2	PC4234	hypothetical prote	186	4	5.0	42	2	T07324	hypothetical prote
114	4	5.0	28	2	A49829	T-cell receptor va	187	4	5.0	42	2	D81730	hypothetical prote
115	4	5.0	28	2	A41476	probable antigen 1	188	4	5.0	42	2	B82657	hypothetical prote
116	4	5.0	29	2	S05032	photosystem II pro	189	4	5.0	43	2	S43195	methionyl aminopep
117	4	5.0	29	2	I49732	NADH2 dehydrogenas	190	4	5.0	43	2	S68006	araalkylamine N-ace
118	4	5.0	30	2	P00723	parvalbumin (limpor	191	4	5.0	43	2	PD0025	28k surface antige
119	4	5.0	30	2	A53415	lectin chain A - I	192	4	5.0	44	2	B38075	N-acetylglactosam
120	4	5.0	30	2	G81031	hypothetical prote	193	4	5.0	44	2	A95166	hypothetical prote
121	4	5.0	30	2	A22498	2-enoate reductase	194	4	5.0	44	2	H90641	hypothetical prote
122	4	5.0	30	2	A34874	transforming prote	195	4	5.0	44	2	G84300	hypothetical prote
123	4	5.0	30	2	B81346	hypothetical prote	196	4	5.0	44	2	T07452	hypothetical prote
124	4	5.0	30	2	A27375	photosystem I iron	197	4	5.0	44	2	A82865	hypothetical prote
125	4	5.0	31	2	S61558	chymotrypsin Pml -	198	4	5.0	44	2	H85492	hypothetical prote
126	4	5.0	31	2	S18356	chymotrypsin (EC 3	199	4	5.0	44	2	D64732	hypothetical prote
127	4	5.0	31	2	A34448	myosin heavy chain	200	4	5.0	44	2	C34327	troponin T, fast 8
128	4	5.0	31	2	S14615	hypothetical prote	201	4	5.0	44	2	IMBP10	hypothetical immun
129	4	5.0	31	2	H82241	hypothetical prote	202	4	5.0	45	2	B29548	mast cell proteina
130	4	5.0	32	2	S11610	ribosomal protein	203	4	5.0	45	2	H44530	T-cell receptor al
131	4	5.0	32	2	S01730	hexon protein - hu	204	4	5.0	45	2	S43149	Ig epsilon chain -
132	4	5.0	32	2	A80785	hypothetical prote	205	4	5.0	45	2	B45292	component for volt
133	4	5.0	32	2	D95225	hypothetical prote	206	4	5.0	45	2	S07932	hypothetical prote
134	4	5.0	32	2	C81569	hypothetical prote	207	4	5.0	45	2	F95184	hypothetical prote
135	4	5.0	32	2	S68901	xanthine dehydroge	208	4	5.0	45	2	B85921	hypothetical prote
136	4	5.0	32	2	A30505	pyruvate, phosphat	209	4	5.0	46	1	ACBP74	gene ac protein -
137	4	5.0	33	2	A60601	keratin, 55k, nucl	210	4	5.0	46	2	PF0034	baseplate protein
138	4	5.0	33	2	I46600	myosin - pig (frag	211	4	5.0	46	2	B82371	hypothetical prote
139	4	5.0	33	2	S52151	hypothetical prote	212	4	5.0	46	2	D82363	hypothetical prote
140	4	5.0	34	2	S67972	apolipoprotein AI	213	4	5.0	46	2	D82037	hypothetical prote
141	4	5.0	34	2	G55151	hypothetical prote	214	4	5.0	46	2	C69745	hypothetical prote
142	4	5.0	34	2	D70249	hypothetical prote	215	4	5.0	46	2	G53613	plectoxin IX - spi
143	4	5.0	34	2	S65371	tRNA-guanine trans	216	4	5.0	46	2	B81717	hypothetical prote
144	4	5.0	34	2	I49145	homeobox protein -	217	4	5.0	46	2	A41814	somatotropin recep
145	4	5.0	35	2	B42762	proteasome endopep	218	4	5.0	47	2	A18825	phospholipase A2 (
146	4	5.0	35	2	F87622	hypothetical prote	219	4	5.0	47	2	S13486	transferrin - bovi
147	4	5.0	35	2	B84674	hypothetical prote	220	4	5.0	47	2	G91196	hypothetical prote
148	4	5.0	35	2	C44918	lactococcin G pept	221	4	5.0	47	2	T37086	probable IS elemen
149	4	5.0	35	2	D69330	hypothetical prote	222	4	5.0	48	2	A38882	GRP-binding protei
150	4	5.0	35	2	F85847	unknown protein en	223	4	5.0	48	2	S20779	Ig heavy chain V r
151	4	5.0	35	2	A83041	conserved hypothet	224	4	5.0	48	2	S78287	ribosomal protein
152	4	5.0	36	2	A27682	39K whey protein -	225	4	5.0	48	2	S74261	troponin T3f, fast
153	4	5.0	36	2	S22222	probable lipid tra	226	4	5.0	48	2	T05927	heme A farnesyltra
154	4	5.0	36	2	A59064	egg-laying hormone	227	4	5.0	48	2	T01745	hypothetical prote
155	4	5.0	36	2	A58864	cereolysin O - Bac	228	4	5.0	48	2	T01702	hypothetical prote
156	4	5.0	36	2	S20679	Mx protein - pig (229	4	5.0	48	2	T22176	hypothetical prote
157	4	5.0	36	2	S16552	hypothetical prote	230	4	5.0	48	2	D82817	hypothetical prote
158	4	5.0	36	2	T30064	hypothetical prote	231	4	5.0	49	2	D70228	hypothetical prote
159	4	5.0	37	2	S70801	probable membrane-	232	4	5.0	49	2	T42123	perD protein - bac
160	4	5.0	37	2	S06217	transforming prote	233	4	5.0	50	2	H90596	hypothetical prote
161	4	5.0	37	2	S17684	thauartin homolog	234	4	5.0	50	2	S19624	ornatin E - leech
162	4	5.0	37	2	B95121	hypothetical prote	235	4	5.0	50	2	A82772	hypothetical prote
163	4	5.0	38	2	S21710	carboxyl reductase	236	4	5.0	50	2	B82702	hypothetical prote
164	4	5.0	38	2	I66797	troponin T 3f - ra	237	4	5.0	50	2	T50878	hypothetical solub
165	4	5.0	38	2	S71918	myo-inositol 1-pho	238	4	5.0	50	2	D90706	hypothetical prote
166	4	5.0	38	2	S33484	hypothetical prote	239	4	5.0	51	2	S36377	Ig heavy chain V r
167	4	5.0	38	2	B42799	photosystem I iron	240	4	5.0	51	2	I66796	fetal troponin T 3
168	4	5.0	39	2	A05331	colipase - spiny d	241	4	5.0	51	2	T07346	hypothetical prote
169	4	5.0	39	2	A11034	hypothetical prote	242	4	5.0	51	2	C71822	hypothetical prote
170	4	5.0	39	2	H85135	hypothetical prote	243	4	5.0	51	2	G69870	prolactin receptor
171	4	5.0	39	2	S63530	hypothetical prote	244	4	5.0	51	2	I56840	hypothetical prote
172	4	5.0	40	2	S33409	Ig heavy chain V r	245	4	5.0	51	2	F83800	hypothetical prote
173	4	5.0	40	2	C87675	hypothetical prote	246	4	5.0	51	2	AF1456	hypothetical prote
174	4	5.0	40	2	T07560	hypothetical prote	247	4	5.0	51	2	B98174	hypothetical prote
175	4	5.0	40	2	H71330	hypothetical prote	248	4	5.0	51	2	AD1839	hypothetical prote

249	4	5.0	52	2	S52963	probable H+-transp	322	4	5.0	57	2	D96953	hypothetical prote
250	4	5.0	52	2	H27578	T-cell receptor be	323	4	5.0	57	2	D97204	lactoylglutathione
251	4	5.0	52	2	S01945	myosin catalytic 1	324	4	5.0	57	2	C89981	hypothetical prote
252	4	5.0	52	2	T06503	hypothetical prote	325	4	5.0	57	2	AF1381	hypothetical prote
253	4	5.0	52	2	G87562	hypothetical prote	326	4	5.0	57	2	AG1750	hypothetical prote
254	4	5.0	52	2	D81214	hypothetical prote	327	4	5.0	57	2	A56665	solanidine UDP-glu
255	4	5.0	52	2	T32956	hypothetical prote	328	4	5.0	58	2	I53690	cytochrome P450 2B
256	4	5.0	52	2	T33694	hypothetical prote	329	4	5.0	58	2	E36491	phosphoprotein pho
257	4	5.0	52	2	S19623	ornatin C - leech	330	4	5.0	58	2	S46922	lysine-tRNA ligase
258	4	5.0	52	2	H97804	hypothetical prote	331	4	5.0	58	2	PQ0129	34.5K linker prote
259	4	5.0	52	2	A64727	yabQ protein Esc	332	4	5.0	58	2	A64910	hypothetical prote
260	4	5.0	52	2	AS9935	nitrogenase (EC 1.	333	4	5.0	58	2	S58143	gene 14 protein -
261	4	5.0	53	1	F2BGR	photosystem II pro	334	4	5.0	58	2	G81896	hypothetical prote
262	4	5.0	53	2	S41957	naringenin-chalcon	335	4	5.0	58	2	F69163	hypothetical prote
263	4	5.0	53	2	S56727	calcium-dependent	336	4	5.0	58	2	S73287	hypothetical prote
264	4	5.0	53	2	S56726	calcium-dependent	337	4	5.0	58	2	S58756	hypothetical prote
265	4	5.0	53	2	AG0053	probable exported	338	4	5.0	58	2	B82565	hypothetical prote
266	4	5.0	53	2	P95066	hypothetical prote	339	4	5.0	58	2	T12949	hypothetical prote
267	4	5.0	53	2	D90189	protein translatio	340	4	5.0	58	2	B97333	hypothetical prote
268	4	5.0	53	2	D69103	hypothetical prote	341	4	5.0	58	2	AF0058	ferredoxin [import
269	4	5.0	53	2	H81673	conserved hypothet	342	4	5.0	58	2	AD2390	hypothetical prote
270	4	5.0	53	2	F97104	probable membrane	343	4	5.0	59	1	C56273	sakacin A precurs
271	4	5.0	53	2	H98038	degenerate transpo	344	4	5.0	59	2	T07976	dihydrokaempferol
272	4	5.0	54	2	S03468	T-cell receptor al	345	4	5.0	59	2	A01117	anthranilate synth
273	4	5.0	54	2	P00022	beta-galactoside-b	346	4	5.0	59	2	S74260	tropoin T1f, fast
274	4	5.0	54	2	S01993	gene 34 protein -	347	4	5.0	59	2	S11812	opacity protein (c
275	4	5.0	54	2	E95069	hypothetical prote	348	4	5.0	59	2	AF1072	hypothetical prote
276	4	5.0	54	2	C90857	hypothetical prote	349	4	5.0	59	2	A86137	hypothetical prote
277	4	5.0	54	2	T42306	hypothetical prote	350	4	5.0	59	2	F95204	conserved domain p
278	4	5.0	54	2	T42318	hypothetical prote	351	4	5.0	59	2	C72203	hypothetical prote
279	4	5.0	54	2	T45629	hypothetical prote	352	4	5.0	59	2	B70243	hypothetical prote
280	4	5.0	54	2	D82851	hypothetical prote	353	4	5.0	59	2	F70251	hypothetical prote
281	4	5.0	54	2	C97135	hypothetical prote	354	4	5.0	59	2	D81133	hypothetical prote
282	4	5.0	54	2	G85762	probable transposa	355	4	5.0	59	2	C64024	hypothetical prote
283	4	5.0	54	2	B56557	PfEMP2/ME8A (clone	356	4	5.0	59	2	D69807	hypothetical prote
284	4	5.0	55	1	BGMS	spermatid transiti	357	4	5.0	59	2	D83672	hypothetical prote
285	4	5.0	55	1	BGRT	protein kinase AK1	358	4	5.0	59	2	B83830	hypothetical prote
286	4	5.0	55	2	S66331	ribosomal protein	359	4	5.0	59	2	G71340	hypothetical prote
287	4	5.0	55	2	E75314	DNA-dependent RNA	360	4	5.0	59	2	D82580	hypothetical prote
288	4	5.0	55	2	A69152	conserved hypothet	361	4	5.0	59	2	S56139	membrane protein n
289	4	5.0	55	2	AC0562	hypothetical prote	362	4	5.0	59	2	E97178	probable transcrip
290	4	5.0	55	2	D81987	hypothetical prote	363	4	5.0	59	2	G97790	lysosome homolog [
291	4	5.0	55	2	C69944	hypothetical prote	364	4	5.0	59	2	C36493	H+-transporting tw
292	4	5.0	55	2	T25692	hypothetical prote	365	4	5.0	59	2	A42461	hypothetical prote
293	4	5.0	55	2	G84007	hypothetical prote	366	4	5.0	60	1	T5EP2J	short toxin 2 homo
294	4	5.0	55	2	C82850	hypothetical prote	367	4	5.0	60	1	T5EP2V	short toxin 2 - we
295	4	5.0	55	2	S53148	H+-transporting tw	368	4	5.0	60	1	LFSE5	lantibiotic Pep5 p
296	4	5.0	55	2	AE2044	hypothetical prote	369	4	5.0	60	2	S10356	probable rubB prot
297	4	5.0	55	2	AH2396	hypothetical prote	370	4	5.0	60	2	G95026	T-cell receptor be
298	4	5.0	56	1	TIPG	pancreatic secreto	371	4	5.0	60	2	G95026	ribosomal protein
299	4	5.0	56	2	T48952	ribosomal S29-like	372	4	5.0	60	2	G97897	50S ribosomal prot
300	4	5.0	56	2	S74259	troponin T 3, fast	373	4	5.0	60	2	F83868	small acid-soluble
301	4	5.0	56	2	I53073	fetal troponin T 2	374	4	5.0	60	2	S62076	M-like protein pre
302	4	5.0	56	2	S10402	finger protein kox	375	4	5.0	60	2	F87332	hypothetical prote
303	4	5.0	56	2	A10756	hypothetical prote	376	4	5.0	60	2	C40128	probable antigen 1
304	4	5.0	56	2	G85054	hypothetical prote	377	4	5.0	60	2	A90942	hypothetical prote
305	4	5.0	56	2	T09177	ydaG protein - Esc	378	4	5.0	60	2	E86867	prophage p83 prote
306	4	5.0	56	2	B71570	hypothetical prote	379	4	5.0	60	2	F84281	hypothetical prote
307	4	5.0	56	2	T32552	small hypothetical	380	4	5.0	60	2	I61886	zinc finger protei
308	4	5.0	56	2	A85956	hypothetical prote	381	4	5.0	60	2	H72785	probable repressor
309	4	5.0	56	2	B90010	hypothetical prote	382	4	5.0	60	2	E85790	hypothetical prote
310	4	5.0	56	2	AB2565	hypothetical prote	383	4	5.0	60	2	A97781	hypothetical prote
311	4	5.0	56	2	C60157	hypothetical prote	384	4	5.0	60	2	B97840	hypothetical prote
312	4	5.0	57	2	S66332	protein kinase AK1	385	4	5.0	60	2	D84940	hypothetical prote
313	4	5.0	57	2	A61479	cytochrome c - try	386	4	5.0	60	2	AH2737	hypothetical prote
314	4	5.0	57	2	E86680	hypothetical prote	387	4	5.0	60	2	F98317	hypothetical prote
315	4	5.0	57	2	C84312	hypothetical prote	388	4	5.0	60	2	AB2227	hypothetical prote
316	4	5.0	57	2	T03080	hypothetical prote	389	4	5.0	60	2	AD2522	hypothetical prote
317	4	5.0	57	2	S43810	hypothetical prote	390	4	5.0	60	2	B93376	ferredoxin (fdx-6)
318	4	5.0	57	2	D70255	hypothetical prote	391	4	5.0	60	2	S05708	homeotic protein c
319	4	5.0	57	2	T35655	50S ribosomal prote	392	4	5.0	61	1	A59136	short neurotoxin 1
320	4	5.0	57	2	G64372	hypothetical prote	393	4	5.0	61	1	N1NJ1B	short neurotoxin 1
321	4	5.0	57	2	D82854	hypothetical prote	394	4	5.0	61	1	N1NJ1P	short neurotoxin 1

395	4	5.0	61	1	N1NJ1R	short neurotoxin 1	468	4	5.0	64	2	S52615	hypothetical prote
396	4	5.0	61	1	N1NJ1S	short neurotoxin 1	469	4	5.0	64	2	D81172	hypothetical prote
397	4	5.0	61	1	N1NJ2P	short neurotoxin 1	470	4	5.0	64	2	B70512	hypothetical prote
398	4	5.0	61	1	N1RI1	short neurotoxin 1	471	4	5.0	64	2	T35034	hypothetical prote
399	4	5.0	61	1	RGBP22	regulatory protein	472	4	5.0	64	2	F69231	hypothetical prote
400	4	5.0	61	2	G81267	50S ribosomal prot	473	4	5.0	64	2	T13381	hypothetical prote
401	4	5.0	61	2	S11461	annexin, isoform P	474	4	5.0	64	2	A60246	Kinogen, HMW - chi
402	4	5.0	61	2	S60796	M protein precurs	475	4	5.0	64	2	I54385	aspartylglucosamin
403	4	5.0	61	2	H5100	hypothetical prote	476	4	5.0	64	2	S22576	hypothetical prote
404	4	5.0	61	2	A69337	conserved hypot	477	4	5.0	64	2	C82843	hypothetical prote
405	4	5.0	61	2	G95049	hypothetical prote	478	4	5.0	64	2	D82811	hypothetical prote
406	4	5.0	61	2	H90437	hypothetical prote	479	4	5.0	64	2	F82697	hypothetical prote
407	4	5.0	61	2	A81898	hypothetical prote	480	4	5.0	64	2	T12921	hypothetical prote
408	4	5.0	61	2	C75321	preprotein translo	481	4	5.0	64	2	D97165	flagellar protein
409	4	5.0	61	2	H59107	hypothetical prote	482	4	5.0	64	2	D97727	hypothetical prote
410	4	5.0	61	2	F81510	hypothetical prote	483	4	5.0	64	2	AC2544	hypothetical prote
411	4	5.0	61	2	H82853	hypothetical prote	484	4	5.0	64	2	AF2495	hypothetical prote
412	4	5.0	62	1	N1NJ1M	short neurotoxin 1	485	4	5.0	65	1	R5KT35	ribosomal protein
413	4	5.0	62	2	B39327	short neurotoxin 1	486	4	5.0	65	1	E69970	spore coat protein
414	4	5.0	62	2	B35866	short neurotoxin 1	487	4	5.0	65	2	S49486	trichosanthes try
415	4	5.0	62	2	D35866	short neurotoxin d	488	4	5.0	65	2	C72233	ribosomal protein
416	4	5.0	62	2	C35866	short neurotoxin c	489	4	5.0	65	2	S73191	50S ribosomal prot
417	4	5.0	62	2	F25866	short neurotoxin c	490	4	5.0	65	2	AD2234	dnak-type molecula
418	4	5.0	62	2	E25866	short neurotoxin C	491	4	5.0	65	2	I79540	conserved hypot
419	4	5.0	62	2	G35866	short neurotoxin b	492	4	5.0	65	2	F69385	hypothetical prote
420	4	5.0	62	2	T33997	aquaporin - common	493	4	5.0	65	2	S16483	hypothetical prote
421	4	5.0	62	2	C90761	probable division	494	4	5.0	65	2	S3704	hypothetical prote
422	4	5.0	62	2	H85624	hypothetical prote	495	4	5.0	65	2	S27026	alpha-2-microglobu
423	4	5.0	62	2	B70245	conserved hypot	496	4	5.0	65	2	AB0610	hypothetical prote
424	4	5.0	62	2	E70257	conserved hypot	497	4	5.0	65	2	H95007	hypothetical prote
425	4	5.0	62	2	A98181	hypothetical prote	498	4	5.0	65	2	E86709	hypothetical prote
426	4	5.0	62	2	S25778	hypothetical prote	499	4	5.0	65	2	E86516	hypothetical prote
427	4	5.0	62	2	C84002	alkaliphily relate	500	4	5.0	65	2	T28606	hypothetical prote
428	4	5.0	62	2	T00188	hypothetical prote	501	4	5.0	65	2	S74661	hypothetical prote
429	4	5.0	62	2	D86027	hypothetical prote	502	4	5.0	65	2	G69385	hypothetical prote
430	4	5.0	62	2	S47759	hypothetical prote	503	4	5.0	65	2	T15591	H8R protein - vari
431	4	5.0	62	2	AF2059	hypothetical prote	504	4	5.0	65	2	G72172	hypothetical prote
432	4	5.0	62	2	AG1956	hypothetical prote	505	4	5.0	65	2	F72105	hypothetical prote
433	4	5.0	62	2	AG2432	hypothetical prote	506	4	5.0	65	2	H82524	hypothetical prote
434	4	5.0	62	2	B59147	conotoxin Tx5.1 pr	507	4	5.0	65	2	B71158	probable nusa prot
435	4	5.0	62	2	D59147	conotoxin Gm5.2 pr	508	4	5.0	65	2	D71070	probable zinc fing
436	4	5.0	63	2	F82058	ribosomal protein	509	4	5.0	65	2	E97099	hypothetical prote
437	4	5.0	63	2	AF0984	probable membrane	510	4	5.0	65	2	H97193	hypothetical prote
438	4	5.0	63	2	C87074	conserved hypot	511	4	5.0	65	2	F89906	hypothetical prote
439	4	5.0	63	2	H86251	protein F25C20.5 [512	4	5.0	65	2	AF0303	conserved hypot
440	4	5.0	63	2	T37351	RNA polymerase sub	513	4	5.0	65	2	AC2285	hypothetical prote
441	4	5.0	63	2	T28506	hypothetical prote	514	4	5.0	65	2	AE1937	hypothetical prote
442	4	5.0	63	2	F71571	hypothetical prote	515	4	5.0	66	1	RCBPL	regulatory protein
443	4	5.0	63	2	I38244	gene SPHAR protein	516	4	5.0	66	2	I39586	cold shock protein
444	4	5.0	63	2	B72159	16r protein - vari	517	4	5.0	66	2	T2222	mercuric reductase
445	4	5.0	63	2	G97341	hypothetical prote	518	4	5.0	66	2	A86729	Cro repressor [imp
446	4	5.0	63	2	AH1757	hypothetical prote	519	4	5.0	66	2	C90663	T-cell-stimulating
447	4	5.0	63	2	AC3155	non-heme chloroper	520	4	5.0	66	2	A43602	probable membrane
448	4	5.0	63	2	F98132	hypothetical prote	521	4	5.0	66	2	AH0816	hypothetical prote
449	4	5.0	63	2	AC2145	hypothetical prote	522	4	5.0	66	2	A99455	hypothetical prote
450	4	5.0	63	2	AD2276	hypothetical prote	523	4	5.0	66	2	T17934	hypothetical prote
451	4	5.0	63	2	AH1856	conotoxin P5.1 pre	524	4	5.0	66	2	S77592	hypothetical prote
452	4	5.0	63	2	F59147	ribosomal protein	525	4	5.0	66	2	T51323	CoOT [imported] -
453	4	5.0	64	1	R3EG18	small acid-soluble	526	4	5.0	66	2	PN0644	hypothetical prote
454	4	5.0	64	1	WHIHB2	3b protein - avian	527	4	5.0	66	2	T36227	hypothetical prote
455	4	5.0	64	1	WHIHB5	3b protein - avian	528	4	5.0	66	2	E69464	hypothetical prote
456	4	5.0	64	1	WHIHB5	restriction inhibi	529	4	5.0	66	2	S11155	cold and ABA induc
457	4	5.0	64	1	QABP22	serpin Spi2 (clone	530	4	5.0	66	2	B85890	hypothetical prote
458	4	5.0	64	2	S15633	serpin Spi2 (clone	531	4	5.0	66	2	AF3083	hypothetical prote
459	4	5.0	64	2	S15635	T-cell receptor al	532	4	5.0	66	2	S15536	homeotic protein H
460	4	5.0	64	2	JH0338	Ig heavy chain V r	533	4	5.0	67	2	B56888	ribosomal protein
461	4	5.0	64	2	I77394	ribosomal protein	534	4	5.0	67	2	E97284	ribosomal protein
462	4	5.0	64	2	T8298	preprotein translo	535	4	5.0	67	2	T62270	troponin T 1, fast
463	4	5.0	64	2	E83664	conserved hypot	536	4	5.0	67	2	S48660	M-like protein em
464	4	5.0	64	2	B69384	Myf5 homolog - chi	537	4	5.0	67	2	S61817	sec-independent pr
465	4	5.0	64	2	A48411	prophage ps2 prote	538	4	5.0	67	2	AC0580	homolog of virulen
466	4	5.0	64	2	B86689	hypothetical prote	539	4	5.0	67	2	AB0787	BlpN protein [impo
467	4	5.0	64	2	T30405		540	4	5.0	67	2	H95062	

541	4	5.0	67	2	E90798	hypothetical prote	614	4	5.0	71	2	I51705	stathmin - African
542	4	5.0	67	2	A86838	ferredoxin [import	615	4	5.0	71	2	S06279	ferritin heavy cha
543	4	5.0	67	2	T10153	hypothetical prote	616	4	5.0	71	2	T17587	hypothetical prote
544	4	5.0	67	2	JU0399	Ki1A.1 protein - p	617	4	5.0	71	2	E83054	conserved hypothet
545	4	5.0	67	2	T17830	hypothetical prote	618	4	5.0	71	2	A81160	hypothetical prote
546	4	5.0	67	2	T37079	hypothetical prote	619	4	5.0	71	2	A81829	hypothetical prote
547	4	5.0	67	2	B69529	hypothetical prote	620	4	5.0	71	2	T42025	hypothetical prote
548	4	5.0	67	2	T01958	hypothetical prote	621	4	5.0	71	2	H64454	hypothetical prote
549	4	5.0	67	2	T14410	pollen coat protei	622	4	5.0	71	2	T29194	hypothetical prote
550	4	5.0	67	2	T14467	hypothetical prote	623	4	5.0	71	2	B82791	conserved hypothet
551	4	5.0	67	2	C83925	hypothetical prote	624	4	5.0	71	2	E81674	hypothetical prote
552	4	5.0	67	2	B85511	hypothetical prote	625	4	5.0	71	2	T12840	hypothetical prote
553	4	5.0	67	2	AD2150	hypothetical prote	626	4	5.0	71	2	AD0201	conserved hypothet
554	4	5.0	67	2	AF1982	Nifr protein [limpo	627	4	5.0	72	1	TIVTOA	proteinase inhibit
555	4	5.0	67	2	AF2126	hypothetical prote	628	4	5.0	72	1	F1BC1	translation initia
556	4	5.0	67	2	F69308	2-ketoglutarate fe	629	4	5.0	72	2	T32629	hypothetical prote
557	4	5.0	68	2	S35174	cytochrome P450 (c	630	4	5.0	72	2	AH0610	initiation factor
558	4	5.0	68	2	JH0113	protein-tyrosine k	631	4	5.0	72	2	G85613	protein chain init
559	4	5.0	68	2	D27578	T-cell receptor be	632	4	5.0	72	2	A99750	protein chain init
560	4	5.0	68	2	S60797	M protein precurs	633	4	5.0	72	2	H86660	hypothetical prote
561	4	5.0	68	2	S60688	env protein - huma	634	4	5.0	72	2	G84918	hypothetical prote
562	4	5.0	68	2	JC7133	antioxidant protei	635	4	5.0	72	2	T17496	hypothetical prote
563	4	5.0	68	2	T18018	hypothetical prote	636	4	5.0	72	2	S8489	hypothetical prote
564	4	5.0	68	2	B43940	lactococcin B prec	637	4	5.0	72	2	B70517	hypothetical prote
565	4	5.0	68	2	B69534	hypothetical prote	638	4	5.0	72	2	T31028	hypothetical prote
566	4	5.0	68	2	T46012	hypothetical prote	639	4	5.0	72	2	T32793	hypothetical prote
567	4	5.0	68	2	S01743	hypothetical prote	640	4	5.0	72	2	T38324	ORF MSV163 hypothe
568	4	5.0	68	2	H95316	FixU nitrogen fixa	641	4	5.0	72	2	G85909	partial probable t
569	4	5.0	68	2	C89987	hypothetical prote	642	4	5.0	72	2	A97771	probable RND efflu
570	4	5.0	68	2	AC1093	hypothetical prote	643	4	5.0	72	2	D37711	cation efflux syst
571	4	5.0	68	2	AD3215	hypothetical prote	644	4	5.0	72	2	H97808	hypothetical prote
572	4	5.0	68	2	A11956	hypothetical prote	645	4	5.0	72	2	G89851	hypothetical prote
573	4	5.0	68	2	I49136	dopamine transport	646	4	5.0	72	2	AC2793	hypothetical prote
574	4	5.0	69	2	S78845	hypothetical prote	647	4	5.0	72	2	AH2557	hypothetical prote
575	4	5.0	69	2	S42314	gene 5.7 protein -	648	4	5.0	72	2	S49186	ferredoxin 2[4fe-4
576	4	5.0	69	2	S65749	CDP-tyvelose 2-epi	649	4	5.0	72	2	S54448	hypothetical prote
577	4	5.0	69	2	A87339	hypothetical prote	650	4	5.0	73	2	S59954	ribosomal protein
578	4	5.0	69	2	G84303	snRNP homolog [imp	651	4	5.0	73	2	AG0609	cold shock-like pr
579	4	5.0	69	2	D72857	Acof-59 protein -	652	4	5.0	73	2	P90556	acyl carrier prote
580	4	5.0	69	2	A64527	hypothetical prote	653	4	5.0	73	2	S71521	M protein type 3 -
581	4	5.0	69	2	A83044	hypothetical prote	654	4	5.0	73	2	AF1886	hypothetical prote
582	4	5.0	69	2	JQ1703	hypothetical 7.3k	655	4	5.0	73	2	T07335	hypothetical prote
583	4	5.0	69	2	S72828	hypothetical prote	656	4	5.0	73	2	B86552	hypothetical prote
584	4	5.0	69	2	B69355	hypothetical prote	657	4	5.0	73	2	I36840	C18L protein - var
585	4	5.0	69	2	T51881	hypothetical prote	658	4	5.0	73	2	T28476	hypothetical prote
586	4	5.0	69	2	D97777	hypothetical prote	659	4	5.0	73	2	T03182	hypothetical prote
587	4	5.0	69	2	AB1561	B. subtilis YkzG p	660	4	5.0	73	2	A41376	64K outer sheath p
588	4	5.0	69	2	AD1203	B. subtilis YkzG p	661	4	5.0	73	2	H83204	conserved hypothet
589	4	5.0	69	2	AD2483	hypothetical prote	662	4	5.0	73	2	A83242	hypothetical prote
590	4	5.0	69	2	AI2235	hypothetical prote	663	4	5.0	73	2	S04874	hypothetical prote
591	4	5.0	70	1	RGBPHK	regulatory protein	664	4	5.0	73	2	H82119	hypothetical prote
592	4	5.0	70	2	I45914	gene K-ras protein	665	4	5.0	73	2	D84078	slx protein homol
593	4	5.0	70	2	JQ0343	T-cell receptor al	666	4	5.0	73	2	F75527	hypothetical prote
594	4	5.0	70	2	I60231	alpha 2u-globulin	667	4	5.0	73	2	H69791	hypothetical prote
595	4	5.0	70	2	D85634	cold shock-like pr	668	4	5.0	73	2	T07454	hypothetical prote
596	4	5.0	70	2	C64840	cold shock protein	669	4	5.0	73	2	D72155	E14L protein - var
597	4	5.0	70	2	H90771	cold shock-like pr	670	4	5.0	73	2	E72072	hypothetical prote
598	4	5.0	70	2	G90478	hypothetical prote	671	4	5.0	73	2	A82804	hypothetical prote
599	4	5.0	70	2	S92881	fixU protein - Rhi	672	4	5.0	73	2	H82772	hypothetical prote
600	4	5.0	70	2	C81126	hypothetical prote	673	4	5.0	73	2	E95921	glucose-1-phosphat
601	4	5.0	70	2	F75602	hypothetical prote	674	4	5.0	73	2	H97170	acyl carrier prote
602	4	5.0	70	2	E70701	hypothetical trans	675	4	5.0	73	2	C97776	hypothetical prote
603	4	5.0	70	2	B69100	hypothetical prote	676	4	5.0	73	2	AI0290	hypothetical prote
604	4	5.0	70	2	C83688	hypothetical prote	677	4	5.0	73	2	AE1213	TN916 ORF19 homolo
605	4	5.0	70	2	E83791	hypothetical prote	678	4	5.0	73	2	AH1594	Portein gp28 (Bact
606	4	5.0	70	2	A97794	hypothetical prote	679	4	5.0	74	1	GSFF7	salivary glue prot
607	4	5.0	70	2	F97762	hypothetical prote	680	4	5.0	74	2	A29597	kinase-related tra
608	4	5.0	70	2	F97777	hypothetical prote	681	4	5.0	74	2	S63632	H+-transporting tw
609	4	5.0	70	2	F98033	transposase, uncha	682	4	5.0	74	2	T40546	60S ribosomal prot
610	4	5.0	70	2	AB2376	hypothetical prote	683	4	5.0	74	2	B85600	cold shock protein
611	4	5.0	71	1	RCBP4	regulatory protein	684	4	5.0	74	2	F90749	cold shock protein
612	4	5.0	71	2	G27578	T-cell receptor be	685	4	5.0	74	2	H64826	cold shock protein
613	4	5.0	71	2	S75774	ribosomal protein	686	4	5.0	74	2	S38900	regulatory protein

687	4	5.0	74	2	C64346	hypothetical prote	760	4	5.0	77	2	JC6324	element c protein
688	4	5.0	74	2	B82939	hypothetical prote	761	4	5.0	77	2	B84390	ferredoxin 2[4Fe-4
689	4	5.0	74	2	C82919	hypothetical prote	762	4	5.0	77	2	G95019	ROK family protein
690	4	5.0	74	2	C50923	hypothetical prote	763	4	5.0	77	2	B90885	hypothetical prote
691	4	5.0	74	2	H90973	hypothetical prote	764	4	5.0	77	2	D90127	probable small nuc
692	4	5.0	74	2	B70135	flagellar protein	765	4	5.0	77	2	C84333	hypothetical prote
693	4	5.0	74	2	A81953	SLYX protein homol	766	4	5.0	77	2	C72868	Acorf-145 protein
694	4	5.0	74	2	S23539	hypothetical prote	767	4	5.0	77	2	C42519	A19L 8.3K protein
695	4	5.0	74	2	A05192	hypothetical prote	768	4	5.0	77	2	H72353	hypothetical prote
696	4	5.0	74	2	D82775	hypothetical prote	769	4	5.0	77	2	F71642	hypothetical prote
697	4	5.0	74	2	AE0227	conserved hypotHet	770	4	5.0	77	2	D69010	hypothetical prote
698	4	5.0	74	2	A69097	ferredoxin - Metha	771	4	5.0	77	2	F84141	hypothetical prote
699	4	5.0	74	2	I41662	hypothetical prote	772	4	5.0	77	2	E82617	hypothetical prote
700	4	5.0	75	1	YBBY2	protease B inhib	773	4	5.0	77	2	A85882	hypothetical prote
701	4	5.0	75	1	TNLJ51	trans-activating t	774	4	5.0	77	2	A97042	hypothetical prote
702	4	5.0	75	2	G69394	H+-transporting AT	775	4	5.0	77	2	B85733	hypothetical prote
703	4	5.0	75	2	S78159	H+-transporting tw	776	4	5.0	77	2	E97808	hypothetical prote
704	4	5.0	75	2	S58773	H+-transporting tw	777	4	5.0	77	2	A97885	transporter trunc
705	4	5.0	75	2	A81342	30S ribosomal prot	778	4	5.0	77	2	T01738	hypothetical prote
706	4	5.0	75	2	A72355	ribosomal protein	779	4	5.0	77	2	AG3462	hypothetical prote
707	4	5.0	75	2	B97307	acyl carrier prote	780	4	5.0	77	2	A64897	hypothetical prote
708	4	5.0	75	2	F64423	hypothetical prote	781	4	5.0	78	1	B69526	conserved hypotHet
709	4	5.0	75	2	B75106	probable snrnp PAB	782	4	5.0	78	2	B54897	dermaseptin b I pr
710	4	5.0	75	2	T44096	hypothetical prote	783	4	5.0	78	2	JH0344	T-cell receptor al
711	4	5.0	75	2	E91249	C4-type zinc finger	784	4	5.0	78	2	T36595	probable ribosomal
712	4	5.0	75	2	S03594	fil protein - phag	785	4	5.0	78	2	A27683	heat shock 90K pro
713	4	5.0	75	2	T14933	hypothetical prote	786	4	5.0	78	2	B81748	conserved hypotHet
714	4	5.0	75	2	F75345	hypothetical prote	787	4	5.0	78	2	E71487	hypothetical prote
715	4	5.0	75	2	G69544	hypothetical prote	788	4	5.0	78	2	AG0997	conserved hypotHet
716	4	5.0	75	2	T29576	hypothetical prote	789	4	5.0	78	2	B91094	type III secretion
717	4	5.0	75	2	B24853	hypothetical prote	790	4	5.0	78	2	D91160	hypothetical prote
718	4	5.0	75	2	A84068	hypothetical prote	791	4	5.0	78	2	E87068	hypothetical prote
719	4	5.0	75	2	D2616	hypothetical prote	792	4	5.0	78	2	F84461	hypothetical prote
720	4	5.0	75	2	G64755	ykgL protein - Esc	793	4	5.0	78	2	JQ1781	Salp6R 8.8K protei
721	4	5.0	75	2	AB1849	hypothetical prote	794	4	5.0	78	2	I69151	perD protein - Esc
722	4	5.0	75	2	D71028	probable small nuc	795	4	5.0	78	2	A75442	hypothetical prote
723	4	5.0	75	2	I51341	homeo box protein	796	4	5.0	78	2	F69790	conserved hypotHet
724	4	5.0	76	2	E58933	ATP synthase prote	797	4	5.0	78	2	A70026	hypothetical prote
725	4	5.0	76	2	H83029	30S ribosomal prot	798	4	5.0	78	2	T35207	hypothetical prote
726	4	5.0	76	2	A36104	GTP-binding regula	799	4	5.0	78	2	C64338	hypothetical prote
727	4	5.0	76	2	C82236	cold shock-like pr	800	4	5.0	78	2	T21426	hypothetical prote
728	4	5.0	76	2	S22203	photosystem I chai	801	4	5.0	78	2	T21427	hypothetical prote
729	4	5.0	76	2	S61818	M-like protein enn	802	4	5.0	78	2	C86006	hypothetical prote
730	4	5.0	76	2	E64324	DNA-directed RNA p	803	4	5.0	78	2	D98860	conserved hypotHet
731	4	5.0	76	2	A69391	DNA-directed RNA p	804	4	5.0	78	2	H89853	hypothetical prote
732	4	5.0	76	2	E36966	rfc 3'-region hypo	805	4	5.0	78	2	F85939	type III secretion
733	4	5.0	76	2	T36251	probable lysyl-TRN	806	4	5.0	78	2	A13363	transcription regu
734	4	5.0	76	2	B36850	A19L protein - var	807	4	5.0	78	2	E65136	hypothetical 8.7 k
735	4	5.0	76	2	T28561	hypothetical prote	808	4	5.0	78	2	AF3003	conserved hypotHet
736	4	5.0	76	2	T17797	hypothetical prote	809	4	5.0	78	2	AG2805	hypothetical prote
737	4	5.0	76	2	F83566	hypothetical prote	810	4	5.0	78	2	C98280	hypothetical prote
738	4	5.0	76	2	E82154	probable transcrip	811	4	5.0	78	2	I51342	homeo box protein
739	4	5.0	76	2	H64393	hypothetical prote	812	4	5.0	79	2	S39850	FKBP immunophilin
740	4	5.0	76	2	T48430	hypothetical prote	813	4	5.0	79	2	B87405	ribosomal protein
741	4	5.0	76	2	T26894	hypothetical prote	814	4	5.0	79	2	B95179	ribosomal protein
742	4	5.0	76	2	T09476	hypothetical prote	815	4	5.0	79	2	A98046	30S ribosomal prot
743	4	5.0	76	2	A39034	neurogranin - bovi	816	4	5.0	79	2	T36351	probable ribosomal
744	4	5.0	76	2	A72166	A20L protein - var	817	4	5.0	79	2	D97286	ribosomal protein
745	4	5.0	76	2	D82787	hypothetical prote	818	4	5.0	79	2	I50549	acetylcholine rece
746	4	5.0	76	2	A01442	gp37-1 (bacterioph	819	4	5.0	79	2	S62078	M-like protein pre
747	4	5.0	76	2	H81272	probable acyl carr	820	4	5.0	79	2	C84077	nitrogen fixation
748	4	5.0	76	2	S82850	NADH2 dehydrogenas	821	4	5.0	79	2	G75155	hypothetical prote
749	4	5.0	76	2	B69110	ferredoxin - Metha	822	4	5.0	79	2	A64334	hypothetical prote
750	4	5.0	76	2	B36359	VSG expression sit	823	4	5.0	79	2	H95035	conserved hypotHet
751	4	5.0	77	1	INSH	insulin precursor	824	4	5.0	79	2	F95210	conserved domain p
752	4	5.0	77	2	A47070	ferredoxin (EC	825	4	5.0	79	2	G86731	exodeoxyribonuclea
753	4	5.0	77	2	JC2189	peptidylprolyl iso	826	4	5.0	79	2	C46026	group I intron end
754	4	5.0	77	2	A01259	complement C3 - pi	827	4	5.0	79	2	D81188	hypothetical prote
755	4	5.0	77	2	A01265	c-H-ras 2 protein	828	4	5.0	79	2	D75326	hypothetical prote
756	4	5.0	77	2	S25229	ubiquitin - Entamo	829	4	5.0	79	2	E69966	hypothetical prote
757	4	5.0	77	2	S29238	chemoreceptor prot	830	4	5.0	79	2	G64375	hypothetical prote
758	4	5.0	77	2	E36943	reverse transcript	831	4	5.0	79	2	F83880	acyl-carrier prote
759	4	5.0	77	2	S63586		832	4	5.0	79	2	F97856	hypothetical prote

833	4	5.0	79	2	B89761	hypothetical prote	906	3	3.8	10	2	S33844	alpha-2-macroglobu
834	4	5.0	79	2	E97906	conserved hypothet	907	3	3.8	10	2	S33995	hypertrehalosemic h
835	4	5.0	79	2	AH1418	hypothetical prote	908	3	3.8	10	2	JC1416	hypertrehalosemic
836	4	5.0	79	2	AB2323	hypothetical prote	909	3	3.8	10	2	S09138	hypertrehalosemic
837	4	5.0	79	2	A12512	hypothetical prote	910	3	3.8	10	2	H28027	protein P11 - curl
838	4	5.0	80	2	PC4098	Ha-ras protein - r	911	3	3.8	10	2	H61308	hemocyanin subunit
839	4	5.0	80	2	PC4097	Ha-ras protein - E	912	3	3.8	10	2	A61622	vitellogenin, 190k
840	4	5.0	80	2	A35572	seminalplasma pre	913	3	3.8	10	2	A35556	hypothetical prote
841	4	5.0	80	2	S06905	ferritin heavy cha	914	3	3.8	10	2	PT0212	T-cell receptor al
842	4	5.0	80	2	S61801	M-like protein enu	915	3	3.8	10	2	C30572	T-cell receptor be
843	4	5.0	80	2	A89860	hypothetical prote	916	3	3.8	10	2	B61440	polygalacturonase
844	4	5.0	80	2	D63492	conserved hypothet	917	3	3.8	10	2	D61440	polygalacturonase
845	4	5.0	80	2	S16200	photosystem I iron	918	3	3.8	10	2	A58365	neuropeptide FRFa
846	4	5.0	80	2	A32364	photosystem I iron	919	3	3.8	10	2	S77990	cytochrome-c oxida
847	4	5.0	80	2	S68677	cytochrome c551 -	920	3	3.8	10	2	T17063	cytochrome-c oxida
848	4	5.0	80	2	A60699	hypothetical prote	921	3	3.8	10	2	H60787	sperm-activating p
849	4	5.0	80	2	P90782	hypothetical prote	922	3	3.8	10	2	F60787	sperm-activating p
850	4	5.0	80	2	A90898	probable damage-in	923	3	3.8	10	2	C60787	sperm-activating p
851	4	5.0	80	2	H91230	hypothetical prote	924	3	3.8	10	2	D60787	sperm-activating p
852	4	5.0	80	2	B90337	conserved hypothet	925	3	3.8	10	2	B60787	sperm-activating p
853	4	5.0	80	2	B90368	conserved hypothet	926	3	3.8	10	2	D60588	sperm-activating p
854	4	5.0	80	2	D95111	hypothetical prote	927	3	3.8	10	2	B60588	sperm-activating p
855	4	5.0	80	2	H84281	hypothetical prote	928	3	3.8	10	2	C60588	sperm-activating p
856	4	5.0	80	2	S02225	hypothetical prote	929	3	3.8	10	2	D60527	sperm-activating p
857	4	5.0	80	2	E72295	hypothetical prote	930	3	3.8	10	2	D60527	sperm-activating p
858	4	5.0	80	2	A29385	conserved hypothet	931	3	3.8	10	2	C39572	sperm-activating p
859	4	5.0	80	2	T39148	hydrophobic seed p	932	3	3.8	10	2	F60527	sperm-activating p
860	4	5.0	80	2	A54059	hypothetical prote	933	3	3.8	10	2	C60527	sperm-activating p
861	4	5.0	80	2	S03560	protein kinase C (934	3	3.8	10	2	E60527	sperm-activating p
862	4	5.0	80	2	G82597	transition protein	935	3	3.8	10	2	G60527	sperm-activating p
863	4	5.0	80	2	C69917	hypothetical prote	936	3	3.8	10	2	E39572	sperm-activating p
864	4	5.0	80	2	G86077	hypothetical prote	937	3	3.8	10	2	D60788	sperm-activating p
865	4	5.0	80	2	E97800	hypothetical prote	938	3	3.8	10	2	E60788	sperm-activating p
866	4	5.0	80	2	G97805	hypothetical prote	939	3	3.8	10	2	C60788	sperm-activating p
867	4	5.0	80	2	H89802	30S ribosomal prot	940	3	3.8	10	2	F60589	sperm-activating p
868	4	5.0	80	2	S40834	hypothetical prote	941	3	3.8	10	2	C60589	sperm-activating p
869	4	5.0	80	2	E97572	hypothetical prote	942	3	3.8	10	2	D60589	sperm-activating p
870	4	5.0	80	2	S02067	glycerol kinase (E	943	3	3.8	10	2	A60527	sperm-activating p
871	4	3.8	5	2	S70615	endo-1,4-beta-xyla	944	3	3.8	10	2	A60787	sperm-activating p
872	3	3.8	5	2	PT0267	Ig heavy chain CND	945	3	3.8	10	2	A60588	sperm-activating p
873	3	3.8	5	2	PT0585	T-cell receptor be	946	3	3.8	10	2	A60788	sperm-activating p
874	3	3.8	6	2	B60110	repetitive protein	947	3	3.8	11	1	GMROL	leucosulfakinin -
875	3	3.8	6	2	PT0605	T-cell receptor be	948	3	3.8	11	2	A38841	rhodopsin homolog
876	3	3.8	6	2	I79564	hypothetical TCU3	949	3	3.8	11	2	I41946	T-cell receptor ga
877	3	3.8	7	2	PT0666	T-cell receptor be	950	3	3.8	11	2	S33519	probable secreted
878	3	3.8	7	2	PT0683	T-cell receptor be	951	3	3.8	11	2	PC4267	ribosomal protein
879	3	3.8	7	2	B35890	RNA-directed DNA p	952	3	3.8	11	2	S71304	amine oxidase (cop
880	3	3.8	7	4	S15597	orf 4 rara 5'-regi	953	3	3.8	11	2	A60656	perisulfakinin - A
881	3	3.8	8	2	A33995	adipokinetic hormo	954	3	3.8	11	2	A32428	amine oxidase (cop
882	3	3.8	8	2	B44960	neuropeptide Led-C	955	3	3.8	11	2	S68637	acetylcholinestera
883	3	3.8	8	2	S08996	hypertrehalosemic	956	3	3.8	11	2	S54347	tubulin beta chain
884	3	3.8	8	2	B49823	adipokinetic hormo	957	3	3.8	11	2	S23306	substance P - Atla
885	3	3.8	8	2	PT0527	T-cell receptor be	958	3	3.8	11	2	A26930	ermG leader peptid
886	3	3.8	8	2	PT0509	T-cell receptor be	959	3	3.8	12	2	S09082	proteasome chain 1
887	3	3.8	8	2	A21440	variant surface gl	960	3	3.8	12	2	S26552	T-cell receptor be
888	3	3.8	8	2	B24749	neuropeptide B - b	961	3	3.8	12	2	S26549	T-cell receptor be
889	3	3.8	8	4	I55411	hypothetical hista	962	3	3.8	12	2	S26553	T-cell receptor be
890	3	3.8	8	2	A28495	conopressin G - co	963	3	3.8	12	2	S26559	T-cell receptor be
891	3	3.8	9	2	A24244	adipokinetic hormo	964	3	3.8	12	2	C58502	58K bile and gallb
892	3	3.8	9	2	PC2197	zymogen granule me	965	3	3.8	12	2	D28551	hypothetical prote
893	3	3.8	9	2	G56978	collagen alpha 1(I	966	3	3.8	12	2	C33099	148K exoantigen -
894	3	3.8	9	2	A42266	peptidylglycine mo	967	3	3.8	12	2	S47360	T-cell antigen rec
895	3	3.8	9	2	B30572	T-cell receptor be	968	3	3.8	12	2	PH1188	T-cell receptor al
896	3	3.8	9	2	S39040	lysine-conopressin	969	3	3.8	12	2	PH1481	T-cell receptor be
897	3	3.8	9	2	I54379	gene NF2 protein -	970	3	3.8	12	2	PH1466	T-cell receptor be
898	3	3.8	9	2	A60427	macrophage cytotox	971	3	3.8	12	2	PH1469	T-cell receptor be
899	3	3.8	9	2	S66635	alpha-2-macroglobu	972	3	3.8	12	2	E58502	43.2K bile stone p
900	3	3.8	9	2	I46016	cytokerin 4 - bo	973	3	3.8	12	2	S71034	potB protein - Sal
901	3	3.8	9	2	PC7074	translation elonga	974	3	3.8	12	2	I40663	bma protein - Clos
902	3	3.8	9	2	PC7078	unidentified 48.7K	975	3	3.8	12	2	PN0162	malate dehydrogena
903	3	3.8	9	2	QDRB	delta sleep-induci	976	3	3.8	12	2	S21205	Ig heavy chain V r
904	3	3.8	9	4	I73804	hypothetical E2 pr	977	3	3.8	12	2	S71380	lebetin 1 isoform
905	3	3.8	10	2	S28055	cytochrome b559 co	978	3	3.8	12	2	S10059	tachykinin - Afric

```
979 3 3.8 12 2 S65409 histone H2B - huma
980 3 3.8 13 2 A33208 calreticulin, hepa
981 3 3.8 13 2 A37390 traA protein - Esc
982 3 3.8 13 2 H64124 hypothetical prote
983 3 3.8 13 2 PA0031 protein QA300045 -
984 3 3.8 13 2 B44957 protein L7 - commo
985 3 3.8 13 2 S47362 T-cell antigen rec
986 3 3.8 13 2 S47388 T-cell antigen rec
987 3 3.8 13 2 B61233 conceptus protein
988 3 3.8 13 2 S66235 sperm motility inh
989 3 3.8 13 2 B36042 oxfK protein - Esc
990 3 3.8 13 2 S09733 photosystem I prot
991 3 3.8 13 2 S66558 serine proteinase
992 3 3.8 13 2 S01904 H+-transporting tw
993 3 3.8 14 1 QMVHP2 mastoparan C - Eur
994 3 3.8 14 1 QMWAVV mastoparan C - Yello
995 3 3.8 14 1 LFECW trp operon leader
996 3 3.8 14 2 A47421 leukotriene B-4 12
997 3 3.8 14 2 C40944 hypothetical prote
998 3 3.8 14 2 S21247 H+-transporting tw
999 3 3.8 14 2 A60622 somatostatin - spo
1000 3 3.8 14 2 A60840 somatostatin I - E

ALIGNMENTS

RESULT 1
S03353
plastocyanin - Microcystis aeruginosa (fragment)
C:Species: Microcystis aeruginosa
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03353
R/Tan, S.; Ho, K.K.
Biochim. Biophys. Acta 973, 111-117, 1989
A>Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.
A:Reference number: S03353; MUID:89134784; PMID:2537099
A:Accession: S03353
A:Molecule type: protein
A:Residues: 1-15 <FAN>
A:Cross-references: UNIPROT:P10625; UNIPARC:UPI0000131BAF

Query Match 7.5%; Score 6; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 ETFTVK 67
Db 1 ETFTVK 6

RESULT 2
H35057
MHC class II histocompatibility antigen DO-B beta chain - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 31-Dec-2004
C:Accession: H35057
R:Gyllenstein, U.B.; Lashkari, D.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1835-1839, 1990
A>Title: Allelic diversification at the class II DOB locus of the mammalian major histoc
A:Reference number: A35054; MUID:90175391; PMID:2308943
A:Accession: H35057
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-57 <GYL>
A:Cross-references: UNIPROT:Q02712; UNIPROT:Q9TPB4; UNIPARC:UPI0000176PDE
C:Superfamily: immunoglobulin homology

Query Match 7.5%; Score 6; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 KDVLFT 63
```

Db 45 KDVLFT 50

RESULT 3

H82927

hypothetical protein UUI51 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: H82927

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A>Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min

A:Reference number: A82870

A:Accession: H82927

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-60 <GLA>

A:Cross-references: UNIPARC:UPI0000139389; GB:AE002115; GB:AF222894; NID:G6899102; PIDN

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: UUI51

A:Genetic code: SGC3

Query Match 7.5%; Score 6; DB 2; Length 60;

Best Local Similarity 100.0%; Pred. No. 59;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEVIKE 8

Db 50 DEVIKE 55

RESULT 4

PQ0469

cysteine proteinase inhibitor - potato (fragment)

N:Alternate names: wound-induced protein

C:Species: Solanum tuberosum (potato)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: PQ0469; S24768

R:Hildmann, T.; Ebnet, M.; Pena-Cortes, H.; Sanchez-Serrano, J.J.; Willmitzer, L.; Prat

Plant Cell 4, 1157-1170, 1992

A>Title: General roles of abscisic and jasmonic acids in gene activation as a result of

A:Reference number: QJL692; MUID:93005746; PMID:1392612

A:Accession: PQ0469

A:Molecule type: mRNA

A:Residues: 1-66 <HIL>

A:Cross-references: UNIPROT:Q03196; UNIPARC:UPI0000128D7E; EMBL:X67844; NID:G21440; PIDN

A:Experimental source: strain desiree

C:Keywords: cysteine proteinase inhibitor

F:18-22/Region: inhibitory

Query Match 7.5%; Score 6; DB 2; Length 66;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEF 12

Db 53 KEVQEF 58

RESULT 5

D64538

hypothetical protein HP0148 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: D64538

R:Tombs, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: D64538
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-68 <TOM>
A:Cross-references: UNIPROT:Q24959; UNIPARC:UPI00000C07EB; GB:AE000536; GB:AE000511; NID

Query Match 7.5%; Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TLKAIH 35
|||
DB 25 TLKAIH 30

RESULT 6
S42781
relaxin - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S42781
R:Evans, B.B.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42776
A:Accession: S42781
A:Molecule type: DNA
A:Residues: 1-33 <EVA>
A:Cross-references: UNIPROT:Q28782; UNIPARC:UPI000008691D; EMBL:Z27230; NID:G415992; PID

C:Genetics:
C:Superfamily: insulin
C:Keywords: disulfide bond; hormone
P:1-33/Domain: relaxin chain 2B (fragment) #status predicted <RXB2>

Query Match 6.2%; Score 5; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DEVIK 7
|||
DB 5 DEVIK 9

RESULT 7
A61232
pregnancy-associated glycoprotein - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Aug-2004
C:Accession: A61232
R:Zoli, A.P.; Beckers, J.F.; Wouters-Ballman, P.; Closset, J.; Falmagne, P.; Ectors, P.
Biol. Reprod. 45, 1-10, 1991
A:Title: Purification and characterization of a bovine pregnancy-associated glycoprotein
A:Reference number: A61232; MUID:91346259; PMID:1908709
A:Accession: A61232
A:Molecule type: protein
A:Residues: 1-39 <ZOL>
A:Cross-references: UNIPROT:Q7M318; UNIPARC:UPI0000175D6D
C:Superfamily: Pepsin
C:Keywords: glycoprotein

Query Match 6.2%; Score 5; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 KDEPQ 27
|||
DB 25 KDEPQ 29

RESULT 8
S23804
homeotic protein lim-2B - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: S23804
R:Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.
Genes Dev. 6, 356-366, 1992

A:Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in t
A:Reference number: S23802; MUID:92192449; PMID:1347750

A:Accession: S23804
A:Molecule type: mRNA
A:Residues: 1-39 <TAI>
A:Cross-references: UNIPROT:P37138; UNIPARC:UPI000012E698; EMBL:Z11588; NID:G64832; PID

C:Genetics:
A:Gene: lim-2B

C:Superfamily: homeotic protein lim-3; homeobox homology; LIM metal-binding repeat homo
C:Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulati
P:1-39/Domain: homeobox homology (fragment) <HOX>

Query Match 6.2%; Score 5; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETLKA 33
|||
DB 6 ETLKA 10

RESULT 9
S23803
homeotic protein lim-2A - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 15-Mar-2004
C:Accession: S23803
R:Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.
Genes Dev. 6, 356-366, 1992

A:Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in t
A:Reference number: S23802; MUID:92192449; PMID:1347750

A:Accession: S23803
A:Molecule type: mRNA
A:Residues: 1-39 <TAI>
A:Cross-references: UNIPARC:UPI000017155C; EMBL:Z11587; NID:G64831; PIDN:CAA77672.1; PI

A:Note: the authors translated the codon ATT for residue 13 as Ala

C:Genetics:
A:Gene: lim-2A

C:Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulati
P:1-39/Domain: homeobox homology (fragment) <HOX>

Query Match 6.2%; Score 5; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETLKA 33
|||
DB 6 ETLKA 10

RESULT 10
C37264
E2 Glycoprotein - Barmah Forest virus (fragment)
C:Species: Barmah Forest virus
C:Date: 30-Aug-1991 #sequence_revision 30-Jan-1993 #text_change 31-Dec-2004
C:Accession: C37264
R:Bell, J.R.; Kinney, R.M.; Trent, D.W.; Strauss, E.G.; Strauss, J.H.
Proc. Natl. Acad. Sci. U.S.A. 81, 4702-4706, 1984

A:Title: An evolutionary tree relating eight alphaviruses, based on amino-terminal sequ

A:Reference number: A31774; MUID:84272701; PMID:6087344
A:Accession: C37264
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-39 <BEL>
A:Cross-references: UNIPROT:P89946; UNIPARC:UPI000017855E

C:Keywords: glycoprotein

Query Match 6.2%; Score 5; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;
QY 41 CGLAG 45
|||||
Db 21 CGLAG 25

RESULT 11
H81591
hypothetical protein CP0304 [imported] - Chlamydophila pneumoniae (strain AR39)
C:Species: Chlamydophila pneumoniae; Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: H81591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-40 <REA>
A:Cross-references: UNIPROT:Q9K298; UNIPARC:UPI00000CCCS57; GB:AE002192; GB:AE002161; NID
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0304

Query Match 6.2%; Score 5; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 18 NKCLKT 22
|||||
Db 9 NKCLKT 13

RESULT 12
PQ0560
nonstructural protein 3 (clone 8) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: PQ0560
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A:Title: Distribution of plural HCV types in Japan.
A:Reference number: PQ0554; MUID:92068204; PMID:1720309
A:Accession: PQ0560
A:Molecule type: mRNA
A:Residues: 1-41 <KAT>
A:Cross-references: UNIPROT:Q81252; UNIPARC:UPI00000F397A; GB:D10563; GB:D90519; NID:g22
A:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: nonstructural protein

Query Match 6.2%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 43 LAGGV 47
|||||
Db 2 LAGGV 6

RESULT 13
PQ0563
nonstructural protein 3 (clone 11) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: PQ0563
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A:Title: Distribution of plural HCV types in Japan.
A:Reference number: PQ0554; MUID:92068204; PMID:1720309

A:Accession: PQ0563
A:Molecule type: mRNA
A:Residues: 1-41 <KAT>
A:Cross-references: UNIPROT:Q81248; UNIPARC:UPI00000EE322; GB:D10566; GB:D90522; NID:g22
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: nonstructural protein

Query Match 6.2%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 43 LAGGV 47
|||||
Db 2 LAGGV 6

RESULT 14
PQ0564
nonstructural protein 3 (clone 4) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: PQ0564
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A:Title: Distribution of plural HCV types in Japan.
A:Reference number: PQ0554; MUID:92068204; PMID:1720309
A:Accession: PQ0564
A:Molecule type: mRNA
A:Residues: 1-41 <KAT>
A:Cross-references: UNIPROT:Q81251; UNIPARC:UPI00000F69F4; GB:D10567; GB:D90523; NID:g22
A:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: nonstructural protein

Query Match 6.2%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 43 LAGGV 47
|||||
Db 2 LAGGV 6

RESULT 15
PQ0562
nonstructural protein 3 (clone 10) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: PQ0562
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A:Title: Distribution of plural HCV types in Japan.
A:Reference number: PQ0554; MUID:92068204; PMID:1720309
A:Accession: PQ0562
A:Molecule type: mRNA
A:Residues: 1-41 <KAT>
A:Cross-references: UNIPROT:Q81247; UNIPARC:UPI00000F65F6; GB:D10565; GB:D90521; NID:g22
A:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: nonstructural protein

Query Match 6.2%; Score 5; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 43 LAGGV 47
|||||
Db 2 LAGGV 6

Search completed: January 20, 2006, 17:50:58
Job time : 25 secs

105	5	6.2	49	2	Q87418_SIVCZ	Q87418 chimpanzee	178	5	6.2	59	2	Q7UFE3_RHOBA	Q7ufe3 rhodopirell
106	5	6.2	50	1	VHUU_METJA	P81335 methanococc	179	5	6.2	59	2	Q39817_ENCVC	Q39817 encephalomy
107	5	6.2	50	2	Q7RGH1_PLAYO	Q7fgh1 plasmodium	180	5	6.2	59	2	Q80Q55_9VIRU	Q80q55 sen virus.
108	5	6.2	50	2	Q4HKY1_CAMLA	Q4hky1 campylobact	181	5	6.2	59	2	Q90WQ4_9PERO	Q90wq4 paralabrax
109	5	6.2	50	2	Q88FV5_PSEPK	Q88fv5 pseudomonas	182	5	6.2	59	2	Q87394_SIVCZ	Q87394 chimpanzee
110	5	6.2	50	2	Q8XH86_CLOPE	Q8xh86 clostridium	183	5	6.2	59	2	Q4GZX9_9HIV1	Q4gzx9 human immun
111	5	6.2	50	2	Q8HJ54_RHILO	Q8hj54 rhizobium 1	184	5	6.2	59	2	Q4GZX8_9HIV1	Q4gzx8 human immun
112	5	6.2	51	2	Q9HBM4_HUMAN	Q9hbm4 homo sapien	185	5	6.2	59	2	Q9U4L3_OXYTR	Q9u4l3 oxytricha t
113	5	6.2	51	2	P96297_ALCEU	P96297 alcaligenes	186	5	6.2	60	2	Q8HWV2_DYUMA	Q8hmv2 daubentonia
114	5	6.2	51	2	Q7UJX5_SYNXP	Q7ujx5 synechococc	187	5	6.2	60	2	Q8HWV2_DYUMA	Q8hmv2 daubentonia
115	5	6.2	51	2	Q8FP13_COREF	Q8fp13 corynebacte	188	5	6.2	60	2	Q5GTC1_WOLTR	Q5gtc1 wolbachia s
116	5	6.2	51	2	Q8XMC1_CLOPE	Q8xmc1 clostridium	189	5	6.2	60	2	Q81RQ0_BACAN	Q81rq0 bacillus a
117	5	6.2	52	2	Q9S6X0_MYCBO	Q9s6x0 mycobacteri	190	5	6.2	60	2	Q9ZC06_STRCO	Q9zc06 streptomyc
118	5	6.2	52	2	Q65VF1_MANSM	Q65vf1 manheimia	191	5	6.2	60	2	Q4RDJ3_TETNG	Q4rdj3 tetraodon n
119	5	6.2	52	2	Q8P062_LEPIN	Q8p062 leptospira	192	5	6.2	60	2	Q87435_SIVCZ	Q87435 chimpanzee
120	5	6.2	52	2	Q31335_ALIMI	Q31335 alligator m	193	5	6.2	61	1	PPDL_BOVIN	P15396 bos taurus
121	5	6.2	52	2	Q31337_ALIMI	Q31337 alligator m	194	5	6.2	61	2	Q4X1X1_ASPFU	Q4x1x1 aspergillus
122	5	6.2	53	2	Q33SD2_HUMAN	Q33sd2 homo sapien	195	5	6.2	61	2	Q5BZY6_SCHJA	Q5bzy6 schistosoma
123	5	6.2	53	2	Q54HU1_DICTDI	Q54hu1 dictyosteli	196	5	6.2	61	2	Q9BPF9_CONTE	Q9bpf9 conus texti
124	5	6.2	53	2	Q7RJH6_PLAYO	Q7rjh6 plasmodium	197	5	6.2	61	2	Q6JDX0_9DIPT	Q6jdx0 cuterebra g
125	5	6.2	53	2	Q4XSV2_PLACH	Q4xsv2 plasmodium	198	5	6.2	61	2	Q4KPE5_PSEFS	Q4kfe5 pseudomonas
126	5	6.2	53	2	Q4Z5L8_PLABE	Q4z5l8 plasmodium	199	5	6.2	61	2	Q8CZ64_STRR6	Q8cz64 streptococc
127	5	6.2	53	2	Q30452_EQUAS	Q30452 equus asinu	200	5	6.2	61	2	Q8P1S7_STRP8	Q8p1s7 streptococc
128	5	6.2	53	2	Q30469_HORSE	Q30469 equus cabal	201	5	6.2	61	2	Q75QV1_HRSV	Q75qv1 human respi
129	5	6.2	53	2	Q30472_HORSE	Q30472 equus cabal	202	5	6.2	61	2	Q8JL51_9CAUD	Q8jls1 virus phich
130	5	6.2	53	2	Q30473_HORSE	Q30473 equus cabal	203	5	6.2	61	2	Q4TFM4_TETNG	Q4tfm4 tetraodon n
131	5	6.2	53	2	Q30474_HORSE	Q30474 equus cabal	204	5	6.2	61	2	Q87352_SIVCZ	Q87352 chimpanzee
132	5	6.2	53	2	Q30477_HORSE	Q30477 equus cabal	205	5	6.2	61	2	Q87432_SIVCZ	Q87432 chimpanzee
133	5	6.2	53	2	Q30478_HORSE	Q30478 equus cabal	206	5	6.2	62	1	QX54A_CONMR	Q6pn82 conus marmo
134	5	6.2	53	2	Q30480_HORSE	Q30480 equus cabal	207	5	6.2	62	2	Q54V25_DICTDI	Q54v25 dictyosteli
135	5	6.2	53	2	Q9BCX7_HORSE	Q9bcx7 equus cabal	208	5	6.2	62	2	Q64995_9ERIC	Q64995 rhododendro
136	5	6.2	53	2	Q6XQ83_9CAUD	Q6xqe3 enterobacte	209	5	6.2	62	2	Q64996_9ERIC	Q64996 gaultheria
137	5	6.2	53	2	Q75Z86_ECOLI	Q75ze6 escherichia	210	5	6.2	62	2	Q8E1C2_STRAS	Q8e1c2 streptococc
138	5	6.2	53	2	Q4LAI0_STAHH	Q4lai0 staphylococ	211	5	6.2	62	2	Q8R7E0_THETN	Q8r7e0 thermoanaer
139	5	6.2	53	2	Q81EHO_BACCR	Q81eho bacillus ce	212	5	6.2	62	2	Q6APL1_DESPS	Q6apl1 desulfotale
140	5	6.2	53	2	Q5RGF4_BRARE	Q5rgf4 brachydanio	213	5	6.2	63	1	CSRA_HA3IN	P44879 haemophilus
141	5	6.2	53	2	P88733_9HIV1	P88733 human immun	214	5	6.2	63	1	QX51_CONGL	Q9u6z9 conus glori
142	5	6.2	53	2	P88743_9HIV1	P88743 human immun	215	5	6.2	63	1	PER_MOOTH	P02023 moorella th
143	5	6.2	53	2	P88747_9HIV1	P88747 human immun	216	5	6.2	63	2	Q9BPG7_CONTE	Q9bpg7 conus texti
144	5	6.2	54	1	QX54B_CONMR	Q68ip5 conus marmo	217	5	6.2	63	2	Q9BPH0_CONTE	Q9bph0 conus texti
145	5	6.2	54	1	QX5B_CONVC	P67f66 conus victo	218	5	6.2	63	2	Q4Z9J0_9VIRU	Q4z9j0 bacterioph
146	5	6.2	54	2	Q7R1E9_GIALA	P7r1e9 giardia lam	219	5	6.2	63	2	Q6M799_CORGL	Q6m799 corynebacte
147	5	6.2	54	2	Q7RMS3_PLAYO	Q7rms3 plasmodium	220	5	6.2	63	2	Q938X2_CAMJE	Q938x2 campylobact
148	5	6.2	54	2	Q8LNP6_ORYSA	Q8lnp6 oryza sativ	221	5	6.2	63	2	Q9EUM6_LISIN	Q9eum6 listeria in
149	5	6.2	55	2	Q4XUD5_PLACH	Q4xud5 plasmodium	222	5	6.2	63	2	Q9EUM0_LISIV	Q9eum0 listeria iv
150	5	6.2	55	2	Q56Z81_ARATH	Q56z81 arabidopsi	223	5	6.2	63	2	Q4QM87_HAB18	Q4qmh7 haemophilus
151	5	6.2	55	2	Q83A77_COXBU	Q83ay7 coxiella bu	224	5	6.2	64	1	QX51A_CONMR	Q6pn86 conus marmo
152	5	6.2	56	2	Q4YGT7_PLABE	Q4ygt7 plasmodium	225	5	6.2	64	1	QX53_CONMR	Q6pn83 conus marmo
153	5	6.2	56	2	Q69TP0_ORYSA	Q69tp0 oryza sativ	226	5	6.2	64	1	NINH_BP933	P69176 bacterioph
154	5	6.2	56	2	Q6GHR8_STAAR	Q6ghe8 staphylococ	227	5	6.2	64	1	NINH_BP919	P69177 bacterioph
155	5	6.2	56	2	Q7ASW8_STAAR	Q7asu8 staphylococ	228	5	6.2	64	2	NINH_BPVT2	Q777w6 bacterioph
156	5	6.2	56	2	Q99U16_STAAM	Q99u16 staphylococ	229	5	6.2	64	2	Q7Y277_9CAUD	Q7y277 phage phi 4
157	5	6.2	57	2	Q17546_CABEL	Q17546 caenorhabdi	230	5	6.2	64	2	Q8X5E8_9VIRU	Q8x5e8 bacterioph
158	5	6.2	57	2	Q5DN40_9CAUD	Q5dn40 bacterioph	231	5	6.2	64	2	Q93756_YEREN	Q937s6 versinia en
159	5	6.2	57	2	Q65J65_BACLD	Q65j65 bacillus li	232	5	6.2	64	2	Q93MP6_CAMJE	Q93mp6 campylobact
160	5	6.2	57	2	Q8K6T6_STRP3	Q8k6t6 streptococ	233	5	6.2	64	2	Q49384_MYCGE	Q49384 mycoplasma
161	5	6.2	57	2	Q4PR74_CASFI	Q4pr74 castor fibe	234	5	6.2	64	2	Q50FZ8_CAMJE	Q50fz8 campylobact
162	5	6.2	57	2	Q4PR73_CASFI	Q4pr73 castor fibe	235	5	6.2	64	2	Q7AK37_ECO57	Q7ak37 escherichia
163	5	6.2	57	2	Q4PR71_CASFI	Q4pr71 castor fibe	236	5	6.2	64	2	Q4MUJ5_BACCE	Q4muj5 bacillus ce
164	5	6.2	57	2	Q4PR70_CASFI	Q4pr70 castor fibe	237	5	6.2	64	2	Q4MUJ2_BACCE	Q4muj2 bacillus ce
165	5	6.2	57	2	Q4PR69_CASFI	Q4pr69 castor fibe	238	5	6.2	64	2	Q9EUV3_LISWE	Q9euv3 listeria we
166	5	6.2	57	2	Q4PR66_CASFI	Q4pr66 castor fibe	239	5	6.2	64	2	Q650L5_BACFR	Q650l5 bacteroides
167	5	6.2	57	2	Q6JKD3_9NUCL	Q6jkd3 neodiprion	240	5	6.2	64	2	Q650L5_BACFR	Q650l5 bacteroides
168	5	6.2	57	2	Q6J8I6_9CALL	Q6j8i6 neorwalk-li	241	5	6.2	64	2	Q8FIH8_LEPIN	Q8filh leptospira
169	5	6.2	58	1	AXPI_ANTAP	P81547 anthopleura	242	5	6.2	64	2	Q6N4V1_RHOPA	Q6n4v1 rhodopseu
170	5	6.2	58	2	Q8GIT8_SYNPF	Q8git8 synechococc	243	5	6.2	64	2	Q82LX8_STRAW	Q82lx8 streptomyce
171	5	6.2	58	2	Q5NY78_AZOSE	Q5ny78 azoarcus sp	244	5	6.2	65	1	AMYL_LACAM	P80696 lactobacill
172	5	6.2	58	2	Q7US83_RHOBA	Q7use3 rhodopirell	245	5	6.2	65	1	QX51B_CONMR	Q6pn85 conus marmo
173	5	6.2	58	2	Q87382_SIVCZ	Q87382 chimpanzee	246	5	6.2	65	1	SAS3_EACME	Q15072 bacillus me
174	5	6.2	59	1	VXIS_EPL54	P20710 bacterioph	247	5	6.2	65	2	Q6TYT5_ORYSA	Q6tyt5 oryza sativ
175	5	6.2	59	2	Q4ZB09_9VIRU	Q4zb09 bacterioph	248	5	6.2	65	2	Q8LLD2_SCUBA	Q8lld2 scutellaria
176	5	6.2	59	2	Q4ZBP0_9VIRU	Q4zbp0 bacterioph	249	5	6.2	65	2	Q7BRU8_BACME	Q7bru8 bacillus me
177	5	6.2	59	2	Q4ZDJ6_9VIRU	Q4zdj6 bacterioph	250	5	6.2	65	2	Q5GRX8_WOLTR	Q5grx8 wolbachia s

251	5	6.2	65	2	Q5XCUS_STRP6	Q5xcu5 streptococc	324	5	6.2	68	2	Q8ATQ9_9HIV1	Q8atq9 human immun
252	5	6.2	65	2	Q9A0F2_STRPY	Q9a0f2 streptococc	325	5	6.2	68	2	Q8ATR0_9HIV1	Q8atr0 human immun
253	5	6.2	65	2	Q5L2L4_STRT1	Q5l2l4 streptococc	326	5	6.2	68	2	Q8ATR1_9HIV1	Q8atr1 human immun
254	5	6.2	65	2	Q5M467_STRT2	Q5m467 streptococc	327	5	6.2	68	2	Q8ATR2_9HIV1	Q8atr2 human immun
255	5	6.2	65	2	Q5NGL6_STRAT	Q5ngl6 francisella	328	5	6.2	68	2	Q8ATR6_9HIV1	Q8atr6 human immun
256	5	6.2	65	2	Q7NUH6_GLOVI	Q7njh6 gloebacter	329	5	6.2	68	2	Q8ATR7_9HIV1	Q8atr7 human immun
257	5	6.2	65	2	Q8NSJ8_CORGL	Q8nsj8 corynebacte	330	5	6.2	68	2	Q8ATR9_9HIV1	Q8atr9 human immun
258	5	6.2	65	2	Q7CF93_STRP3	Q7cf93 streptococc	331	5	6.2	68	2	Q8ATS2_9HIV1	Q8ats2 human immun
259	5	6.2	65	2	Q7CNC6_STRP8	Q7cnc6 streptococc	332	5	6.2	68	2	Q8QEH7_9HIV1	Q8qeh7 human immun
260	5	6.2	65	2	Q8DYT6_STRAS	Q8dyt6 streptococc	333	5	6.2	68	2	Q8QEH8_9HIV1	Q8qeh8 human immun
261	5	6.2	65	2	Q8E4E4_STRAS	Q8e4e4 streptococc	334	5	6.2	68	2	Q8QEH9_9HIV1	Q8qeh9 human immun
262	5	6.2	65	2	Q80212_MOUSE	Q80212 mus musculu	335	5	6.2	68	2	Q8QEI0_9HIV1	Q8qei0 human immun
263	5	6.2	65	2	Q6XD88_9REOV	Q6xd88 human rotav	336	5	6.2	68	2	Q8QEI1_9HIV1	Q8qei1 human immun
264	5	6.2	65	2	Q9MMJ1_9EMBB	Q9mmj1 geospiza co	337	5	6.2	68	2	Q8QEI8_9HIV1	Q8qei8 human immun
265	5	6.2	65	2	Q9MMJ7_9EMBE	Q9mmj7 geospiza co	338	5	6.2	68	2	Q8QEI9_9HIV1	Q8qei9 human immun
266	5	6.2	66	1	CX52_CONMR	Q6pu84 conus marmo	339	5	6.2	69	1	SEM1_ASHGO	P62499 ashbya goss
267	5	6.2	66	1	RL35_BRAJA	Q89wh9 bradyrhizob	340	5	6.2	69	1	YFXZ_AZOCA	P26486 azornisoblu
268	5	6.2	66	1	RL35_CAUCR	Q9a9e2 caulobacter	341	5	6.2	69	2	Q95ZG8_DICDI	Q95z98 dictyosteli
269	5	6.2	66	1	RL35_RHOPA	Q6ndr5 rhodopseudo	342	5	6.2	69	2	Q4YRL2_PLABE	Q4yr12 plasmodium
270	5	6.2	66	1	Q54B11_DICDI	Q54b11 dictyosteli	343	5	6.2	69	2	Q4Z755_PLABE	Q4z755 plasmodium
271	5	6.2	66	2	Q5F6D5_NEIG1	Q5f6d5 neisseria g	344	5	6.2	69	2	Q93YL6_BRANA	Q93yl6 brassica na
272	5	6.2	66	2	Q5F7Q0_NEIG1	Q5f7q0 neisseria g	345	5	6.2	69	2	Q9LZ32_ARATH	Q9lz32 arabidopsis
273	5	6.2	66	2	Q5P9C4_NEIG1	Q5p9c4 neisseria g	346	5	6.2	69	2	Q4TSC3_9SPHN	Q4tsc3 erythrobact
274	5	6.2	66	2	Q5FH68_EHRRG	Q5fh68 ehrlichia r	347	5	6.2	69	2	Q5P5W6_AZOSE	Q5p5w6 azoarcus sp
275	5	6.2	66	2	Q8PLS3_STRP3	Q8pls3 streptococc	348	5	6.2	69	2	Q72UT4_LEPIC	Q72ut4 leptospira
276	5	6.2	66	2	Q5LLE3_SILPO	Q5lle3 silicibacte	349	5	6.2	69	2	Q8OSG0_9PICO	Q8osg0 human rhino
277	5	6.2	66	2	Q5XB43_SILPO	Q5xb43 streptococc	350	5	6.2	69	2	Q8OSG2_9PICO	Q8osg2 human rhino
278	5	6.2	66	2	Q99Y22_STRPY	Q99y22 streptococc	351	5	6.2	69	2	Q8OSG4_9PICO	Q8osg4 human rhino
279	5	6.2	66	2	Q7CNE4_STRP8	Q7cne4 streptococc	352	5	6.2	69	2	Q8OSG6_9PICO	Q8osg6 human rhino
280	5	6.2	66	2	Q5PEV4_ANAMH	Q5pev4 anaplasma m	353	5	6.2	69	2	Q8OSH0_9PICO	Q8osh0 human rhino
281	5	6.2	66	2	Q5HC38_EHRRW	Q5hc38 ehrlichia r	354	5	6.2	69	2	Q8OSH1_9PICO	Q8osh1 human rhino
282	5	6.2	66	2	Q52KL6_MOUSE	Q52kl6 mus musculu	355	5	6.2	69	2	Q8OSH4_9PICO	Q8osh4 human rhino
283	5	6.2	66	2	Q4SBW7_TETNG	Q4sbw7 tetraodon n	356	5	6.2	69	2	Q8OSH7_9PICO	Q8osh7 human rhino
284	5	6.2	67	1	RL35_RICPR	Q9zcv1 rickettsia	357	5	6.2	69	2	Q8OSH8_9PICO	Q8osh8 human rhino
285	5	6.2	67	2	Q4XM94_PLACH	Q4xm94 plasmodium	358	5	6.2	69	2	Q8OSI2_9PICO	Q8osi2 human rhino
286	5	6.2	67	2	Q8SNQ8_PROVE	Q8snq8 propithecus	359	5	6.2	69	2	Q8OSI3_9PICO	Q8osi3 human rhino
287	5	6.2	67	2	Q5CBP4_9THEM	Q5cbp4 thermotoga	360	5	6.2	69	2	Q8OSI4_9PICO	Q8osi4 human rhino
288	5	6.2	67	2	Q4V1P8_BACCZ	Q4v1p8 bacillus ce	361	5	6.2	69	2	Q8OSI5_9PICO	Q8osi5 human rhino
289	5	6.2	67	2	Q4R2T6_HYDTH	Q4r2t6 hydrognoaba	362	5	6.2	69	2	Q8OSI6_9PICO	Q8osi6 human rhino
290	5	6.2	67	2	Q4NKB4_9DELT	Q4nkb4 anaeronyxob	363	5	6.2	69	2	Q8OSJ2_9PICO	Q8osj2 human rhino
291	5	6.2	67	2	Q4L8X1_BACCR	Q4l8x1 bacillus ce	364	5	6.2	69	2	Q8OSJ5_9PICO	Q8osj5 human rhino
292	5	6.2	67	2	Q5NNC0_ZYMMO	Q5nnc0 zymomonas m	365	5	6.2	69	2	Q8OSJ6_9PICO	Q8osj6 human rhino
293	5	6.2	67	2	Q9QEI0_9HIV1	Q9qei0 human immun	366	5	6.2	69	2	Q8OSJ7_9PICO	Q8osj7 human rhino
294	5	6.2	68	1	IPA3_YEAST	P01094 saccharomyc	367	5	6.2	69	2	Q8OSJ8_9PICO	Q8osj8 human rhino
295	5	6.2	68	1	RL35_RICCN	Q92hb3 rickettsia	368	5	6.2	69	2	Q8OSJ9_9PICO	Q8osj9 human rhino
296	5	6.2	68	1	RL35_WOLPM	Q73gr8 wolbachia p	369	5	6.2	69	2	Q8OSK0_9PICO	Q8osk0 human rhino
297	5	6.2	68	1	Y1110_HALSA	P17104 halobacteri	370	5	6.2	69	2	Q8OSK1_9PICO	Q8osk1 human rhino
298	5	6.2	68	2	Q973K1_SULTO	Q973k1 sulfolobus	371	5	6.2	69	2	Q8OSK2_9PICO	Q8osk2 human rhino
299	5	6.2	68	2	Q95304_HUMAN	Q95304 homo sapien	372	5	6.2	69	2	Q8OSK3_9PICO	Q8osk3 human rhino
300	5	6.2	68	2	Q5XYZ4_BORGA	Q5xyz4 borrelia ga	373	5	6.2	69	2	Q8OSK4_9PICO	Q8osk4 human rhino
301	5	6.2	68	2	Q6SHM8_9BACT	Q6shm8 uncultured	374	5	6.2	69	2	Q8OSK5_9PICO	Q8osk5 human rhino
302	5	6.2	68	2	Q7P970_RICSI	Q7p970 rickettsia	375	5	6.2	69	2	Q8OSK9_9PICO	Q8osk9 human rhino
303	5	6.2	68	2	Q4UMK7_RICFE	Q4umk7 rickettsia	376	5	6.2	69	2	Q8OSL0_9PICO	Q8osl0 human rhino
304	5	6.2	68	2	Q4FNH7_RICCK	Q4fnh7 candidatus	377	5	6.2	69	2	Q8OSL2_9PICO	Q8osl2 human rhino
305	5	6.2	68	2	Q73F41_BACCI	Q73f41 bacillus ce	378	5	6.2	69	2	Q8OSL5_9PICO	Q8osl5 human rhino
306	5	6.2	68	2	Q73F42_BACCI	Q73f42 bacillus ce	379	5	6.2	69	2	Q8OSL6_9PICO	Q8osl6 human rhino
307	5	6.2	68	2	Q92MT2_HELPJ	Q9zmt2 helicobacte	380	5	6.2	69	2	Q8OSL8_9PICO	Q8osl8 human rhino
308	5	6.2	68	2	Q81QAI_BACAN	Q8lqai bacillus an	381	5	6.2	69	2	Q8OSL9_9PICO	Q8osl9 human rhino
309	5	6.2	68	2	Q6N0Z6_RHOPA	Q6n0z6 rhodopseudo	382	5	6.2	69	2	Q8OSM0_9PICO	Q8osm0 human rhino
310	5	6.2	68	2	Q68WD1_RICTY	Q68wd1 rickettsia	383	5	6.2	69	2	Q8OSM1_9PICO	Q8osm1 human rhino
311	5	6.2	68	2	Q8V0Q2_PMV	Q8v0q2 papaya mosa	384	5	6.2	69	2	Q8OSM3_9PICO	Q8osm3 human rhino
312	5	6.2	68	2	Q8V0Q5_PMV	Q8v0q5 papaya mosa	385	5	6.2	69	2	Q8OSM5_9PICO	Q8osm5 human rhino
313	5	6.2	68	2	Q8ATP5_9HIV1	Q8atp5 human immun	386	5	6.2	69	2	Q8OSM7_9PICO	Q8osm7 human rhino
314	5	6.2	68	2	Q8ATP6_9HIV1	Q8atp6 human immun	387	5	6.2	69	2	Q8OSM9_9PICO	Q8osm9 human rhino
315	5	6.2	68	2	Q8ATP7_9HIV1	Q8atp7 human immun	388	5	6.2	69	2	Q8OSM8_9PICO	Q8osm8 human rhino
316	5	6.2	68	2	Q8ATP9_9HIV1	Q8atp9 human immun	389	5	6.2	69	2	Q8OSM9_9PICO	Q8osm9 human rhino
317	5	6.2	68	2	Q8ATQ0_9HIV1	Q8atq1 human immun	390	5	6.2	69	2	Q8OSN0_9PICO	Q8osn0 human rhino
318	5	6.2	68	2	Q8ATQ1_9HIV1	Q8atq1 human immun	391	5	6.2	69	2	Q8OSN4_9PICO	Q8osn4 human rhino
319	5	6.2	68	2	Q8ATQ2_9HIV1	Q8atq2 human immun	392	5	6.2	69	2	Q8OSN5_9PICO	Q8osn5 human rhino
320	5	6.2	68	2	Q8ATQ3_9HIV1	Q8atq3 human immun	393	5	6.2	69	2	Q8OSN6_HRV23	Q8osn6 human rhino
321	5	6.2	68	2	Q8ATQ4_9HIV1	Q8atq4 human immun	394	5	6.2	69	2	Q8OSN7_9PICO	Q8osn7 human rhino
322	5	6.2	68	2	Q8ATQ5_9HIV1	Q8atq5 human immun	395	5	6.2	69	2	Q8OSN8_9PICO	Q8osn8 human rhino
323	5	6.2	68	2	Q8ATQ7_9HIV1	Q8atq7 human immun	396	5	6.2	69	2	Q8OSP0_9PICO	Q8osp0 human rhino

397	5	6.2	69	2	Q80SP1_9PICO	Q80sp1 human rhino	470	5	6.2	75	2	Q57BT4_BRUAB	Q57bt4 brucella ab
398	5	6.2	69	2	Q80SP3_HRV16	Q80sp3 human rhino	471	5	6.2	75	2	Q72P13_LEPIC	Q72p13 leptospira
399	5	6.2	69	2	Q80SP4_9PICO	Q80sp4 human rhino	472	5	6.2	75	2	Q8FZA3_BRUSU	Q8fza3 brucella su
400	5	6.2	69	2	Q80SP5_9PICO	Q80sp5 human rhino	473	5	6.2	75	2	Q8YIL3_BRUME	Q8yil3 brucella me
401	5	6.2	69	2	Q80SP7_9PICO	Q80sp7 human rhino	474	5	6.2	75	2	Q7AK74_922Z2	Q7ak74 plasmid r10
402	5	6.2	69	2	Q80SP8_9PICO	Q80sp8 human rhino	475	5	6.2	75	2	Q5Y1H1_9HEPC	Q5y1h1 hepatitis c
403	5	6.2	69	2	Q80SP9_9PICO	Q80sp9 human rhino	476	5	6.2	75	2	Q8JM20_9NUCL	Q8jm20 mamestra co
404	5	6.2	69	2	Q80SQ1_9PICO	Q80sq1 human rhino	477	5	6.2	75	2	Q9WK35_ENMCV	Q9wk35 encephalomy
405	5	6.2	69	2	Q80SQ6_HRV2	Q80sq6 human rhino	478	5	6.2	75	2	Q9YPA2_ENMCV	Q9ypa2 porcine enc
406	5	6.2	69	2	Q80SQ7_HRV1A	Q80sq7 human rhino	479	5	6.2	76	1	PIA1_PLEOS	Q7m4t6 pleurotus o
407	5	6.2	69	2	Q8JYL7_9REOV	Q8jyl7 bovine rota	480	5	6.2	76	1	PIA2_PLEOS	Q7m4t5 pleurotus o
408	5	6.2	69	2	Q8QWH4_9ENTO	Q8qwh4 human coxsa	481	5	6.2	76	2	Q28492_ARCFU	Q28492 archaeoglob
409	5	6.2	70	2	Q8NKU7_ACIAM	Q8nku7 acidianus a	482	5	6.2	76	2	Q46813_EQUAS	Q46813 equus asinu
410	5	6.2	70	2	Q5UWV4_HALMA	Q5uwv4 haloarcula	483	5	6.2	76	2	Q46815_EQUAS	Q46815 equus asinu
411	5	6.2	70	2	Q858N7_9CAUD	Q858n7 lactococcus	484	5	6.2	76	2	Q7Y3W1_9CAUD	Q7y3w1 bacterioph
412	5	6.2	70	2	Q88165_SGCEE	Q88165 secale cere	485	5	6.2	76	2	Q8HAA4_9CAUD	Q8haa4 salmonella
413	5	6.2	70	2	Q94KK3_LOLPR	Q94kk3 lolium pere	486	5	6.2	76	2	Q69SR5_ORYSA	Q69sr5 oryza sativ
414	5	6.2	70	2	Q9F654_ECOLI	Q9f654 escherichia	487	5	6.2	76	2	Q6Z4F9_ORYSA	Q6z4f9 oryza sativ
415	5	6.2	70	2	Q4HB47_9DEIO	Q4hb47 deinococcus	488	5	6.2	76	2	Q761Z1_ORYSA	Q761z1 oryza sativ
416	5	6.2	70	2	Q8A758_BACTN	Q8a758 bacteroides	489	5	6.2	76	2	Q9S953_MESCR	Q9s953 mesembryant
417	5	6.2	70	2	Q8RE06_FUSNN	Q8re06 fusobacteri	490	5	6.2	76	2	Q87892_NEIME	Q87892 neisseria m
418	5	6.2	70	2	Q80XV5_9MURI	Q80xv5 rattus sp.	491	5	6.2	76	2	Q7P3X3_FUSNV	Q7p3x3 fusobacteri
419	5	6.2	71	2	Q8TZV7_PYRFU	Q8tzv7 pyrococcus	492	5	6.2	76	2	Q9CKJ0_PASMU	Q9ckj0 pasteurella
420	5	6.2	71	2	Q68YW3_LEPMC	Q68yw3 leptospira	493	5	6.2	76	2	Q8AKB9_DESPS	Q8akb9 desulfotale
421	5	6.2	71	2	Q80146_9CAUD	Q80146 bacterioph	494	5	6.2	76	2	Q8JX76_9VIRU	Q8jx76 sen virus.
422	5	6.2	71	2	Q9PDH9_XYLFA	Q9pdh9 xylella fas	495	5	6.2	76	2	Q4T4C9_TETNG	Q4t4c9 tetraodon n
423	5	6.2	71	2	Q6G9S6_STAAS	Q6g9s6 staphylococ	496	5	6.2	77	2	Q8W1M3_SOLCH	Q8w1m3 solanum cha
424	5	6.2	71	2	Q7P197_CHRVO	Q7p197 chromobacte	497	5	6.2	77	2	Q62UM1_BACLD	Q62um1 bacillus li
425	5	6.2	71	2	Q5HGE4_STAAC	Q5hge4 staphylococ	498	5	6.2	77	2	Q97LU9_CIOAB	Q97lu9 clostridium
426	5	6.2	71	2	Q8NMY2_STAAC	Q8nmy2 staphylococ	499	5	6.2	77	2	Q8G2J6_BRUSU	Q8g2j6 brucella su
427	5	6.2	71	2	Q9WK37_ENMCV	Q9wk37 encephalomy	500	5	6.2	77	2	Q8QTI3_9INFA	Q8qti3 influenza a
428	5	6.2	71	2	Q9VPL9_ENMCV	Q9vpl9 encephalomy	501	5	6.2	77	2	Q8QTI4_9INFA	Q8qti4 influenza a
429	5	6.2	71	2	Q9YF53_9HIV1	Q9yf53 human immun	502	5	6.2	77	2	Q4T544_TETNG	Q4t544 tetraodon n
430	5	6.2	71	2	Q9YF54_9HIV1	Q9yf54 human immun	503	5	6.2	78	1	RR16_ADICA	Q85fn9 adiantum ca
431	5	6.2	72	1	X358_MANSN	Q65vp5 mantheimia	504	5	6.2	78	1	Y022_CHICV	Q824w6 chlamydothi
432	5	6.2	72	2	Q4YFM4_PLABE	Q4yfm4 plasmodium	505	5	6.2	78	1	Y720_CHLNP	Q9v2k5 pyrococcus
433	5	6.2	72	2	Q6A211_GORBE	Q6a211 gorilla gor	506	5	6.2	78	2	Q9V2K5_PVRAB	Q9v2k5 pyrococcus
434	5	6.2	72	2	Q6A215_GORBE	Q6a215 gorilla gor	507	5	6.2	78	2	Q8ND26_HUMAN	Q8nd26 homo sapien
435	5	6.2	72	2	Q6A216_GORBE	Q6a216 gorilla gor	508	5	6.2	78	2	Q7RAS0_PLAYO	Q7ras0 plasmodium
436	5	6.2	72	2	Q6A218_GORGO	Q6a218 gorilla gor	509	5	6.2	78	2	Q5NVK9_PONPY	Q5nvk9 pongo pygma
437	5	6.2	72	2	Q6A219_GORGO	Q6a219 gorilla gor	510	5	6.2	78	2	Q6W3R0_ACIJB	Q6w3r0 acinonyx ju
438	5	6.2	72	2	Q76FP0_CANFA	Q76fp0 canis fami	511	5	6.2	78	2	Q66T53_GOSHI	Q66t53 gossypium h
439	5	6.2	72	2	Q6X3F8_PSEAE	Q6x3f8 pseudomonas	512	5	6.2	78	2	Q7P9U1_RICSI	Q7p9u1 rickettsia
440	5	6.2	72	2	Q4L5A4_STAHI	Q4l5a4 staphylococ	513	5	6.2	78	2	Q5L788_CHLAB	Q5l788 chlamydothi
441	5	6.2	72	2	Q88VB0_LACPL	Q88vb0 lactobacill	514	5	6.2	78	2	Q88VY2_RICTY	Q88vy2 rickettsia
442	5	6.2	72	2	Q74L22_LACJO	Q74l22 lactobacill	515	5	6.2	79	1	Y1306_LISMO	P67288 listeria mo
443	5	6.2	72	2	Q5HQ79_STAEO	Q5hq79 staphylococ	516	5	6.2	79	1	Y1324_LISMF	P67285 listeria mo
444	5	6.2	72	2	Q8CT15_STAEP	Q8ct15 staphylococ	517	5	6.2	79	1	Y1344_LISIN	P67289 listeria in
445	5	6.2	73	2	Q56H83_9EUC	Q56h83 farfantepen	518	5	6.2	79	2	Q7S8A7_NEUCR	Q7s8a7 neurospora
446	5	6.2	73	2	Q56H84_9EUC	Q56h84 farfantepen	519	5	6.2	79	2	Q8IFB4_PLAFA	Q8ifb4 plasmodium
447	5	6.2	73	2	Q58LL3_9CAUD	Q58ll3 cyanophaga	520	5	6.2	79	2	Q4BP73_9CAEN	Q4bp73 conus tessu
448	5	6.2	73	2	Q6K3N0_ORISA	Q6k3n0 oryza sativ	521	5	6.2	79	2	Q4XHV5_PLACH	Q4xhv5 plasmodium
449	5	6.2	73	2	Q72CU5_DBSVH	Q72cu5 desulfovibr	522	5	6.2	79	2	Q30465_HORSE	Q30465 equus cabal
450	5	6.2	73	2	Q9YPL4_ENMCV	Q9ypl4 encephalomy	523	5	6.2	79	2	Q80833_ARATH	Q80833 arabidopsis
451	5	6.2	73	2	Q9YPL8_ENMCV	Q9ypl8 encephalomy	524	5	6.2	79	2	Q8H365_ORYSA	Q8h365 oryza sativ
452	5	6.2	73	2	Q4S123_TETNG	Q4s123 tetraodon n	525	5	6.2	79	2	Q81883_ARATH	Q81883 arabidopsis
453	5	6.2	73	2	Q85464_9RETR	Q85464 avian sarco	526	5	6.2	79	2	P77060_ECOLI	P77060 escherichia
454	5	6.2	74	2	Q8ZWG6_PYRAE	Q8zwg6 pyrobaculum	527	5	6.2	79	2	Q77060_ECOLI	Q77060 escherichia
455	5	6.2	74	2	Q8ZZW1_PYRAE	Q8zzw1 pyrobaculum	528	5	6.2	79	2	Q9AIU5_ZOORA	Q9aius zoogloea ra
456	5	6.2	74	2	Q6ILS0_DROME	Q6ils0 drosophila	529	5	6.2	79	2	Q34958_BACSU	Q34958 bacillus su
457	5	6.2	74	2	Q4X551_PLACH	Q4x551 plasmodium	530	5	6.2	79	2	Q9WZ91_THEME	Q9wz91 thermotoga
458	5	6.2	74	2	Q6LE72_SALTY	Q6le72 salmonella	531	5	6.2	79	2	Q7NZN4_CHRVO	Q7nzn4 chlamydothi
459	5	6.2	74	2	Q4UZ19_XANCP	Q4uz19 xanthomonas	532	5	6.2	79	2	Q65K03_BACLD	Q65k03 bacillus li
460	5	6.2	74	2	Q831J4_ENTFA	Q831j4 enterococcu	533	5	6.2	79	2	Q8CER2_MOUSE	Q8cer2 mus musculu
461	5	6.2	74	2	Q77AU0_XANCP	Q77au0 xanthomonas	534	5	6.2	80	2	Q8V3G9_SWPV	Q8v3g9 swinepox vi
462	5	6.2	74	2	Q77AU0_XANCP	Q77au0 xanthomonas	535	5	6.2	80	2	Q95575_HUMAN	Q95575 homo sapien
463	5	6.2	74	2	Q9W8B2_ENMCV	Q9w8b2 encephalomy	536	5	6.2	80	2	Q54SB2_DICDI	Q54sb2 dictyosteli
464	5	6.2	75	1	TRAY3_ECOLI	P05835 escherichia	537	5	6.2	80	2	Q85J60_ANTGR	Q85j60 anthonomus
465	5	6.2	75	2	Q552L0_DICDI	Q552l0 dictyosteli	538	5	6.2	80	2	Q76FN9_CANFA	Q76fn9 canis fami
466	5	6.2	75	2	Q5ZCF4_ORYSA	Q5zcf4 oryza sativ	539	5	6.2	80	2	Q4FLJ6_GRICK	Q4flj6 candidatus
467	5	6.2	75	2	Q05554_LEGPN	Q05554 legionella	540	5	6.2	80	2	Q9RZA2_DEIRA	Q9rza2 deinococcus
468	5	6.2	75	2	Q74WA0_YERPE	Q74wa0 yersinia pe	541	5	6.2	80	2	Q5LYA7_STRTI	Q5lya7 streptococ
469	5	6.2	75	2	Q6SJ27_ECOLI	Q6sj27 escherichia	542	5	6.2	80	2	Q9YPL2_ENMCV	Q9ypl2 encephalomy
												Q801C6_LATME	Q801c6 latimeria m

543	4	5.0	9	1	CB22_SPIOL	Q9t2k9 spinacia ol	616	4	5.0	19	2	Q01057_KLULA	Q01057 kluyveromy
544	4	5.0	2	Q7M2N7_BOSIN	Q7m2n7 bos indicus	617	4	5.0	19	2	Q8IVK8_HUMAN	Q8ivk8 homo sapien	
545	4	5.0	9	P82568_STRPY	P82568 streptococ	618	4	5.0	19	2	Q9UC73_HUMAN	Q9uc73 homo sapien	
546	4	5.0	11	ODAIF_SARBU	P83518 sarcophaga	619	4	5.0	19	2	Q9UKU5_HUMAN	Q9uku5 homo sapien	
547	4	5.0	11	Q6LC30_FASHE	Q6l330 fasciola he	620	4	5.0	19	2	Q8TAJ9_HUMAN	Q8taj9 homo sapien	
548	4	5.0	11	Q91UY9_9ZZZZ	Q91uy9 transposon	621	4	5.0	19	2	Q26321_LYMST	Q26321 lymnaea sta	
549	4	5.0	12	SOIS_BACSU	P80863 bacillus su	622	4	5.0	19	2	Q5SBS5_SCHJA	Q5sbes schistosoma	
550	4	5.0	12	Q5KSP0_SYMFO	Q5kep0 symlocarpu	623	4	5.0	19	2	Q9QV38_9MURI	Q9qv38 mus sp. erp	
551	4	5.0	12	Q6WPN0_ARATH	Q6wpn0 arabidopsis	624	4	5.0	19	2	Q9PRG2_SALSA	Q9prg2 salmo salar	
552	4	5.0	13	RS19_ASHYP	Q44592 ash yellowa	625	4	5.0	20	1	CHY3_PAGMA	P83547 pagrus majo	
553	4	5.0	13	Q50038_MYCLE	Q50038 mycobacteri	626	4	5.0	20	1	CRP_MUSCA	P19094 mustelus ca	
554	4	5.0	13	Q6RSM3_COXBU	Q6rsm3 coxiella bu	627	4	5.0	20	1	DAH51_LITDA	P84267 litoria dah	
555	4	5.0	13	Q6LCB1_RAT	Q6lcb1 rattus norv	628	4	5.0	20	1	NF03_NAEFO	P83998 naegleria f	
556	4	5.0	14	HLPI_HYLFU	P84292 hyla puncta	629	4	5.0	20	2	Q7SAL6_NEUCR	Q7sali6 neurospora	
557	4	5.0	14	MAST_VESMA	P04205 vespa manda	630	4	5.0	20	2	Q7M4Q0_HUMAN	Q7m4q0 homo sapien	
558	4	5.0	14	MAST_VBSOR	P17238 vespa orien	631	4	5.0	20	2	Q9UCA0_HUMAN	Q9uca0 homo sapien	
559	4	5.0	14	Q5BR70_SCHJA	Q5br70 schistosoma	632	4	5.0	20	2	Q96B47_HUMAN	Q96b47 homo sapien	
560	4	5.0	14	Q8HYM2_FELCA	Q8hym2 felis silve	633	4	5.0	20	2	Q7R7X6_PLAYO	Q7r7x6 plasmodium	
561	4	5.0	14	Q56ZE8_ARATH	Q56ze8 arabidopsis	634	4	5.0	20	2	Q4XKU0_PLACH	Q4xku0 plasmodium	
562	4	5.0	14	Q52638_ECOLI	Q52638 escherichia	635	4	5.0	20	2	Q4YCL5_PLABE	Q4ycl5 plasmodium	
563	4	5.0	14	Q52636_9ZZZZ	Q52636 plasmid r12	636	4	5.0	20	2	Q4Z2C1_PLABE	Q4z2c1 plasmodium	
564	4	5.0	14	Q661E1_BORGA	Q661e1 borrelia ga	637	4	5.0	20	2	Q9SMJ7_TARSY	Q9smj7 tarsius syr	
565	4	5.0	14	Q6LDY1_9ZZZZ	Q6ldy1 plasmid r38	638	4	5.0	20	2	Q9SMJ8_GALMO	Q9smj8 galago moho	
566	4	5.0	14	Q6LEH6_9ZZZZ	Q6leh6 plasmid r53	639	4	5.0	20	2	Q9SMK3_ATEBE	Q9smk3 ateles belz	
567	4	5.0	14	Q6LEH7_9ZZZZ	Q6leh7 plasmid r10	640	4	5.0	20	2	Q9SMK4_CHEMA	Q9smk4 cheirogaleu	
568	4	5.0	14	Q6LEH8_9ZZZZ	Q6leh8 plasmid col	641	4	5.0	20	2	Q9SMK5_VARVR	Q9smk5 varecia var	
569	4	5.0	14	Q6LEH9_9ZZZZ	Q6leh9 plasmid col	642	4	5.0	20	2	Q9SMK6_EULCO	Q9smk6 eulemur cor	
570	4	5.0	14	Q6LEH10_9ZZZZ	Q6leh10 plasmid col	643	4	5.0	20	2	Q5IGY2_9CAUD	Q5igy2 bacterioph	
571	4	5.0	14	Q56127_9CIRC	Q56127 porcine cir	644	4	5.0	20	2	Q9R4Y5_HELPI	Q9r4y5 helicobacte	
572	4	5.0	14	Q93202_9CIRC	Q93202 porcine cir	645	4	5.0	20	2	Q9PSI4_ONCKI	Q9psi4 oncorhynch	
573	4	5.0	14	Q77NR3_9CIRC	Q77nr3 porcine cir	646	4	5.0	21	1	DAH52_LITDA	P84268 litoria dah	
574	4	5.0	14	Q77RC0_9CIRC	Q77rc0 porcine cir	647	4	5.0	21	1	MCPT3_MOUSE	P21843 mus musculu	
575	4	5.0	14	Q77RM6_9CIRC	Q77rm6 porcine cir	648	4	5.0	21	2	Q9UWH7_9CREN	Q9uwh7 sulfolobus	
576	4	5.0	14	Q77S02_9CIRC	Q77s02 porcine cir	649	4	5.0	21	2	Q7JPS8_LYMST	Q7jps8 lymnaea sta	
577	4	5.0	14	Q77S09_9CIRC	Q77s09 porcine cir	650	4	5.0	21	2	Q7R9Y0_PLAYO	Q7r9y0 plasmodium	
578	4	5.0	14	Q77S13_9CIRC	Q77s13 porcine cir	651	4	5.0	21	2	Q4XLR2_PLACH	Q4xlr2 plasmodium	
579	4	5.0	15	Q7SBM4_NEUCR	Q7sbm4 neurospora	652	4	5.0	21	2	Q4YCP3_PLABE	Q4ycp3 plasmodium	
580	4	5.0	15	Q9UR90_YEAST	Q9ur90 saccharomyc	653	4	5.0	21	2	Q8HYM1_FELCA	Q8hym1 felis silve	
581	4	5.0	15	Q5K6Q7_CRAGI	Q5k6q7 crassostrea	654	4	5.0	21	2	Q8N4X2_HUMAN	Q8n4x2 homo sapien	
582	4	5.0	15	Q6LDF5_TRICO	Q6ldf5 trichostron	655	4	5.0	22	2	Q9BZM3_HUMAN	Q9bzm3 homo sapien	
583	4	5.0	15	Q7M319_9META	Q7m319 macropus ep	656	4	5.0	22	2	Q5BY01_SCHJA	Q5by01 schistosoma	
584	4	5.0	15	Q52304_9ZZZZ	Q52304 plasmid r1-	657	4	5.0	22	2	Q9NFG2_PLAFA	Q9nfg2 plasmodium	
585	4	5.0	15	Q80X05_MESAU	Q80x05 mesocricetu	658	4	5.0	22	2	Q7RLB6_PLAYO	Q7rlb6 plasmodium	
586	4	5.0	15	Q79ED5_9ZZZZ	Q79ed5 plasmid r12	659	4	5.0	22	2	Q7RMV4_PLAYO	Q7rmv4 plasmodium	
587	4	5.0	15	Q9PTM6_POEGU	Q9ptm6 poephila gu	660	4	5.0	22	2	Q4XI70_PLACH	Q4xi70 plasmodium	
588	4	5.0	16	Q5B8M1_EMENI	Q5b8m1 aspergillus	661	4	5.0	22	2	Q4XS26_PLACH	Q4xs26 plasmodium	
589	4	5.0	16	Q9URB8_YEAST	Q9urb8 saccharomyc	662	4	5.0	22	2	Q4YG66_PLABE	Q4yg66 plasmodium	
590	4	5.0	16	Q9TRA2_PIG	Q9tra2 sus scrofa	663	4	5.0	22	2	P82162_SPIOL	P82162 spinacia ol	
591	4	5.0	16	P82161_SPIOL	P82161 spinacia ol	664	4	5.0	22	2	Q34195_EHRII	Q34195 ehrlichia r	
592	4	5.0	16	Q6RSJ3_COXBU	Q6rsj3 coxiella bu	665	4	5.0	22	2	Q9ZG44_CHLTR	Q9zg44 chlamydia t	
593	4	5.0	16	Q9R5K1_PSEPU	Q9r5k1 pseudomonas	666	4	5.0	22	2	Q9QV15_9MURI	Q9qv15 mus sp. syn	
594	4	5.0	16	Q6LBX8_PSEAE	Q6lxb8 pseudomonas	667	4	5.0	22	2	Q9QM14_9MURI	Q9qm14 mus sp. p	
595	4	5.0	16	Q9PRY2_PETMA	Q9pry2 petromyzon	668	4	5.0	23	1	ACHG_ELEEL	P09692 electrophor	
596	4	5.0	17	UN15_CLOPA	P81354 clostridium	669	4	5.0	23	1	AUR41_LITAU	P82397 litoria aur	
597	4	5.0	17	Q9GZT7_HUMAN	Q9gz77 homo sapien	670	4	5.0	23	1	AUR42_LITAU	P69025 litoria aur	
598	4	5.0	17	Q9UD18_HUMAN	Q9ud18 homo sapien	671	4	5.0	23	1	PS3_PSEPD	P69024 litoria ran	
599	4	5.0	17	Q6LER4_HUMAN	Q6ler4 homo sapien	672	4	5.0	23	1	PS4_PSEPD	P83190 pseudis par	
600	4	5.0	17	P90402_9HIV1	P90402 human immun	673	4	5.0	23	1	Q5DVF3_9CREN	Q5dvf3 sulfolobus	
601	4	5.0	17	Q8UT86_9HIV1	Q8ut86 human immun	674	4	5.0	23	1	Q8N5P5_HUMAN	Q8n5p5 homo sapien	
602	4	5.0	17	Q90709_9HIV1	Q90709 human immun	675	4	5.0	23	2	Q7RJKO_PLAYO	Q7rjko plasmodium	
603	4	5.0	18	Q69Y10_HUMAN	Q69y10 homo sapien	676	4	5.0	23	2	Q7RLB8_PLAYO	Q7rlb8 plasmodium	
604	4	5.0	18	Q9UBT8_HUMAN	Q9ubt8 homo sapien	677	4	5.0	23	2	Q4XNB0_PLACH	Q4xnb0 plasmodium	
605	4	5.0	18	Q6RSD8_9DIPT	Q6rsd8 chironomus	678	4	5.0	23	2	Q4XY15_PLACH	Q4xy15 plasmodium	
606	4	5.0	18	Q4TZV7_PAPHA	Q4tzv7 papio hamad	679	4	5.0	23	2	Q4Y655_PLACH	Q4y655 plasmodium	
607	4	5.0	18	Q9X3N3_NEIME	Q9x3n3 neisseria m	680	4	5.0	23	2	Q4Y6B6_PLACH	Q4y6b6 plasmodium	
608	4	5.0	18	P95811_STRPY	P95811 streptococ	681	4	5.0	23	2	Q4YGG2_PLABE	Q4ygg2 plasmodium	
609	4	5.0	18	P97166_STRPY	P97166 streptococ	682	4	5.0	23	2	Q4YIN7_PLABE	Q4yin7 plasmodium	
610	4	5.0	18	Q81CS8_BACCR	Q81cs8 bacillus ce	683	4	5.0	23	2	Q9S8D9_MAIZE	Q9s8d9 zea mays m	
611	4	5.0	18	Q9DSS9_ADE04	Q9ds9 human adeno	684	4	5.0	23	2	Q9R410_BORPE	Q9r410 bordetella	
612	4	5.0	19	H170_RAT	P21794 rattus norv	685	4	5.0	23	2	Q9R5T0_TREDE	Q9r5t0 treponema d	
613	4	5.0	19	NF37_NAEFO	P83727 naegleria f	686	4	5.0	23	2	Q43887_ANAAZ	Q43887 anabaena az	
614	4	5.0	19	UKA1_HUMAN	P31940 homo sapien	687	4	5.0	23	2	Q6LXK6_9PICO	Q6ldx6 human rhino	
615	4	5.0	19	Q9UWJ8_ARCFU	Q9uwj8 archaeglob	688	4	5.0	23	2			

689	4	5.0	24	1	CT31_LITCI	P81851	litoria cit	762	4	5.0	27	2	Q9Q193_9HEPC	Q9qi93	hepatitis c
690	4	5.0	24	1	IR31_HAEIN	P35756	haemophilus	763	4	5.0	27	2	Q9Q194_9HEPC	Q9qi94	hepatitis c
691	4	5.0	24	2	Q6QNX8_9CNID	Q6qnx8	anthopleura	764	4	5.0	27	2	Q9Q195_9HEPC	Q9qi95	hepatitis c
692	4	5.0	24	2	Q4X3I5_PLACH	Q4x3i5	plasmodium	765	4	5.0	27	2	Q9Q196_9HEPC	Q9qi96	hepatitis c
693	4	5.0	24	2	Q4XC56_PLACH	Q4xc56	plasmodium	766	4	5.0	27	2	Q9Q197_9HEPC	Q9qi97	hepatitis c
694	4	5.0	24	2	Q4YMI4_PLABE	Q4ymi4	plasmodium	767	4	5.0	27	2	Q9Q198_9HEPC	Q9qi98	hepatitis c
695	4	5.0	24	2	Q4THA3_TETNG	Q4tha3	tetraodon n	768	4	5.0	27	2	Q9Q199_9HEPC	Q9qi99	hepatitis c
696	4	5.0	24	1	CHY1_PAGMA	P83545	pagrus major	769	4	5.0	27	2	Q9Q200_9HEPC	Q9qiao	hepatitis c
697	4	5.0	25	1	CHY2_PAGMA	P83546	pagrus major	770	4	5.0	27	2	Q9Q201_9HEPC	Q9qiao	hepatitis c
698	4	5.0	25	2	Q9UWG3_SULSO	Q9uwg3	sulfolobus	771	4	5.0	27	2	Q9Q202_9HEPC	Q9qiao	hepatitis c
699	4	5.0	25	2	Q9BQJ6_HUMAN	Q9bqj6	homo sapien	772	4	5.0	27	2	Q9Q203_9HEPC	Q9qiao	hepatitis c
700	4	5.0	25	2	Q5C4Z9_SCHJA	Q5c4z9	schistosoma	773	4	5.0	27	2	Q9Q204_9HEPC	Q9qiao	hepatitis c
701	4	5.0	25	2	Q9BM60_9BILA	Q9bm60	sagitta sp.	774	4	5.0	27	2	Q9Q205_9HEPC	Q9qiao	hepatitis c
702	4	5.0	25	2	Q4XK95_PLACH	Q4xk95	plasmodium	775	4	5.0	27	2	Q9Q206_9HEPC	Q9qiao	hepatitis c
703	4	5.0	25	2	Q7M3G0_BOVIN	Q7m3g0	bos taurus	776	4	5.0	27	2	Q9Q207_9HEPC	Q9qiao	hepatitis c
704	4	5.0	25	2	Q9LSW1_ARATH	Q9lsw1	arabidopsis	777	4	5.0	27	2	Q9Q208_9HEPC	Q9qiao	hepatitis c
705	4	5.0	25	2	Q9K2K4_STAAU	Q9k2k4	staphylococ	778	4	5.0	27	2	Q9Q209_9HEPC	Q9qiao	hepatitis c
706	4	5.0	25	2	Q9X9U4_STRCO	Q9x9u4	streptomyce	779	4	5.0	27	2	Q9Q210_9HEPC	Q9qiao	hepatitis c
707	4	5.0	25	2	Q4LA85_STAHI	Q4la85	staphylococ	780	4	5.0	27	2	Q9Q211_9HEPC	Q9qiao	hepatitis c
708	4	5.0	25	2	Q8RVE7_MESAU	Q8rve7	mesocricetu	781	4	5.0	27	2	Q9Q212_9HEPC	Q9qiao	hepatitis c
709	4	5.0	25	2	Q9QUZ2_9MURI	Q9quz2	mus sp. . 5	782	4	5.0	27	2	Q9Q213_9HEPC	Q9qiao	hepatitis c
710	4	5.0	25	2	Q69474_HHV1	Q69474	human herpe	783	4	5.0	27	2	Q9Q214_9HEPC	Q9qiao	hepatitis c
711	4	5.0	25	2	Q9PSB0_XENBO	Q9psb0	xenopus bor	784	4	5.0	27	2	Q9Q215_9HEPC	Q9qiao	hepatitis c
712	4	5.0	25	2	Q8Q30_9HIV1	Q8q30	human immun	785	4	5.0	27	2	Q9Q216_9HEPC	Q9qiao	hepatitis c
713	4	5.0	25	2	Q8Q37_9HIV1	Q8q37	human immun	786	4	5.0	27	2	Q9Q217_9HEPC	Q9qiao	hepatitis c
714	4	5.0	25	2	Q8Q68_9HIV1	Q8q68	human immun	787	4	5.0	27	2	Q9Q218_9HEPC	Q9qiao	hepatitis c
715	4	5.0	25	2	Q8Q98_9HIV1	Q8q98	human immun	788	4	5.0	27	2	Q9Q219_9HEPC	Q9qiao	hepatitis c
716	4	5.0	25	2	Q8QAS_9HIV1	Q8qas	human immun	789	4	5.0	27	2	Q9Q220_9HEPC	Q9qiao	hepatitis c
717	4	5.0	25	2	Q9WRF2_9HIV1	Q9wrf2	human immun	790	4	5.0	27	2	Q9Q221_9HEPC	Q9qiao	hepatitis c
718	4	5.0	26	1	ARALB_ARABL	P83573	axalia elat	791	4	5.0	27	2	Q9Q222_9HEPC	Q9qiao	hepatitis c
719	4	5.0	26	1	STP_BFLZ3	P62766	bacterioph	792	4	5.0	27	2	Q9Q223_9HEPC	Q9qiao	hepatitis c
720	4	5.0	26	1	STP_BFLZ5	P62767	bacterioph	793	4	5.0	27	2	Q9Q224_9HEPC	Q9qiao	hepatitis c
721	4	5.0	26	1	STP_BFLZ4	P62765	bacterioph	794	4	5.0	27	2	Q9Q225_9HEPC	Q9qiao	hepatitis c
722	4	5.0	26	1	Y507_HELPF	P64662	helicobacte	795	4	5.0	27	2	Q9Q226_9HEPC	Q9qiao	hepatitis c
723	4	5.0	26	1	Y560_HELPF	P64661	helicobacte	796	4	5.0	27	2	Q9Q227_9HEPC	Q9qiao	hepatitis c
724	4	5.0	26	1	YFHA_KLEOX	P21710	klebsiella	797	4	5.0	27	2	Q9Q228_9HEPC	Q9qiao	hepatitis c
725	4	5.0	26	2	Q9UMG7_SULSO	Q9umg7	sulfolobus	798	4	5.0	27	2	Q9Q229_9HEPC	Q9qiao	hepatitis c
726	4	5.0	26	2	Q50833_METVA	Q50835	methanococc	799	4	5.0	27	2	Q9Q230_9HEPC	Q9qiao	hepatitis c
727	4	5.0	26	2	Q468K4_DROMR	Q468k4	drosophila	800	4	5.0	27	2	Q9Q231_9HEPC	Q9qiao	hepatitis c
728	4	5.0	26	2	Q4XE15_PLACH	Q4xe15	plasmodium	801	4	5.0	27	2	Q9Q232_9HEPC	Q9qiao	hepatitis c
729	4	5.0	26	2	Q4XQ31_PLACH	Q4xq31	plasmodium	802	4	5.0	27	2	Q9Q233_9HEPC	Q9qiao	hepatitis c
730	4	5.0	26	2	Q4YE51_PLABE	Q4ye51	plasmodium	803	4	5.0	27	2	Q9Q234_9HEPC	Q9qiao	hepatitis c
731	4	5.0	26	2	Q8HYW8_BOVIN	Q8hyw8	bos taurus	804	4	5.0	27	2	Q9Q235_9HEPC	Q9qiao	hepatitis c
732	4	5.0	26	2	Q38084_9CAUD	Q38084	bacterioph	805	4	5.0	27	2	Q9Q236_9HEPC	Q9qiao	hepatitis c
733	4	5.0	26	2	Q56289_THIFE	Q56289	thiobacillu	806	4	5.0	27	2	Q9Q237_9HEPC	Q9qiao	hepatitis c
734	4	5.0	26	2	Q6V7G4_VIBCH	Q6v7g4	vibrio chol	807	4	5.0	27	2	Q9Q238_9HEPC	Q9qiao	hepatitis c
735	4	5.0	26	2	Q8VVF8_STRSU	Q8vvf8	streptococc	808	4	5.0	27	2	Q9Q239_9HEPC	Q9qiao	hepatitis c
736	4	5.0	26	2	Q64FW9_9VIRU	Q64fw9	cauliflowe	809	4	5.0	27	2	Q9Q240_9HEPC	Q9qiao	hepatitis c
737	4	5.0	26	2	Q13159_CHICK	Q13159	gallus gall	810	4	5.0	27	2	Q9Q241_9HEPC	Q9qiao	hepatitis c
738	4	5.0	26	2	Q8UVE1_CHICK	Q8uve1	gallus gall	811	4	5.0	27	2	Q9Q242_9HEPC	Q9qiao	hepatitis c
739	4	5.0	26	2	Q9PSB3_XENLA	Q9psb3	xenopus lae	812	4	5.0	27	2	Q9Q243_9HEPC	Q9qiao	hepatitis c
740	4	5.0	26	2	Q4PU49_9HIV1	Q4pu49	human immun	813	4	5.0	27	2	Q9Q244_9HEPC	Q9qiao	hepatitis c
741	4	5.0	26	2	Q4PU54_9HIV1	Q4pu54	human immun	814	4	5.0	27	2	Q9Q245_9HEPC	Q9qiao	hepatitis c
742	4	5.0	26	2	Q4PU59_9HIV1	Q4pu59	human immun	815	4	5.0	27	2	Q9Q246_9HEPC	Q9qiao	hepatitis c
743	4	5.0	27	1	RN2CB_FANCL	P82879	rana clamit	816	4	5.0	27	2	Q9Q247_9HEPC	Q9qiao	hepatitis c
744	4	5.0	27	2	Q8MTK3_CHRQI	Q8mtk4	chrysosora q	817	4	5.0	27	2	Q9Q248_9HEPC	Q9qiao	hepatitis c
745	4	5.0	27	2	Q4Y2T0_PLACH	Q4y2t0	plasmodium	818	4	5.0	27	2	Q9Q249_9HEPC	Q9qiao	hepatitis c
746	4	5.0	27	2	Q4YE00_PLABE	Q4ye00	plasmodium	819	4	5.0	27	2	Q9Q250_9HEPC	Q9qiao	hepatitis c
747	4	5.0	27	2	Q4YVK2_PLABE	Q4yvk2	plasmodium	820	4	5.0	27	2	Q9Q251_9HEPC	Q9qiao	hepatitis c
748	4	5.0	27	2	Q46119_CAMJE	Q46119	campylobact	821	4	5.0	27	2	Q9Q252_9HEPC	Q9qiao	hepatitis c
749	4	5.0	27	2	Q4NGE1_BACCE	Q4nge1	bacillus ce	822	4	5.0	27	2	Q9Q253_9HEPC	Q9qiao	hepatitis c
750	4	5.0	27	2	Q9QVS1_9MURI	Q9qvs1	mus sp. . 1	823	4	5.0	27	2	Q9Q254_9HEPC	Q9qiao	hepatitis c
751	4	5.0	27	2	O57153_9BETA	O57153	human herpe	824	4	5.0	27	2	Q9Q255_9HEPC	Q9qiao	hepatitis c
752	4	5.0	27	2	O57154_9BETA	O57154	human herpe	825	4	5.0	27	2	Q9Q256_9HEPC	Q9qiao	hepatitis c
753	4	5.0	27	2	Q6SXX2_9HEPC	Q6sxx2	hepatitis c	826	4	5.0	27	2	Q9Q257_9HEPC	Q9qiao	hepatitis c
754	4	5.0	27	2	Q9QHC2_9HEPC	Q9qhc2	hepatitis c	827	4	5.0	27	2	Q9Q258_9HEPC	Q9qiao	hepatitis c
755	4	5.0	27	2	Q9QHC5_9HEPC	Q9qhc5	hepatitis c	828	4	5.0	27	2	Q9Q259_9HEPC	Q9qiao	hepatitis c
756	4	5.0	27	2	Q9QHC9_9HEPC	Q9qhc9	hepatitis c	829	4	5.0	27	2	Q9Q260_9HEPC	Q9qiao	hepatitis c
757	4	5.0	27	2	Q9QHD4_9HEPC	Q9qhd4	hepatitis c	830	4	5.0	27	2	Q9Q261_9HEPC	Q9qiao	hepatitis c
758	4	5.0	27	2	Q9Q146_9HEPC	Q9q146	hepatitis c	831	4	5.0	27	2	Q9Q262_9HEPC	Q9qiao	hepatitis c
759	4	5.0	27	2	Q9Q191_9HEPC	Q9q191	hepatitis c	832	4	5.0	27	2	Q9Q263_9HEPC	Q9qiao	hepatitis c
760	4	5.0	27	2	Q9Q192_9HEPC	Q9q192	hepatitis c	833	4	5.0	27	2	Q9Q264_9HEPC	Q9qiao	hepatitis c
761	4	5.0	27	2	Q9Q193_9HEPC	Q9q193	hepatitis c	834	4	5.0	27	2	Q9Q265_9HEPC	Q9qiao	hepatitis c

835	4	5.0	27	2	Q4TX84_9HEPC	Q4tx84 hepatitis c	908	4	5.0	30	2	Q7M241_ORYSA	Q7m241 oryza sativ
836	4	5.0	27	2	Q4TX85_9HEPC	Q4tx85 hepatitis c	909	4	5.0	30	2	Q8GP81_STRTR	Q8gp81 streptococc
837	4	5.0	27	2	Q4TX86_9HEPC	Q4tx86 hepatitis c	910	4	5.0	30	2	Q4LB43_ECOLI	Q4lb43 escherichia
838	4	5.0	27	2	Q4TX88_9HEPC	Q4tx88 hepatitis c	911	4	5.0	30	2	Q4MUK5_BACCE	Q4muk5 bacillus ce
839	4	5.0	27	2	Q4TX90_9HEPC	Q4tx90 hepatitis c	912	4	5.0	30	2	Q4HI47_CAWCO	Q4hi47 campylobact
840	4	5.0	27	2	Q4TX93_9HEPC	Q4tx93 hepatitis c	913	4	5.0	30	2	Q4JVV9_CORJK	Q4jvv9 corynebacte
841	4	5.0	27	2	Q4TX95_9HEPC	Q4tx95 hepatitis c	914	4	5.0	30	2	Q7MVC5_PORGI	Q7mvc5 porphyromon
842	4	5.0	27	2	Q4TX98_9HEPC	Q4tx98 hepatitis c	915	4	5.0	30	2	Q8EJP3_SHEON	Q8ejp3 shewanella
843	4	5.0	27	2	Q4TX99_9HEPC	Q4tx99 hepatitis c	916	4	5.0	30	2	Q9PPG5_CAWJE	Q9ppg5 campylobact
844	4	5.0	27	2	Q4TXA1_9HEPC	Q4txa1 hepatitis c	917	4	5.0	30	2	Q8JB13_CXBU	Q8jb13 coxiella bu
845	4	5.0	27	2	Q4TXA2_9HEPC	Q4txa2 hepatitis c	918	4	5.0	30	2	Q8HIF8_STAAC	Q8hif8 staphylococ
846	4	5.0	27	2	Q71608_CHICK	Q73608 gallus gall	919	4	5.0	30	2	Q981L4_RHILO	Q981l4 rhizobium l
847	4	5.0	27	2	Q4SQF1_TETNG	Q4sqf1 tetraodon n	920	4	5.0	30	2	Q9JXT7_NEIMB	Q9jxt7 neisseria m
848	4	5.0	27	2	LECA_TRIHO	P36230 iris hollan	921	4	5.0	30	2	Q7M031_RAT	Q7m031 rattus norv
849	4	5.0	28	1	ORND_PLAOR	P25513 placobdella	922	4	5.0	30	2	Q88549_MSAU	Q88549 mesocricetu
850	4	5.0	28	2	Q26318_LYMST	Q26318 lymnaea sta	923	4	5.0	30	2	Q96630_ADEB2	Q96630 bovine aden
851	4	5.0	28	2	Q26319_LYMST	Q26319 lymnaea sta	924	4	5.0	30	2	Q8QFV5_LAMFL	Q8qfv5 lampetra fl
852	4	5.0	28	2	Q27356_LYMST	Q27356 lymnaea sta	925	4	5.0	31	1	CTRP_PENMO	Q35002 penaeus mon
853	4	5.0	28	2	Q5C2P0_SCHJA	Q4xv0 schistosoma	926	4	5.0	31	1	PETL_PORPU	P51221 porphyra pu
854	4	5.0	28	2	Q4XV0_PLACH	Q4xv0 schistosoma	927	4	5.0	31	2	Q9USG3_SCHPO	Q9usg3 schizosacch
855	4	5.0	28	2	Q4XV8_PLACH	Q4xv8 plasmodium	928	4	5.0	31	2	Q9BZZ6_HUMAN	Q9bzz6 homo sapien
856	4	5.0	28	2	Q4YC14_PLABE	Q4yc14 plasmodium	929	4	5.0	31	2	Q5BZR3_SCHJA	Q5bzz3 schistosoma
857	4	5.0	28	2	Q4YXA7_PLABE	Q4yya7 plasmodium	930	4	5.0	31	2	Q7RPU7_PLAYO	Q7rpu7 plasmodium
858	4	5.0	28	2	Q7SRX0_IPONI	Q75rx0 ipomoea nil	931	4	5.0	31	2	QAXGX2_PLACH	Q4xgx2 plasmodium
859	4	5.0	28	2	Q7APD1_ORYSA	Q7xpd1 oryza sativ	932	4	5.0	31	2	Q53411_BACSU	Q53411 bacillus su
860	4	5.0	28	2	Q9XK42_9STRA	Q9xk42 aureococcus	933	4	5.0	31	2	Q57CN6_BRUAB	Q57cn6 brucella ab
861	4	5.0	28	2	Q4W565_ECOLI	Q4w565 escherichia	934	4	5.0	31	2	Q4L3L7_STAHL	Q4l3l7 staphylococ
862	4	5.0	28	2	Q9R5E6_THEAQ	Q9r5e6 thermus aqu	935	4	5.0	31	2	Q8DTU2_STRMU	Q8dtu2 streptococc
863	4	5.0	28	2	Q9P1E6_MOUSE	Q9p19 mus musculu	936	4	5.0	31	2	Q9KZT7_VIBCH	Q9kzt7 vibrio chol
864	4	5.0	28	2	Q8OKG6_9RHAB	Q8okg6 rabies viru	937	4	5.0	31	2	Q6MK47_BDEBA	Q6mk47 bdellovibri
865	4	5.0	28	2	Q8OKK0_9RHAB	Q8okk0 rabies viru	938	4	5.0	31	2	Q87IQ9_VIBPA	Q87iq9 vibrio para
866	4	5.0	28	2	Q9QCD4_ADE02	Q9qcd4 human adeno	939	4	5.0	31	2	Q8G058_BRUSU	Q8g058 brucella su
867	4	5.0	28	2	Q9QCD5_9ADEN	Q9qcd5 human adeno	940	4	5.0	31	2	Q9CMC7_9MURI	Q9cmc7 rattus sp.
868	4	5.0	28	2	Q9QCD6_9ADEN	Q9qcd6 human adeno	941	4	5.0	31	2	Q99KD9_MOUSE	Q99kd9 mus musculu
869	4	5.0	28	2	Q9QCD7_9ADEN	Q9qcd7 human adeno	942	4	5.0	31	2	Q84108_IANT6	Q84108 influenza a
870	4	5.0	28	2	Q9QCD8_ADE08	Q9qcd8 human adeno	943	4	5.0	31	2	Q91AA4_CHICK	Q91aa4 gallus gall
871	4	5.0	28	2	Q9QD08_9RHAB	Q9qcd8 rabies viru	944	4	5.0	31	2	Q85512_9RETR	Q85512 avian eryth
872	4	5.0	28	2	Q9QC15_9HEPC	Q9qc15 hepatitis c	945	4	5.0	32	2	Q7M553_HALSA	Q7m553 haloarcula
873	4	5.0	28	2	Q9YX86_9VIRU	Q9yx86 acute bee p	946	4	5.0	32	2	Q5UWY3_HALMA	Q5uwy3 haloarcula
874	4	5.0	29	1	NUO1_SOLTU	P80267 solanum tub	947	4	5.0	32	2	Q8TGT3_YEAST	Q8tgt3 saccharomyc
875	4	5.0	29	1	PSBI_SYNVU	P12240 synechococc	948	4	5.0	32	2	Q96S24_HUMAN	Q96s24 homo sapien
876	4	5.0	29	1	Q9HDQ3_CANRU	Q9hdq3 candida rug	949	4	5.0	32	2	Q5BRP2_SCHJA	Q5brp2 schistosoma
877	4	5.0	29	2	Q69YR8_HUMAN	Q69yr8 homo sapien	950	4	5.0	32	2	Q4X4Q6_PLACH	Q4x4q6 plasmodium
878	4	5.0	29	2	Q53SD1_HUMAN	Q53sd1 homo sapien	951	4	5.0	32	2	Q4XF05_PLACH	Q4xf05 plasmodium
879	4	5.0	29	2	Q4X6D1_PLACH	Q4x6d1 plasmodium	952	4	5.0	32	2	Q4XHI2_PLACH	Q4xhi2 plasmodium
880	4	5.0	29	2	Q4YFJ4_PLABE	Q4yfj4 plasmodium	953	4	5.0	32	2	Q4Y2Q0_PLACH	Q4y2q0 plasmodium
881	4	5.0	29	2	Q4YJ20_PLABE	Q4yj20 plasmodium	954	4	5.0	32	2	Q4YGI2_PLABE	Q4ygi2 plasmodium
882	4	5.0	29	2	Q4YU46_PLABE	Q4yu46 plasmodium	955	4	5.0	32	2	Q4YUS2_PLABE	Q4yus2 plasmodium
883	4	5.0	29	2	Q7OPH1_PIG	Q7oph1 sus scrofa	956	4	5.0	32	2	Q6J9M8_XENNE	Q6j9m8 xenorhabdus
884	4	5.0	29	2	Q9R658_RHOCA	Q9r658 rhodobacter	957	4	5.0	32	2	Q7M016_CIOSY	Q7m016 clostridium
885	4	5.0	29	2	Q9IQJ6_9HIV1	Q9iqj6 human immun	958	4	5.0	32	2	Q7M018_9FIRM	Q7m018 veillonella
886	4	5.0	30	1	2ENR_CLOTY	P11887 clostridium	959	4	5.0	32	2	Q9K261_CHLPN	Q9k261 chlamydia p
887	4	5.0	30	1	CX2A_CONBE	P58625 conus betul	960	4	5.0	32	2	Q9R5J6_MYCTU	Q9r5j6 mycobacteri
888	4	5.0	30	1	PSAM_MESVI	P82037 uperoleia i	961	4	5.0	32	2	Q57MB8_SALCH	Q57mb8 salmonella
889	4	5.0	30	1	UPB61_UPSIN	P82037 uperoleia i	962	4	5.0	32	2	Q4MFR9_BACCE	Q4mfr9 bacillus ce
890	4	5.0	30	1	UPB62_UPSIN	P82037 uperoleia i	963	4	5.0	32	2	Q4MFR1_BACCE	Q4mfr1 bacillus ce
891	4	5.0	30	2	P78460_HUMAN	P78460 homo sapien	964	4	5.0	32	2	Q4HMX1_CAMLA	Q4hmx1 campylobact
892	4	5.0	30	2	Q26320_LYMST	Q26320 lymnaea sta	965	4	5.0	32	2	Q4MPQ8_BACCE	Q4mpq8 bacillus ce
893	4	5.0	30	2	Q5BR16_SCHJA	Q5br16 schistosoma	966	4	5.0	32	2	Q5PE29_SALPA	Q5pe29 salmonella
894	4	5.0	30	2	Q5C004_SCHJA	Q5c004 schistosoma	967	4	5.0	32	2	Q65WI3_MANSM	Q65wi3 manheimia
895	4	5.0	30	2	Q5CAU1_SCHJA	Q5cau1 schistosoma	968	4	5.0	32	2	Q73EA3_BACCI	Q73ea3 bacillus ce
896	4	5.0	30	2	Q7R4B5_GIALA	Q7r4b5 giardia lam	969	4	5.0	32	2	Q73FJ9_BACCI	Q73fj9 bacillus ce
897	4	5.0	30	2	Q8IHP0_PLAF7	Q8ihp0 plasmodium	970	4	5.0	32	2	Q8Z582_SALTI	Q8z582 salmonella
898	4	5.0	30	2	Q7RF34_PLAYO	Q7rf34 plasmodium	971	4	5.0	32	2	Q97NT4_STRPN	Q97nt4 streptococc
899	4	5.0	30	2	Q7RIME_PLAYO	Q7rim6 plasmodium	972	4	5.0	32	2	Q81R94_BACAN	Q81r94 bacillus an
900	4	5.0	30	2	Q4XE18_PLACH	Q4xe18 plasmodium	973	4	5.0	32	2	Q83CC7_COXBU	Q83cc7 coxiella bu
901	4	5.0	30	2	Q4XJP6_PLACH	Q4xjp6 plasmodium	974	4	5.0	32	2	Q7VIX4_HELHP	Q7vix4 helicobacte
902	4	5.0	30	2	Q4XVC7_PLACH	Q4xvc7 plasmodium	975	4	5.0	32	2	Q5HQO6_STAEO	Q5hqo6 staphylococ
903	4	5.0	30	2	Q4XXW6_PLACH	Q4xxw6 plasmodium	976	4	5.0	32	2	Q81JD8_BACAN	Q81jd8 bacillus an
904	4	5.0	30	2	Q4Y299_PLACH	Q4y299 plasmodium	977	4	5.0	32	2	Q73F54_BACCI	Q73f54 bacillus ce
905	4	5.0	30	2	Q4Y489_PLACH	Q4y489 plasmodium	978	4	5.0	32	2	Q80WZ8_9MURI	Q80wz8 mus sp. met
906	4	5.0	30	2	Q4YJY1_PLABE	Q4yjy1 plasmodium	979	4	5.0	32	2	Q9QWB2_9MURI	Q9qwb2 rattus sp.
907	4	5.0	30	2	Q5ULW3_9CAUD	Q5ulw3 lactobacill	980	4	5.0	32	2	Q9IWC2_9PAPI	Q9iwc2 phocoena sp

981 4 5.0 32 2 Q502D3 BRARE
 982 4 5.0 32 2 Q4REX4 TETNG
 983 4 5.0 32 2 Q4SUK1 TETNG
 984 4 5.0 33 2 Q13375 HUMAN
 985 4 5.0 33 2 Q9UDT0 HUMAN
 986 4 5.0 33 2 Q4G105 HUMAN
 987 4 5.0 33 2 Q9NGN0 STRPU
 988 4 5.0 33 2 Q4XEP6 PLACH
 989 4 5.0 33 2 Q4XTB8 PLACH
 990 4 5.0 33 2 Q9TSW9 CANFA
 991 4 5.0 33 2 Q29066 PIG
 992 4 5.0 33 2 Q8H9P9 9CAUD
 993 4 5.0 33 2 Q5XZ94 BORGA
 994 4 5.0 33 2 Q711Z4 LACDL
 995 4 5.0 33 2 Q65SM8 MANSM
 996 4 5.0 33 2 Q6MNH5 BDEBA
 997 4 5.0 33 2 Q88AE8 PSESM
 998 4 5.0 33 2 Q9Z298 RAT
 999 4 5.0 33 2 Q7M0E6 RAT
 1000 4 5.0 33 2 Q6EAW6 9CALI

ALIGNMENTS

RESULT 1
 Q4XUQ5 PLACH PRELIMINARY; PRT; 29 AA.

AC Q4XUQ5;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC105993.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.I., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01003007; CAH79356.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 29 AA; 3541 MW; A386F2C2D29442CC CRC64;

Query Match 8.8%; Score 7; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 YNKLKTK 23
 |||||
 Db 2 YNKLKTK 8

RESULT 2
 PLAS_MICAE STANDARD; PRT; 15 AA.
 ID PLAS_MICAE
 AC P10625;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Plastocyanin (Fragment).

GN Name=petE;
 OS Microcystis aeruginosa.
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
 OX NCBI_TaxID=1126;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=89134784; PubMed=2537099;
 RA Tan S., Ho K.-K.;
 RT "Purification of an acidic plastocyanin from Microcystis aeruginosa.";
 RL Biochim. Biophys. Acta 973:111-117(1989).
 CC -!- FUNCTION: Participates in electron transfer between P700 and the
 CC cytochrome b6-f complex in photosystem I.
 CC -!- SIMILARITY: Contains 1 plastocyanin-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR PIR; S03353; S03353.
 DR HAMAP; MF 00566; -; 1.
 DR InterPro; IPR000923; BlueCu 1.
 DR PROSITE; PS00196; COPPER_BLUE; PARTIAL.
 KW Copper; Direct protein sequencing; Electron transport; Metal-binding;
 KW Transport.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1555 MW; 32B6D4662F44F969 CRC64;

Query Match 7.5%; Score 6; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EFTTVK 67
 |||||
 Db 1 EFTTVK 6

RESULT 3

Q93Y77 ATRBE PRELIMINARY; PRT; 37 AA.
 ID Q93Y77 ATRBE PRELIMINARY; PRT; 37 AA.
 AC Q93Y77;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Putative multicystatin (Fragment).
 OS Atropa belladonna (Belladonna) (Deadly nightshade).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Atropa.
 OX NCBI_TaxID=33113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nouar B.;
 RL Thesis (2001), Department of Plant Biotechnology, Universite Libre de
 RL Bruxelles, Brussels, Belgium.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Nouar B., Baucher M., Jaziri M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309374; CAC40744.1; -; mRNA.
 DR HSRF; P09229; IEOK.
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
 DR InterPro; IPR003243; Prot_inh_I25A_B.
 DR ProDom; PD001231; Prot_inh_I25A_B; 1.
 FT NON TER 1
 SQ SEQUENCE 37 AA; 4403 MW; 37285565D81A4284 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEF 12


```

Db          23 KEVQEF 28
|||||
RESULT 4
O53412_BACSU
ID Q53412_BACSU PRELIMINARY; PRT; 42 AA.
AC Q53412;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Clone pS7 product protein (Fragment).
GN Name=clone pS7 product;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94271615; PubMed=7545933;
RA Luo J., Li W., Zhang T., Chai S., Wang H.;
RT "Cloning and sequencing of promoter and signal sequence coding regions
from Bacillus subtilis.";
RL I Chuan Hsueh Pao 21:74-80(1994).
DR EMBL; S70232; AAB31052.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 42 AA; 4834 MW; B868407FA47BE164 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EVIKEV 9
Db 16 EVIKEV 21
|||||

RESULT 5
Q4RNV7_TETNG
ID Q4RNV7_TETNG PRELIMINARY; PRT; 48 AA.
AC Q4RNV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 10 SCAP15009, whole genome shotgun sequence.
GN ORFNames=GSTENG00031353001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Kellis M., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DDAJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015009; CAG09859.1; -; Genomic DNA.
SQ SEQUENCE 51 AA; 5947 MW; 30A95DD8BEA7CA83 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 PKKQVL 61
Db 20 PKKQVL 25
|||||

RESULT 7
Y151_UREPA
ID Y151_UREPA STANDARD; PRT; 60 AA.
AC Q9PQZ3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein UUI151.

```

```
GN OrderedLocusNames=U1151;
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 700970 / Serovar 3;
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Caswell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum.";
RL Nature 407:757-762(2000).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE002115; AAF30557.1; -; Genomic DNA.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 60 AA; 7313 MW; 49AB0B55342E43F3 CRC64;

Query Match 7.5%; Score 6; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 3 DEVIKE 8
DB 50 DEVIKE 55

RESULT 8
Q74EK4 GEOSL
ID Q74EK4 GEOSL PRELIMINARY; PRT; 62 AA.
AC Q74EK4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Lipoprotein, putative.
GN OrderedLocusNames=GSU0958;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34285.1; -; Genomic_DNA.
DR TIGR; GSU0958; -;
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 62 AA; 6629 MW; 189C7B0BE509B16E CRC64;

Query Match 7.5%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 42 GLAGGV 47
DB 16 GLAGGV 21
```

```
RESULT 9
Q4FLM6 GRICK
ID Q4FLM6 GRICK PRELIMINARY; PRT; 63 AA.
AC Q4FLM6
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Ribosomal L29 protein.
GN Name=rpM6; ORFNames=SR11_1109;
OS Candidatus Pelagibacter ubique HTCC1062.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC SAR11 cluster; Candidatus Pelagibacter.
OX NCBI_TaxID=335992;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC1062;
RA Giovannoni S.J., Tripp H.J., Givan S.A., Podar M., Vergin K.L.,
RA Baptista D., Bibbs L., Eads J., Richardson T.H., Noordwehr M.,
RA Rappe M.S., Short J., Carrington J.C., Mathur E.J.;
RT "Genome Streamlining in a Cosmopolitan Oceanic Bacterium.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000084; AAZ21912.1; -; Genomic DNA.
SQ SEQUENCE 63 AA; 7318 MW; A52A50C9AED6670F CRC64;

Query Match 7.5%; Score 6; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 2 KDEVIK 7
DB 11 KDEVIK 16

RESULT 10
CVT_SOLTU
ID CVT_SOLTU STANDARD; PRT; 66 AA.
AC Q03I96;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cysteine proteinase inhibitor (Fragment).
GN Name=CYS-PIN;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Aspermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Desiree; TISSUE=Leaf;
RX MEDLINE=93005746; PubMed=1392612; DOI=10.1105/tpc.4.9.1157;
RA Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J.,
RA Willmitzer L., Prath S.;
RT "General roles of abscisic and jasmonic acids in gene activation as a
RT result of mechanical wounding.";
RL Plant Cell 4:1157-1170(1992).
CC -!- TISSUE SPECIFICITY: In tubers of untreated plants. After ABA
CC treatment or mechanical wounding is mostly accumulated in leaves,
CC to a lesser extent in stems, but not in roots.
CC -!- INDUCTION: By abscisic acid (ABA), jasmonic acid (JA) and
CC wounding.
CC -!- SIMILARITY: Belongs to the cystatin family. Phytocystatin
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X67844; CAA48037.1; -; mRNA.
DR PIR; PQ0469; PQ0469.
```

```

DR InterPro; IPR000010; Prot_inh_cystat.
DR InterPro; IPR003243; Prot_inh_125A_B.
DR Pfam; PF00031; Cystatin; 1.
DR ProDom; PD001231; Prot_inh_125A_B; 1.
DR SMART; SM00043; CV; 1.
DR PROSITE; PS00267; CYSTATIN; 1.
KW Protease inhibitor; Thiol protease inhibitor.
FT MOTIF 18 22 Secondary area of contact.
FT NON_TER 1 1
SQ SEQUENCE 66 AA; 7906 MW; 70C2832D0E777631 CRC64;

Query Match 7.5%; Score 6; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KEVQEF 12
DB 53 KEVQEF 58

RESULT 11
Q7UB3_RHOBA PRELIMINARY; PRT; 67 AA.
AC Q7UB3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE OrderedLocNames=RB3398;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294138; CAD73168.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 67 AA; 7569 MW; 217C390C6105CABE CRC64;

Query Match 7.5%; Score 6; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 ALNCCG 42
DB 46 ALNCCG 51

RESULT 12
O24959_HELPY PRELIMINARY; PRT; 68 AA.
AC O24959;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0148.
DE OrderedLocNames=HP0148;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000536; AAD07229.1; -; Genomic_DNA.
DR PIR; D64538; D64538.
DR TIGR; HP0148; -.
KW Complete proteome.
SQ SEQUENCE 68 AA; 7790 MW; 6329CF386CC93B5D CRC64;

Query Match 7.5%; Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TLKAIH 35
DB 25 TLKAIH 30

RESULT 13
OS2950_BACSU PRELIMINARY; PRT; 71 AA.
ID OS2950;
AC OS2950;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Plasmid pLS32 DNA for thymidine kinase, replication protein, complete
DE cds.
OS Bacillus subtilis.
OG Plasmid pLS32.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM1163;
RX MEDLINE=98149660; PubMed=9490016; DOI=10.1016/S0014-5793(98)00015-5;
RA Tanaka T., Ogura M.;
RT "A novel Bacillus natto plasmid pLS32 capable of replication in
RT Bacillus subtilis.";
RL FEBS Lett. 422:243-246(1998).
DR EMBL; D49467; BAA24874.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase; Plasmid.
SQ SEQUENCE 71 AA; 8171 MW; B7DB456163C5AFDD CRC64;

Query Match 7.5%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETLKAI 34
DB 12 ETLKAI 17

RESULT 14
Q728A1_DESVH PRELIMINARY; PRT; 71 AA.
ID Q728A1;
AC Q728A1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE OrderedLocNames=DVU2703;
GN Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).

```

```
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidse T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; Utterback T.R.,
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559 (2004).
DR EMBL; AE017318; AAS97175.1; -; Genomic_DNA.
DR TIGR; DVU2703; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 71 AA; 7316 MW; A9450594FCA4C18 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GLAGGV 47
DB 52 GLAGGV 57

RESULT 15
QSBQT7 SCHJA PRELIMINARY; PRT; 73 AA.
AC QSBQT7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY915878; AAX31099.1; -; mRNA.
DR InterPro; IPR000074; APOA1_A4_E.
DR InterPro; IPR006121; HeavyMe_Transpt.
DR Pfam; PF00403; HMA; 1.
DR PROSITE; PS50846; HMA_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8059 MW; 8510BE3AF5226877 CRC64;

Query Match 7.5%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DAIKEV 76
DB 32 DAIKEV 37

Search completed: January 20, 2006, 17:50:49
Job time : 94 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:50:54 ; Search time 73 Seconds
(without alignments)
144.453 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58
Perfect score: 24
Sequence: 1 LRFDSQTKSIPQETNNNSPYT 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 939972

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	25.0	6	5	ABP51699 CD9 cell
2	6	25.0	22	9	ADV54659 G protein
3	6	25.0	22	9	ADV55655 G protein
4	6	25.0	23	2	AAW99457 C.albican
5	6	25.0	23	5	AAE19801 First cat
6	6	25.0	23	7	ADM33266 Candida a
7	5	20.8	5	2	AAW00431 Interleuk
8	5	20.8	7	1	AAW71426 Immunomod
9	5	20.8	8	2	AAW11529 Interleuk
10	5	20.8	8	2	AAW11528 Interleuk
11	5	20.8	9	2	AAW47083 Immunogen
12	5	20.8	9	4	ABP12131 HIV A02 s
13	5	20.8	9	5	ABW94781 CTL epit
14	5	20.8	9	5	ABW94700 CTL epit
15	5	20.8	9	5	ABW94890 CTL epit
16	5	20.8	9	5	ABW94512 CTL epit
17	5	20.8	9	5	ABW95000 CTL epit
18	5	20.8	9	5	ABW94602 CTL epit
19	5	20.8	9	5	ABW95087 CTL epit
20	5	20.8	9	5	AAE31350 Human tyr
21	5	20.8	9	5	AAE31351 Human tyr
22	5	20.8	9	5	AAE31352 Human tyr
23	5	20.8	9	6	ABJ20142 MHC bindi
24	5	20.8	9	8	ADP25771 Plasmodiu

25	5	20.8	9	8	ADP25547	Adp25547 Plasmodiu
26	5	20.8	9	8	ADT40166	Adt40166 HSARS vir
27	5	20.8	9	8	ADS79583	Ads79583 SARS viru
28	5	20.8	9	8	ADT37696	Adt37696 HSARS vir
29	5	20.8	9	9	ADZ50678	Adz50678 X. peatis
30	5	20.8	10	4	AAW86662	Aaw86662 Saccharom
31	5	20.8	10	4	AAW86800	Aaw86800 Saccharom
32	5	20.8	10	4	ABP12285	Abp12285 HIV A02 s
33	5	20.8	10	5	ABW94839	Abw94839 CTL epit
34	5	20.8	10	5	ABW95132	Abw95132 CTL epit
35	5	20.8	12	5	ABG93666	Abg93666 Human Mit
36	5	20.8	12	5	ABG93725	Abg93725 Human Mit
37	5	20.8	14	7	ADF71051	Adf71051 Saccharom
38	5	20.8	15	8	ADM36120	Adm36120 RTN3 pept
39	5	20.8	16	4	AAW99487	Aaw99487 Vaccine r
40	5	20.8	16	5	AAE17169	Aae17169 Meningoco
41	5	20.8	17	2	AAW17549	Aaw17549 Beta-B2-C
42	5	20.8	17	5	AAU89944	Aau89944 Insulin/i
43	5	20.8	17	9	AEA43954	Aea43954 Anti-TPO
44	5	20.8	17	9	AEA43960	Aea43960 Anti-TPO
45	5	20.8	18	6	ABP82477	Abp82477 G protein
46	5	20.8	18	6	ABP82915	Abp82915 G protein
47	5	20.8	20	8	ADH16103	Adh16103 Gliadin r
48	5	20.8	20	8	ADH16104	Adh16104 Gliadin r
49	5	20.8	20	8	ADH15373	Adh15373 Gliadin r
50	5	20.8	20	8	ADH15374	Adh15374 Gliadin r
51	5	20.8	20	8	ADM36164	Adm36164 Human RTN
52	5	20.8	21	5	AAU89040	Aau89040 Insulin/i
53	5	20.8	21	6	ADA03870	Ada03870 Insulin r
54	5	20.8	21	7	ADH95083	Adh95083 Insulin r
55	5	20.8	21	7	ADM35382	Adm35382 HLA bindi
56	5	20.8	21	7	ADM34149	Adm34149 HLA bindi
57	5	20.8	21	8	ADL67774	Adl67774 IGF-IR/IR
58	5	20.8	21	8	ADM37619	Adm37619 Aeti-IR f
59	5	20.8	21	9	ADX85360	Adx85360 HIV Gp120
60	5	20.8	22	2	AAV5048	Aav5048 G protein
61	5	20.8	22	9	ADV54935	Adv54935 G protein
62	5	20.8	22	9	ADV55154	Adv55154 G protein
63	5	20.8	22	9	AAW82478	Aaw82478 Neurospor
64	5	20.8	23	2	AAE22579	Aae22579 Drosophil
65	5	20.8	23	5	ADW55733	Adw55733 Neurospor
66	5	20.8	23	8	AAW06593	Aaw06593 Interleuk
67	5	20.8	24	2	AAW06594	Aaw06594 Interleuk
68	5	20.8	25	2	ABG62549	Abg62549 Rubacteri
69	5	20.8	25	4	AAW27137	Aaw27137 Fibronect
70	4	16.7	4	2	AAW44663	Aaw44663 Platelet
71	4	16.7	4	2	AAW44662	Aaw44662 Platelet
72	4	16.7	4	2	AAW00429	Aaw00429 Interleuk
73	4	16.7	4	2	AAW30984	Aaw30984 Non-cross
74	4	16.7	4	2	ABP55543	Abp55543 Hepatitis
75	4	16.7	4	6	ADA26528	Ada26528 Tobacco s
76	4	16.7	4	6	AAE32856	Aae32856 Hepatitis
77	4	16.7	4	6	ADH51741	Adh51741 Novel hum
78	4	16.7	4	9	ADV11616	Adv11616 RGD1 pept
79	4	16.7	4	9	AAW27143	Aaw27143 Fibronect
80	4	16.7	5	2	AAW54176	Aaw54176 CHA255 11
81	4	16.7	5	2	ABW9053	Abw9053 RGD pepti
82	4	16.7	5	3	ABB80034	Abb80034 Oligopept
83	4	16.7	5	4	AAW91904	Aaw91904 Bag cell
84	4	16.7	5	5	AAU85943	Aau85943 Peptide #
85	4	16.7	5	5	ADN03333	Adn03333 Exemplary
86	4	16.7	5	8	ADR42168	Adr42168 gamma-Bag
87	4	16.7	5	8	ADQ95092	Adq95092 Synthetic
88	4	16.7	5	8	ADU48082	Adu48082 Peptide {
89	4	16.7	6	1	AAW71425	Aaw71425 Immunomod
90	4	16.7	6	1	AAW71425	Aaw71425 Immunomod
91	4	16.7	6	2	AAW14820	Aaw14820 Bay thioe
92	4	16.7	6	3	AAW80540	Aaw80540 Bay C18:1
93	4	16.7	6	3	AAW83826	Aaw83826 Pyrrolobe
94	4	16.7	6	4	AAW88728	Aaw88728 Human int
95	4	16.7	6	4	AAW49582	Aaw49582 Rt-loop p
96	4	16.7	6	5	AAE21423	Aae21423 Saccharom
97	4	16.7	6	5	ADO26631	Ado26631 Synthetic

98	4	16.7	6	8	ADO26633	Synthetic	171	4	16.7	9	6	ABR06146	Human can
99	4	16.7	6	9	AE948702	Serine pr	172	4	16.7	9	6	ABR16846	Human can
100	4	16.7	7	2	AD86832	CD9 antiq	173	4	16.7	9	7	ADD88500	Influenza
101	4	16.7	7	2	AAW11530	Interleuk	174	4	16.7	9	7	ADG18265	Influenza
102	4	16.7	7	2	AAW25984	Hypervari	175	4	16.7	9	8	ADM73326	Human eur
103	4	16.7	7	2	AAW34373	PKB subat	176	4	16.7	9	8	ADN92001	Human eur
104	4	16.7	7	4	AB888727	Human int	177	4	16.7	9	8	ADN90431	Human 202
105	4	16.7	7	5	AB808575	Human HCC	178	4	16.7	9	8	ADN91112	Human 202
106	4	16.7	7	5	AB878367	Amino aci	179	4	16.7	9	8	ADN92316	Human 202
107	4	16.7	7	5	AAE14637	Human CD9	180	4	16.7	9	8	ADN93124	Human 202
108	4	16.7	7	6	AAO23188	Template-	181	4	16.7	9	8	ADN89811	Human 202
109	4	16.7	7	6	AAO23194	Template-	182	4	16.7	9	8	ADN90762	Human 202
110	4	16.7	7	6	AAO23193	Template-	183	4	16.7	9	8	ADN92237	Human 202
111	4	16.7	7	6	AAO23195	Template-	184	4	16.7	9	8	ADN92242	Human 202
112	4	16.7	7	7	ABR62643	Human pro	185	4	16.7	9	8	ADN92390	Human 202
113	4	16.7	7	7	ADK35697	Peptide e	186	4	16.7	9	8	ADN90152	Human 202
114	4	16.7	7	7	ABW00439	Human CD9	187	4	16.7	9	8	ADN1691	Human 202
115	4	16.7	7	7	ADK69863	Human CD9	188	4	16.7	9	8	ADN92934	Human 202
116	4	16.7	7	7	ADM08995	Canine im	189	4	16.7	9	8	ADN92778	Human 202
117	4	16.7	7	8	ADL19367	Human CD9	190	4	16.7	9	8	ADN92861	Human 202
118	4	16.7	7	8	ADO15613	N. mening	191	4	16.7	9	8	ADN90803	Human 202
119	4	16.7	7	8	ADN08516	Cotton te	192	4	16.7	9	8	ADN93006	Human 202
120	4	16.7	7	8	ADK68307	Androgen	193	4	16.7	9	8	ADN92214	Human 202
121	4	16.7	7	8	ADK88884	Peptide f	194	4	16.7	9	8	ADN92376	Human 202
122	4	16.7	7	9	AEA89006	Human CD9	195	4	16.7	9	8	ADP25484	Plasmodiu
123	4	16.7	8	2	AAE69615	MHC claa	196	4	16.7	9	8	ADP25705	Plasmodiu
124	4	16.7	8	2	AAI40242	Amino aci	197	4	16.7	9	8	ADP25820	Plasmodiu
125	4	16.7	8	2	AAI40316	Amino aci	198	4	16.7	9	8	ADP25587	Plasmodiu
126	4	16.7	8	2	AAI533467	HIV-1 nef	199	4	16.7	9	8	ADP26040	Plasmodiu
127	4	16.7	8	2	AAI533393	HIV-1 nef	200	4	16.7	9	8	ADP25639	Plasmodiu
128	4	16.7	8	2	AAI26734	HIV-deriv	201	4	16.7	9	8	ADP25516	Plasmodiu
129	4	16.7	8	2	AAI26808	HIV-deriv	202	4	16.7	9	8	ADP25703	Plasmodiu
130	4	16.7	8	4	AB888726	Human int	203	4	16.7	9	8	ADR12491	Anti-canc
131	4	16.7	8	4	ABR52156	Mutant Pe	204	4	16.7	9	8	ADR47098	HLA-Bindi
132	4	16.7	8	4	ABR70259	Peptide #	205	4	16.7	9	8	ADT41381	hsARS vir
133	4	16.7	8	5	ABO88570	Human HCC	206	4	16.7	9	8	ADS80796	SARS virtu
134	4	16.7	8	7	ABW01593	Human TR1	207	4	16.7	9	8	ADT38911	hsARS vir
135	4	16.7	8	8	ADG94480	Human JNM	208	4	16.7	9	8	ADT02851	Human tum
136	4	16.7	8	8	ADI46879	Permeabil	209	4	16.7	9	8	ADT72523	Human RSV
137	4	16.7	8	8	ADI46862	Permeabil	210	4	16.7	9	8	ADT72889	Human RSV
138	4	16.7	8	8	ADN65659	HLA bindi	211	4	16.7	9	8	ADT72890	Human RSV
139	4	16.7	8	8	ADN65651	HLA bindi	212	4	16.7	9	8	ADT90910	Human eur
140	4	16.7	8	8	ADP87055	Junctiona	213	4	16.7	9	8	ADV29616	Human 109
141	4	16.7	8	8	ADP87039	Junctiona	214	4	16.7	9	8	ADV29229	Human 109
142	4	16.7	8	8	ADR05419	S39 subti	215	4	16.7	9	8	ADV30499	Human 109
143	4	16.7	8	8	ADT89656	Human TR1	216	4	16.7	9	8	ADV26688	Human 109
144	4	16.7	8	8	ADU08080	Heat shoc	217	4	16.7	9	8	ADV30066	Human 109
145	4	16.7	9	2	AAW49512	Human leu	218	4	16.7	9	8	ADV26538	Human 109
146	4	16.7	9	2	AAW49266	Human leu	219	4	16.7	9	8	ADV29208	Human 109
147	4	16.7	9	2	AAW43849	Specific	220	4	16.7	9	9	ADW92427	H1N1 inf1
148	4	16.7	9	2	AAW43845	Specific	221	4	16.7	9	9	ADZ00083	Cyclic pe
149	4	16.7	9	4	AB888725	Human int	222	4	16.7	9	9	ADZ86764	Cytotoxic
150	4	16.7	9	4	AAE63616	Complemen	223	4	16.7	10	1	AAE71431	Immunomod
151	4	16.7	9	4	AAJ02654	Hepatitis	224	4	16.7	10	1	AAE71430	Immunomod
152	4	16.7	9	4	AAJ00731	Hepatitis	225	4	16.7	10	2	AAE43942	Bovine Gl
153	4	16.7	9	4	AAJ02116	Hepatitis	226	4	16.7	10	2	AAE49439	Immunomod
154	4	16.7	9	5	ABR94604	CTL epito	227	4	16.7	10	2	AAW41459	Fragment
155	4	16.7	9	5	ABR95085	CTL epito	228	4	16.7	10	2	AAW41459	Fragment
156	4	16.7	9	5	ABR95104	CTL epito	229	4	16.7	10	2	AAI10312	T cell ep
157	4	16.7	9	5	ABR94517	CTL epito	230	4	16.7	10	2	AAI40255	Amino aci
158	4	16.7	9	5	ABR95006	CTL epito	231	4	16.7	10	2	AAI53406	HIV-1 nef
159	4	16.7	9	5	ABR94503	CTL epito	232	4	16.7	10	2	AAI04359	Salmonell
160	4	16.7	9	5	ABR94921	CTL epito	233	4	16.7	10	3	AAI66452	HIV-deriv
161	4	16.7	9	5	ABR94618	CTL epito	234	4	16.7	10	4	AAE88724	Human int
162	4	16.7	9	5	ABG34115	Antigenic	235	4	16.7	10	4	AAE47551	Ag85B(110
163	4	16.7	9	5	ABG80675	Human tum	236	4	16.7	10	4	AAE94982	Human com
164	4	16.7	9	5	ABG80676	Human tum	237	4	16.7	10	4	AAE94982	Human com
165	4	16.7	9	6	ABR16010	Human can	238	4	16.7	10	4	AAE87012	Saccharom
166	4	16.7	9	6	ABR17027	Human can	239	4	16.7	10	4	AAJ02254	Hepatitis
167	4	16.7	9	6	ABR17023	Human can	240	4	16.7	10	4	AAJ02732	Hepatitis
168	4	16.7	9	6	ABR17056	Human can	241	4	16.7	10	5	ABR94634	CTL epito
169	4	16.7	9	6	ABR06295	Human can	242	4	16.7	10	5	ABR94837	CTL epito
170	4	16.7	9	6	ABR16253	Human can	243	4	16.7	10	5	ABR95058	CTL epito

244	4	16.7	10	5	ABB94760	Abb94760 CTL epitope	317	4	16.7	10	8	ADV26570	Adv26570 Human 109
245	4	16.7	10	5	ABJ15234	Abj15234 Immunogen	318	4	16.7	10	9	ADW15724	Adw15724 Novel hum
246	4	16.7	10	5	ABU57443	Abu57443 HIV cytoto	319	4	16.7	10	9	AEb44901	Aeb44901 M tuberc
247	4	16.7	10	5	ABG79994	Abg79994 MHC class	320	4	16.7	11	2	AAR6031	Aar6031 Oligopept
248	4	16.7	10	6	AAE30016	Aae30016 Retinobla	321	4	16.7	11	2	AAR51276	Aar51276 Meningoco
249	4	16.7	10	6	ABP55431	Abp55431 Retinobla	322	4	16.7	11	2	AAR51277	Aar51277 Meningoco
250	4	16.7	10	6	ABRI6899	Abri6899 Human can	323	4	16.7	11	2	AAR83267	Aar83267 NPF motif
251	4	16.7	10	6	ABRI17105	Abri17105 Human can	324	4	16.7	11	2	AAW83267	Aaw83267 NPF motif
252	4	16.7	10	6	ABRI6364	Abri6364 Human can	325	4	16.7	11	2	AAW05147	Aaw05147 HIV Tat p
253	4	16.7	10	6	ABR06177	Abro6177 Human can	326	4	16.7	11	3	AAW98026	Aaw98026 Synthetic
254	4	16.7	10	6	ABRI7348	Abri7348 Human can	327	4	16.7	11	3	AAW98025	Aaw98025 Synthetic
255	4	16.7	10	6	ABRI7692	Abri7692 Human can	328	4	16.7	11	4	AAB88723	Aab88723 Human int
256	4	16.7	10	6	ABRI7291	Abri7291 Human can	329	4	16.7	11	4	AAM99178	Aam99178 Vaccine r
257	4	16.7	10	6	ABR06813	Abro6813 Human can	330	4	16.7	11	4	AAM98099	Aam98099 Human Bre
258	4	16.7	10	6	ABRI17109	Abri17109 Human can	331	4	16.7	11	4	AAB87985	Aab87985 Peptide a
259	4	16.7	10	6	ABR06633	Abro6633 Human can	332	4	16.7	11	4	Aaj02241	Aaj02241 Hepatitis
260	4	16.7	10	6	ABRI6934	Abri6934 Human can	333	4	16.7	11	4	Aaj00754	Aaj00754 Hepatitis
261	4	16.7	10	6	ABRI7275	Abri7275 Human can	334	4	16.7	11	4	Aaj02722	Aaj02722 Hepatitis
262	4	16.7	10	6	ABU70004	Abu70004 Human imm	335	4	16.7	11	6	ADA01464	Ada01464 Human ang
263	4	16.7	10	6	ABU70279	Abu70279 Human imm	336	4	16.7	11	6	ABJ20167	Abj20167 MHC bindi
264	4	16.7	10	7	ADD69231	Add69231 Human hea	337	4	16.7	11	6	ABP1065	Abp1065 TRAF2-bin
265	4	16.7	10	7	ADD23532	Add23532 Breast ca	338	4	16.7	11	6	AAO23202	Aao23202 Template-
266	4	16.7	10	7	ADD96812	Add96812 HIV-1 cro	339	4	16.7	11	7	ABO32492	Ab032492 HIV-1 mul
267	4	16.7	10	7	ADD96537	Add96537 HIV-1 cro	340	4	16.7	11	7	AD871005	Ad871005 HIV-1 Tat
268	4	16.7	10	7	ADM08993	Adm08993 Canine im	341	4	16.7	11	7	ADL94498	Adl94498 HIV-1 Tat
269	4	16.7	10	8	ADG94420	Adg94420 Human JAM	342	4	16.7	11	8	ADG92153	Adg92153 Chemoens
270	4	16.7	10	8	ADG94434	Adg94434 Human JAM	343	4	16.7	11	8	ADS92210	Ads92210 Chemoens
271	4	16.7	10	8	ADG94442	Adg94442 Human JAM	344	4	16.7	11	8	ADT40637	Adt40637 hSARS vir
272	4	16.7	10	8	ADK68931	Adk68931 Epitope 1	345	4	16.7	11	8	ADT40544	Adt40544 hSARS vir
273	4	16.7	10	8	ADI46818	Adi46818 Permeabil	346	4	16.7	11	8	AD800053	Ad800053 SARS viru
274	4	16.7	10	8	ADI46853	Adi46853 Permeabil	347	4	16.7	11	8	ADT79961	Adt79961 SARS viru
275	4	16.7	10	8	ADI46840	Adi46840 Permeabil	348	4	16.7	11	8	ADT38074	Adt38074 hSARS vir
276	4	16.7	10	8	ADI46832	Adi46832 Permeabil	349	4	16.7	11	8	ADT38167	Adt38167 hSARS vir
277	4	16.7	10	8	ADL27224	Adl27224 Peptide f	350	4	16.7	11	9	ADW03581	Adw03581 Human RIN
278	4	16.7	10	8	ADN90892	Adn90892 Human 202	351	4	16.7	12	1	AAP71428	Aap71428 Immunomod
279	4	16.7	10	8	ADN90592	Adn90592 Human 202	352	4	16.7	12	1	AAP71427	Aap71427 Immunomod
280	4	16.7	10	8	ADN93567	Adn93567 Human 202	353	4	16.7	12	1	AAR06818	Aar06818 Cell surf
281	4	16.7	10	8	ADN93693	Adn93693 Human 202	354	4	16.7	12	2	AAR06032	Aar06032 Oligopept
282	4	16.7	10	8	ADN89969	Adn89969 Human 202	355	4	16.7	12	2	AAR20117	Aar20117 MHC class
283	4	16.7	10	8	ADN91826	Adn91826 Human 202	356	4	16.7	12	2	AAR49390	Aar49390 HLA-A2 po
284	4	16.7	10	8	ADN91529	Adn91529 Human 202	357	4	16.7	12	2	AAR49477	Aar49477 HLA-A2 po
285	4	16.7	10	8	ADN93757	Adn93757 Human 202	358	4	16.7	12	2	AAR49401	Aar49401 HLA-Cw9 p
286	4	16.7	10	8	ADN90237	Adn90237 Human 202	359	4	16.7	12	2	AAR69608	Aar69608 MHC class
287	4	16.7	10	8	ADN90940	Adn90940 Human 202	360	4	16.7	12	2	AAW11838	Aaw11838 Peptide s
288	4	16.7	10	8	ADN93400	Adn93400 Human 202	361	4	16.7	12	2	AAV29652	Aav29652 H-ras com
289	4	16.7	10	8	ADN93430	Adn93430 Human 202	362	4	16.7	12	4	AAB88722	Aab88722 Human int
290	4	16.7	10	8	ADN90583	Adn90583 Human 202	363	4	16.7	12	4	AAV97744	Aav97744 Peroxidase
291	4	16.7	10	8	ADN93756	Adn93756 Human 202	364	4	16.7	12	5	AAU09443	Aau09443 Chlamydo
292	4	16.7	10	8	ADN93941	Adn93941 Human 202	365	4	16.7	12	6	ABU11918	Abu11918 Human HGP
293	4	16.7	10	8	ADO22326	Ado22326 Retinobla	366	4	16.7	12	6	ABR39318	AbR39318 Potential
294	4	16.7	10	8	ADP87030	Adp87030 Junctiona	367	4	16.7	12	6	ABU14073	Abu14073 Transadomi
295	4	16.7	10	8	ADP87017	Adp87017 Junctiona	368	4	16.7	12	7	Add23761	Add23761 Breast ca
296	4	16.7	10	8	ADP87009	Adp87009 Junctiona	369	4	16.7	12	8	ADN65155	Adn65155 HLA bindi
297	4	16.7	10	8	ADP86995	Adp86995 Junctiona	370	4	16.7	12	8	ADN05491	Adn05491 Antipeori
298	4	16.7	10	8	ADQ10729	Adq10729 Human imm	371	4	16.7	12	8	ADQ15899	Adq15899 Human MDM
299	4	16.7	10	8	ADRI12499	Adri12499 Anti-canc	372	4	16.7	12	9	ADV59259	Adv59259 G protein
300	4	16.7	10	8	ADRI12506	Adri12506 Anti-canc	373	4	16.7	12	9	ADV59654	Adv59654 G protein
301	4	16.7	10	8	ADRI12498	Adri12498 Anti-canc	374	4	16.7	12	9	ADV57523	Adv57523 G protein
302	4	16.7	10	8	ADRA7105	Adra7105 HLA-bindi	375	4	16.7	12	9	ADV57112	Adv57112 G protein
303	4	16.7	10	8	ADRA7106	Adra7106 HLA-bindi	376	4	16.7	12	9	ADV60057	Adv60057 G protein
304	4	16.7	10	8	ADRA7113	Adra7113 HLA-bindi	377	4	16.7	12	9	ADV57896	Adv57896 G protein
305	4	16.7	10	8	ADSI1209	Adsi1209 Tumour-as	378	4	16.7	12	9	ADV58797	Adv58797 G protein
306	4	16.7	10	8	ADT90925	Adt90925 Human sur	379	4	16.7	12	9	ADV59934	Adv59934 G protein
307	4	16.7	10	8	ADT90917	Adt90917 Human sur	380	4	16.7	13	2	AAR06819	Aar06819 Cell surf
308	4	16.7	10	8	ADT90918	Adt90918 Human sur	381	4	16.7	13	2	AAR20118	Aar20118 MHC class
309	4	16.7	10	8	ADV27455	Adv27455 Human 109	382	4	16.7	13	2	AAR69609	Aar69609 MHC class
310	4	16.7	10	8	ADV31299	Adv31299 Human 109	383	4	16.7	13	2	AAR96474	Aar96474 Hepatitis
311	4	16.7	10	8	ADV30878	Adv30878 Human 109	384	4	16.7	13	2	AAR94321	Aar94321 Anti-thro
312	4	16.7	10	8	ADV27261	Adv27261 Human 109	385	4	16.7	13	2	AAW76600	Aaw76600 Simian im
313	4	16.7	10	8	ADV27204	Adv27204 Human 109	386	4	16.7	13	2	AAW76599	Aaw76599 Simian im
314	4	16.7	10	8	ADV30663	Adv30663 Human 109	387	4	16.7	13	2	AAW54569	Aaw54569 Peptide 8
315	4	16.7	10	8	ADV27014	Adv27014 Human 109	388	4	16.7	13	2	AAW44131	Aaw44131 HLA-A2 pe
316	4	16.7	10	8	ADV27793	Adv27793 Human 109	389	4	16.7	13	2	AAW79341	Aaw79341 Staphyloc

390	4	16.7	13	4	AAB88721	Aab88721 Human int	463	4	16.7	14	8	ADI56797	Adi56797 Melanoma
391	4	16.7	13	4	AAB07209	Aae07209 Human LIV	464	4	16.7	14	8	ADI56772	Adi56772 Flu virus
392	4	16.7	13	4	AAB85938	Aab85938 Lima bean	465	4	16.7	14	8	ADP73498	Adp73498 Neisseria
393	4	16.7	13	4	AAB85937	Aab85937 Chick pea	466	4	16.7	14	8	ADQ94315	Adq94315 Human pre
394	4	16.7	13	5	ABP72103	Abp72103 Beta 1,2-	467	4	16.7	14	8	ADRI2790	Adri2790 N. mening
395	4	16.7	13	5	ADG66697	Adg66697 B. lichen	468	4	16.7	14	8	ADU49898	Adu49898 Human glu
396	4	16.7	13	5	ADG66700	Adg66700 B. lichen	469	4	16.7	14	9	ADM80714	Adm80714 Human pro
397	4	16.7	13	5	ADG66699	Adg66699 B. lichen	470	4	16.7	14	9	ADY53789	Ady53789 Human Ig
398	4	16.7	13	5	ADG66698	Adg66698 B. lichen	471	4	16.7	14	9	ADY53788	Ady53788 Human Ig
399	4	16.7	13	6	ABU08282	Abu08282 Prostate	472	4	16.7	14	9	ADZ00084	Adz00084 Cyclic pe
400	4	16.7	13	6	ADA43109	Ada43109 HLA-DR be	473	4	16.7	14	9	AEA64487	Aea64487 Cyclic pe
401	4	16.7	13	6	ADA43111	Ada43111 HLA-DR be	474	4	16.7	14	9	AEA64482	Aea64482 Cyclic pe
402	4	16.7	13	6	ADA43113	Ada43113 HLA-DR be	475	4	16.7	14	9	AEA64483	Aea64483 Cyclic pe
403	4	16.7	13	6	ADA43110	Ada43110 HLA-DR be	476	4	16.7	14	9	AEA64486	Aea64486 Cyclic pe
404	4	16.7	13	6	ADA43112	Ada43112 HLA-DR be	477	4	16.7	14	9	AEA64485	Aea64485 Cyclic pe
405	4	16.7	13	7	ADD18064	Add18064 Human G-p	478	4	16.7	14	9	AEA64484	Aea64484 Cyclic pe
406	4	16.7	13	8	ADI00496	Adi00496 Influenza	479	4	16.7	14	9	AEA64481	Aea64481 Cyclic pe
407	4	16.7	13	8	ADI56771	Adi56771 Flu virus	480	4	16.7	14	9	AEA64483	Aea64483 Cyclic pe
408	4	16.7	13	8	ADH89766	Adh89766 Cell pene	481	4	16.7	15	2	AAR49389	Aar49389 HLA-A2 po
409	4	16.7	13	8	ADK69701	Adk69701 Novel fus	482	4	16.7	15	2	AAR49633	Aar49633 Camel imm
410	4	16.7	13	8	ADK68462	Adk68462 Peptide s	483	4	16.7	15	2	AAW75601	Aaw75601 M. tuberc
411	4	16.7	13	8	ADK68461	Adk68461 Peptide s	484	4	16.7	15	2	AAW75656	Aaw75656 M. tuberc
412	4	16.7	13	8	ADO21581	Ado21581 Chickpea	485	4	16.7	15	2	AAW75602	Aaw75602 M. tuberc
413	4	16.7	13	8	ADO21582	Ado21582 Lima bean	486	4	16.7	15	2	AAW75655	Aaw75655 M. tuberc
414	4	16.7	13	8	ADO06903	Ado06903 PRRSV gp5	487	4	16.7	15	2	AAW75657	Aaw75657 M. tuberc
415	4	16.7	13	8	ADO06902	Ado06902 PRRSV gp5	488	4	16.7	15	2	AAW92585	Aaw92585 Mouse bet
416	4	16.7	13	8	ADM65154	Adm65154 HLA bindi	489	4	16.7	15	2	AAW92584	Aaw92584 Mouse bet
417	4	16.7	13	9	ADY27605	Ady27605 Alpha-1-3	490	4	16.7	15	3	AAW00051	Aaw00051 Cartilage
418	4	16.7	13	9	ADY14192	Ady14192 Soluble p	491	4	16.7	15	4	AAAB88719	AaB88719 Human int
419	4	16.7	13	9	ADY27630	Ady27630 Alpha-2-3	492	4	16.7	15	4	AAAG65148	AaG65148 Rb derive
420	4	16.7	13	9	ADZ38302	Adz38302 Human kin	493	4	16.7	15	4	ABR51033	AbR51033 Human sec
421	4	16.7	14	2	AAR33244	Aar33244 HIV-NJ-33	494	4	16.7	15	4	ABG78795	Abg78795 Human myo
422	4	16.7	14	2	AAR49400	Aar49400 HLA-Cw9 p	495	4	16.7	15	4	ABP24631	Abp24631 HIV DR su
423	4	16.7	14	2	AAR77226	Aar77226 Hamster i	496	4	16.7	15	4	ABJ03358	Abj03358 Hepatitis
424	4	16.7	14	2	AAW30030	Aaw30030 Mutant hu	497	4	16.7	15	5	ABP58871	Abp58871 Follicle
425	4	16.7	14	2	AAW41922	Aaw41922 Peptide u	498	4	16.7	15	5	ABB07889	Abb07889 Phosphoen
426	4	16.7	14	2	AAW62008	Aaw62008 SEQ ID NO	499	4	16.7	15	5	ABG62749	Abg62749 Eubacteri
427	4	16.7	14	2	AAW66136	Aaw66136 Prosaposi	500	4	16.7	15	5	ABG62484	Abg62484 Eubacteri
428	4	16.7	14	2	AAJ36479	Aaj36479 Fragment	501	4	16.7	15	5	AAE18792	Aae18792 Streptoco
429	4	16.7	14	3	AAJ99943	Aaj99943 HLA class	502	4	16.7	15	5	ABP60052	Abp60052 Motor pro
430	4	16.7	14	3	AAJ98021	Aaj98021 Sunflower	503	4	16.7	15	5	ABU11944	Abu11944 Human HGP
431	4	16.7	14	4	AAJ98714	Aaj98714 Human pep	504	4	16.7	15	6	ABU11956	Abu11956 Human HGP
432	4	16.7	14	4	AAJ97761	Aaj97761 Human pep	505	4	16.7	15	6	ABP59317	Abp59317 Human neu
433	4	16.7	14	4	AAJ988720	Aaj988720 Human int	506	4	16.7	15	6	ABR32307	AbR32307 Human can
434	4	16.7	14	4	AAJ999335	Aaj999335 Vaccine r	507	4	16.7	15	6	ABR34213	AbR34213 Human can
435	4	16.7	14	4	AAU68411	Aau68411 Human Bre	508	4	16.7	15	6	ABR31673	AbR31673 Human can
436	4	16.7	14	4	AAJ980068	Aaj980068 Chemokine	509	4	16.7	15	6	ABR34163	AbR34163 Human can
437	4	16.7	14	5	ABR74646	AbR74646 Retinobla	510	4	16.7	15	6	ABR31911	AbR31911 Human can
438	4	16.7	14	5	ABR05878	AbB05878 Amb a I r	511	4	16.7	15	6	ABR34228	AbR34228 Human can
439	4	16.7	14	5	ABR05950	AbB05950 Amb a I r	512	4	16.7	15	6	ABR31842	AbR31842 Human can
440	4	16.7	14	6	ABP72984	Abp72984 Membrane	513	4	16.7	15	6	ABR32082	AbR32082 Human can
441	4	16.7	14	6	ABU11935	Abu11935 Human HGP	514	4	16.7	15	6	ABR34096	AbR34096 Human can
442	4	16.7	14	6	ABU11936	Abu11936 Human HGP	515	4	16.7	15	6	ABR34203	AbR34203 Human can
443	4	16.7	14	6	ABU11919	Abu11919 Human HGP	516	4	16.7	15	6	ABR31779	AbR31779 Human can
444	4	16.7	14	6	ABU11920	Abu11920 Human HGP	517	4	16.7	15	6	ABR31750	AbR31750 Human can
445	4	16.7	14	6	ABU11937	Abu11937 Human HGP	518	4	16.7	15	6	ABR32083	AbR32083 Human can
446	4	16.7	14	6	ABJ38788	Abj38788 Human G-p	519	4	16.7	15	6	ABR34153	AbR34153 Human can
447	4	16.7	14	6	ABJ38718	Abj38718 Human G-p	520	4	16.7	15	6	ABR34131	AbR34131 Human can
448	4	16.7	14	6	ABJ38764	Abj38764 Human G-p	521	4	16.7	15	6	ABP83373	Abp83373 G protein
449	4	16.7	14	6	ABJ38765	Abj38765 Human G-p	522	4	16.7	15	6	ABU08065	Abu08065 N-termina
450	4	16.7	14	6	ABJ38787	Abj38787 Human G-p	523	4	16.7	15	6	ABU56365	Abu56365 Mycobacte
451	4	16.7	14	6	ABJ38719	Abj38719 Human G-p	524	4	16.7	15	6	ABU56364	Abu56364 Mycobacte
452	4	16.7	14	6	ADA12025	Ada12025 Human nov	525	4	16.7	15	6	ABO45290	AbO45290 Novel hum
453	4	16.7	14	7	ADD18065	Add18065 Human G-p	526	4	16.7	15	6	ABO45270	AbO45270 Protein a
454	4	16.7	14	7	ADD18060	Add18060 Human G-p	527	4	16.7	15	7	ABE39310	Aae39310 M. tuberc
455	4	16.7	14	7	ADE10863	Adel0863 ChimERIC	528	4	16.7	15	7	AAE39311	Aae39311 M. tuberc
456	4	16.7	14	7	ADG44360	Adg44360 Anti-path	529	4	16.7	15	7	AAE39309	Aae39309 M. tuberc
457	4	16.7	14	7	ADM39768	Adm39768 Neisseria	530	4	16.7	15	7	AAE39311	Aae39311 M. tuberc
458	4	16.7	14	7	ADM40850	Adm40850 Neisseria	531	4	16.7	15	7	AAE45025	Aae45025 Human p95
459	4	16.7	14	7	ADM36522	Adm36522 Soybean l	532	4	16.7	15	7	ADP32542	Adp32542 Clostridi
460	4	16.7	14	8	ADG63963	Adg63963 Recombina	533	4	16.7	15	7	ADP45151	Adp45151 M. tuberc
461	4	16.7	14	8	ADI00497	Adi00497 Influenza	534	4	16.7	15	7	ADP45152	Adp45152 M. tuberc
462	4	16.7	14	8	ADI00522	Adi00522 Melanoma-	535	4	16.7	15	7		

536	4	16.7	15	7	ADP45153	Adf45153 M. tuberc	609	4	16.7	16	7	ABO27244	Abo27244 Self-anti
537	4	16.7	15	7	ADP70981	Adf70981 Subtielli	610	4	16.7	16	7	AD88732	Ad88732 Malarial
538	4	16.7	15	7	ADP70982	Adf70982 Subtielli	611	4	16.7	16	7	ADG18497	Adg18497 P. falcip
539	4	16.7	15	7	ADP70980	Adf70980 Subtielli	612	4	16.7	16	7	ADG68018	Adg68018 Human TRP
540	4	16.7	15	7	ADP70979	Adf70979 Subtielli	613	4	16.7	16	7	ADG68004	Adg68004 Human TRP
541	4	16.7	15	7	ADL96063	Adi96063 Human neu	614	4	16.7	16	7	ADJ46091	Adj46091 CS3 subun
542	4	16.7	15	8	ADL35018	Adi35018 Hepatitis	615	4	16.7	16	8	ADH62685	Adh62685 E. coli p
543	4	16.7	15	8	ADL35021	Adi35021 Hepatitis	616	4	16.7	16	8	ADK69565	Adk69565 Epitope l
544	4	16.7	15	8	ADL35020	Adi35020 Hepatitis	617	4	16.7	16	8	ADP69105	Adp69105 Human NOV
545	4	16.7	15	8	ADN94442	Adn94442 Human 202	618	4	16.7	16	8	ADP69105	Adp69105 Human NOV
546	4	16.7	15	8	ADN94444	Adn94444 Human 202	619	4	16.7	16	8	ADP69105	Adp69105 Human NOV
547	4	16.7	15	8	ADN94328	Adn94328 Human 202	620	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
548	4	16.7	15	8	ADN94443	Adn94443 Human 202	621	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
549	4	16.7	15	8	ADN944085	Adn944085 Human 202	622	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
550	4	16.7	15	8	ADN94207	Adn94207 Human 202	623	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
551	4	16.7	15	8	ADN94137	Adn94137 Human 202	624	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
552	4	16.7	15	8	ADN94272	Adn94272 Human 202	625	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
553	4	16.7	15	8	ADN94640	Adn94640 Human 202	626	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
554	4	16.7	15	8	ADN94487	Adn94487 Human 202	627	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
555	4	16.7	15	8	ADQ36837	Ado36837 Majorly a	628	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
556	4	16.7	15	8	ADQ36838	Ado36838 Majorly a	629	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
557	4	16.7	15	8	ADQ36836	Ado36836 Majorly a	630	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
558	4	16.7	15	8	ADP26542	Adp26542 Plasmodiu	631	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
559	4	16.7	15	8	ADQ81257	Adq81257 GW182 pep	632	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
560	4	16.7	15	8	ADT91833	Adt91833 SIV varia	633	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
561	4	16.7	15	8	ADV31616	Adv31616 Human 109	634	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
562	4	16.7	15	8	ADV31524	Adv31524 Human 109	635	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
563	4	16.7	15	8	ADV31553	Adv31553 Human 109	636	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
564	4	16.7	15	8	ADV31447	Adv31447 Human 109	637	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
565	4	16.7	15	8	ADV31856	Adv31856 Human 109	638	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
566	4	16.7	15	8	ADV31685	Adv31685 Human 109	639	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
567	4	16.7	15	8	ADV32081	Adv32081 Human 109	640	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
568	4	16.7	15	8	ADV31857	Adv31857 Human 109	641	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
569	4	16.7	15	8	ADU64212	Adu64212 30 KD pro	642	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
570	4	16.7	15	8	ADU64211	Adu64211 30 KD pro	643	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
571	4	16.7	15	8	ADU64213	Adu64213 30 KD pro	644	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
572	4	16.7	15	8	ADU64270	Adu64270 32 KD pro	645	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
573	4	16.7	15	8	ADU64272	Adu64272 32 KD pro	646	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
574	4	16.7	15	8	ADU64271	Adu64271 32 KD pro	647	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
575	4	16.7	15	9	ADV14736	Adv14736 Protein r	648	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
576	4	16.7	15	9	ADV22664	Adv22664 HIV-1 Tat	649	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
577	4	16.7	15	9	ADV22662	Adv22662 HIV-1 Tat	650	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
578	4	16.7	15	9	ADV22663	Adv22663 HIV-1 Tat	651	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
579	4	16.7	15	9	ADV23401	Adv23401 HBV immun	652	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
580	4	16.7	15	9	ADV23399	Adv23399 HBV immun	653	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
581	4	16.7	15	9	ADV23400	Adv23400 HBV immun	654	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
582	4	16.7	15	9	ADW64465	Adw64465 Wild type	655	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
583	4	16.7	15	9	ADX02678	Adx02678 Neural th	656	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
584	4	16.7	15	9	ADX69408	Adx69408 CDK 2 or	657	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
585	4	16.7	15	9	ADY84962	Ady84962 Nef 218 p	658	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
586	4	16.7	15	9	ADZ71849	Adz71849 p21-deriv	659	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
587	4	16.7	16	2	AAK49461	Aar49461 HLA-A30 p	660	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
588	4	16.7	16	2	AAK88364	Aar88364 CS3 pilus	661	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
589	4	16.7	16	2	AAK85697	Aar85697 HCV-J NG3	662	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
590	4	16.7	16	2	AAW17877	Aaw17877 Photorhab	663	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
591	4	16.7	16	2	AAW75331	Aaw75331 Adenoviru	664	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
592	4	16.7	16	2	AAW85349	Aaw85349 Helper r	665	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
593	4	16.7	16	2	AAW71002	Aaw71002 Epitope f	666	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
594	4	16.7	16	3	AAV59337	Aay59337 Tyrosine	667	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
595	4	16.7	16	4	AAK88718	Aab88718 Human int	668	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
596	4	16.7	16	4	AAK99214	Aam99214 Vaccine r	669	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
597	4	16.7	16	4	AAE12235	Aae12235 Mycobacte	670	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
598	4	16.7	16	4	AAE12235	Aae12235 Mycobacte	671	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
599	4	16.7	16	4	AAE12235	Aae12235 Mycobacte	672	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
600	4	16.7	16	4	AAU29011	Aau29011 Vector pM	673	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
601	4	16.7	16	5	ABO80039	Abo80039 Amino aci	674	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
602	4	16.7	16	5	AAE17168	Aae17168 Meningoco	675	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
603	4	16.7	16	5	AAU77202	Aau77202 Polyspar	676	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
604	4	16.7	16	6	ABO23259	Abo23259 Light cha	677	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
605	4	16.7	16	6	ABP82420	Abp82420 G protein	678	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
606	4	16.7	16	6	ABP82331	Abp82331 G protein	679	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
607	4	16.7	16	6	ABO01417	Abo01417 Single ch	680	4	16.7	16	9	ADW88042	Adw88042 Pilus pro
608	4	16.7	16	7	ABO01256	Abo01256 Single ch	681	4	16.7	16	9	ADW88042	Adw88042 Pilus pro

682	4	16.7	18	2	Aaw06613	Aaw06613	HIV-1 mat	755	4	16.7	19	8	ADR69311	Adr68311	Androgen
683	4	16.7	18	2	Aaw06615	Aaw06615	HIV-1 mat	756	4	16.7	19	8	ADU15798	Adul5798	PDZ domain
684	4	16.7	18	2	Aaw06616	Aaw06616	HIV-1 mat	757	4	16.7	19	9	ADV14076	Adv14076	Yeast N-t
685	4	16.7	18	2	Aaw46687	Aaw46687	Biotinyl	758	4	16.7	19	9	ADV14103	Adv14103	Yeast N-t
686	4	16.7	18	2	Aay24541	Aay24541	Biotinyl	759	4	16.7	19	9	ADW52277	Adw52277	Human PL
687	4	16.7	18	3	Aay99046	Aay99046	HLA class	760	4	16.7	19	9	AEBO7936	Aeb07936	Peptide b
688	4	16.7	18	3	Aay99045	Aay99045	HLA class	761	4	16.7	20	2	AR07710	Aar07710	Rb-15 ant
689	4	16.7	18	3	Aay99043	Aay99043	HLA class	762	4	16.7	20	2	AA27685	Aar27685	Anticocci
690	4	16.7	18	3	Aay99041	Aay99041	HLA class	763	4	16.7	20	2	AA47009	Aar47009	Interleuk
691	4	16.7	18	3	Aay99044	Aay99044	HLA class	764	4	16.7	20	2	AA49383	Aar49383	HLA-A2 po
692	4	16.7	18	4	AA88716	AA88716	Human int	765	4	16.7	20	2	AA49394	Aar49394	HLA-C pos
693	4	16.7	18	4	AAE09921	AAE09921	Human int	766	4	16.7	20	2	AAW99451	Aaw99451	Human par
694	4	16.7	18	5	ABP52503	ABP52503	Fusion pr	767	4	16.7	20	2	AAW71357	Aar71357	Wild type
695	4	16.7	18	5	ABG32409	ABG32409	Peptide #	768	4	16.7	20	2	AAW71358	Aar71358	Conserved
696	4	16.7	18	5	ABG32404	ABG32404	Peptide #	769	4	16.7	20	2	AAW03008	Aaw03008	Peptide f
697	4	16.7	18	5	ABP74746	ABP74746	Proteome	770	4	16.7	20	2	AAW08022	Aaw08022	HIV pep1
698	4	16.7	18	7	AD810872	AD810872	Chimeric	771	4	16.7	20	2	AAW41658	Aaw41658	Immunomod
699	4	16.7	18	7	AD88730	AD88730	Malarial	772	4	16.7	20	2	ABP71216	Abp71216	DRBeta1*0
700	4	16.7	18	7	ADG18495	ADG18495	P. falcip	773	4	16.7	20	2	AAW22209	Aaw22209	Endogenou
701	4	16.7	18	7	ADM39777	ADM39777	N. meningi	774	4	16.7	20	2	AAW37480	Aaw37480	Brevibact
702	4	16.7	18	7	ADM40859	ADM40859	Neisseria	775	4	16.7	20	2	AAW54559	Aaw54559	Peptide f
703	4	16.7	18	8	ADG63972	ADG63972	Recombina	776	4	16.7	20	2	AAW31907	Aay31907	Spider ve
704	4	16.7	18	8	ADL26438	ADL26438	Synthetic	777	4	16.7	20	2	AAW31909	Aay31909	Spider ve
705	4	16.7	18	8	ADP73507	ADP73507	Neisseria	778	4	16.7	20	3	AAW92062	Aay92062	Drosophil
706	4	16.7	18	8	ADR12799	ADR12799	N. mening	779	4	16.7	20	4	AAW88714	Aab88714	Human int
707	4	16.7	18	8	ADS84937	ADS84937	Beta-site	780	4	16.7	20	4	AAW91128	Aab91128	Parathyro
708	4	16.7	18	8	ADU76760	ADU76760	HIV promo	781	4	16.7	20	4	AAE03101	Aae03101	Human gen
709	4	16.7	18	8	ADU76763	ADU76763	HIV promo	782	4	16.7	20	4	AAU01420	Aau01420	Peptide #
710	4	16.7	18	8	ADU76761	ADU76761	HIV promo	783	4	16.7	20	4	AAU01419	Aau01419	Peptide #
711	4	16.7	18	8	ADU76762	ADU76762	HIV promo	784	4	16.7	20	4	AAW74641	Aab74641	Wild-type
712	4	16.7	18	8	ADU76766	ADU76766	HIV promo	785	4	16.7	20	4	AAW74640	Aab74640	Mutant m8
713	4	16.7	18	9	ADV22987	ADV22987	HCV H77 i	786	4	16.7	20	4	AAO05387	Aao05387	Human pol
714	4	16.7	18	9	ADV22986	ADV22986	HCV H77 i	787	4	16.7	20	5	ABG63650	Abg63650	Human alb
715	4	16.7	18	9	ADW64466	ADW64466	Truncated	788	4	16.7	20	5	ABG63278	Abg63278	Human pro
716	4	16.7	18	9	ADW92657	ADW92657	Malaria b	789	4	16.7	20	5	AAO18726	Aao18726	Heparitis
717	4	16.7	19	2	AA49395	AA49395	HLA-A2 pos	790	4	16.7	20	5	ABW84377	Aab84377	H. brasili
718	4	16.7	19	2	AA49384	AA49384	HLA-A2 po	791	4	16.7	20	5	AAU89680	Aau89680	Insulin/i
719	4	16.7	19	2	AA49385	AA49385	HLA-A2 po	792	4	16.7	20	6	AAU57483	Aau57483	Human sec
720	4	16.7	19	2	AA49386	AA49386	HLA-A2 po	793	4	16.7	20	6	ADA41361	Ada41361	Human nef
721	4	16.7	19	2	AA49384	AA49384	Peptide f	794	4	16.7	20	7	ADB67719	Adb67719	HIV-1 nef
722	4	16.7	19	3	AAW04437	AAW04437	Oestrogen	795	4	16.7	20	7	ADB67720	Adb67720	HIV-1 nef
723	4	16.7	19	3	AAW69298	AAW69298	Expressed	796	4	16.7	20	7	ADC61119	Adc61119	Human CD4
724	4	16.7	19	4	AAW21526	AAW21526	Peptide #	797	4	16.7	20	7	ADC61118	Adc61118	Human CD4
725	4	16.7	19	4	AAW88715	AAW88715	Human int	798	4	16.7	20	7	ADC99594	Adc99594	Cancer-re
726	4	16.7	19	4	ABW43871	ABW43871	Peptide #	799	4	16.7	20	7	ADD55623	Add55623	Hepatitis
727	4	16.7	19	4	AAW37788	AAW37788	Peptide #	800	4	16.7	20	7	ADG17820	Adg17820	Binding a
728	4	16.7	19	4	AAW57678	AAW57678	KV.1 PL p	801	4	16.7	20	7	ADG17862	Adg17862	Binding a
729	4	16.7	19	4	AAW74654	AAW74654	Wild type	802	4	16.7	20	7	ADF77801	Adf77801	MALP lipo
730	4	16.7	19	4	AAW74655	AAW74655	Mutant P5	803	4	16.7	20	7	ADH80940	Adh80940	HIV hyper
731	4	16.7	19	4	AAW58088	AAW58088	KV.1 PL p	804	4	16.7	20	7	ADM56182	Adm56182	Synthetic
732	4	16.7	19	4	ABW26797	ABW26797	Protein #	805	4	16.7	20	7	ADN14208	Adn14208	HIV B cel
733	4	16.7	19	4	AAW7598	AAW7598	Human bon	806	4	16.7	20	7	ADW33877	Adw33877	HLA bindi
734	4	16.7	19	4	AAW55816	AAW55816	PL peptid	807	4	16.7	20	8	ADW35110	Adw35110	HLA bindi
735	4	16.7	19	4	AAW64858	AAW64858	Human bra	808	4	16.7	20	8	ADH15375	Adh15375	Gliadin r
736	4	16.7	19	4	ABG59250	ABG59250	Human liv	809	4	16.7	20	8	ADH16105	Adh16105	Gliadin r
737	4	16.7	19	5	AAW75837	AAW75837	Wheat xyl	810	4	16.7	20	8	ADH15372	Adh15372	Gliadin r
738	4	16.7	19	5	ABJ05208	ABJ05208	C-termina	811	4	16.7	20	8	ADH16102	Adh16102	Gliadin r
739	4	16.7	19	5	ABP63231	ABP63231	KV1.3 PL	812	4	16.7	20	8	ADL76915	Adl76915	Albumin f
740	4	16.7	19	6	ABP72985	ABP72985	Membrane	813	4	16.7	20	8	ADL95977	Adl95977	Prostate
741	4	16.7	19	7	ADC61117	ADC61117	Human CD4	814	4	16.7	20	8	ADL95980	Adl95980	Prostate
742	4	16.7	19	7	ADP26606	ADP26606	BGS-19 pe	815	4	16.7	20	8	ADM29147	Adm29147	Hepatitis
743	4	16.7	19	7	ADF14807	ADF14807	SLE/sjogr	816	4	16.7	20	8	ADM29148	Adm29148	Hepatitis
744	4	16.7	19	8	ADQ06898	ADQ06898	PRRSV gp5	817	4	16.7	20	8	ADO08701	Ado08701	HCV epito
745	4	16.7	19	8	ADQ06899	ADQ06899	PRRSV gp5	818	4	16.7	20	8	ADP71365	Adp71365	Sequence
746	4	16.7	19	8	ADQ06897	ADQ06897	PRRSV gp5	819	4	16.7	20	8	ADP71205	Adp71205	HCV E1 pr
747	4	16.7	19	8	ADQ20647	ADQ20647	rNOS PDZ	820	4	16.7	20	8	ADP71339	Adp71339	HIV-1 tat
748	4	16.7	19	8	ADQ20687	ADQ20687	P5D-95 PD	821	4	16.7	20	8	ADQ31345	Adq31345	HIV-1 tat
749	4	16.7	19	8	ADO20751	ADO20751	P5D-95 PD	822	4	16.7	20	8	ADI95227	Adi95227	OSPF-rela
750	4	16.7	19	8	ADO20775	ADO20775	P5D-95 PD	823	4	16.7	20	8	ADI95226	Adi95226	OSPF-rela
751	4	16.7	19	8	ADO20704	ADO20704	P5D-95 PD	824	4	16.7	20	8	ADU78957	Adu78957	Human pop
752	4	16.7	19	8	ADP71362	ADP71362	Sequence	825	4	16.7	20	9	ADU12429	Adu12429	Human pho
753	4	16.7	19	8	ADP71364	ADP71364	Sequence	826	4	16.7	20	9	ADY38344	Ady38344	Antigenic
754	4	16.7	19	8	ADP71363	ADP71363	Sequence	827	4	16.7	20	9	ADZ98096	Adz98096	Human ami

974 4 16.7 25 4 AAm99189
975 4 16.7 25 4 AAm99592
976 4 16.7 25 4 AB38475 Peptide #
977 4 16.7 25 4 AAm31917
978 4 16.7 25 4 AB23631
979 4 16.7 25 4 AAm71620
980 4 16.7 25 4 AAm59087
981 4 16.7 25 4 ABG53302
982 4 16.7 25 5 ABG41432
983 4 16.7 25 5 ABG62214
984 4 16.7 25 5 ABG62627
985 4 16.7 25 5 ABG62526
986 4 16.7 25 5 ABG96124
987 4 16.7 25 7 ADM08232
988 4 16.7 25 7 ADM08239
989 4 16.7 25 7 ADM08240
990 4 16.7 25 7 ADM08247
991 4 16.7 25 7 ADM08208
992 4 16.7 25 7 ADM08206
993 4 16.7 25 7 ADM08211
994 4 16.7 25 7 ADM08236
995 4 16.7 25 7 ADM08210
996 4 16.7 25 7 ADM08245
997 4 16.7 25 7 ADM08241
998 4 16.7 25 7 ADM08243
999 4 16.7 25 7 ADM08203
1000 4 16.7 25 7 ADM08246

ALIGNMENTS

RESULT 1
ADP51699
ID ADP51699 standard; peptide; 6 AA.
AC ADP51699;
XX
DT 01-OCT-2002 (first entry)
XX
DE CD9 cell surface protein peptide.
XX
KW Human; epidermal growth factor receptor; EGFR; immunogenic; cancer;
KW apoptosis; cytostatic; cell surface protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200247613-A2.
XX
PD 20-JUN-2002.
XX
PF 13-NOV-2001; 2001WO-US047734.
XX
PR 27-NOV-2000; 2000US-00723307.
XX
PA (NOUN) UNIV NORTHWESTERN.
XX
PI Calenoff E, Ditlow CC;
PI WPI; 2002-566624/60.
XX
DR Candidates for cancer-specific or cancer-associated antigens useful for
PT diagnosis and treatment of cancer comprise synthetic peptides.
XX
PS Disclosure; Page 16; 53pp; English.
XX
CC The present invention describes a method for identifying candidates that
CC are cancer-specific or cancer-associated antigens. The method involves:
CC (1) mapping hydrophilic regions of amino acid sequences; (2) identifying
CC hydrophilic peptide regions that are glycosylated in non-cancerous cells,
CC but deglycosylated in cancer cells; and (3) synthesizing, labeling and
CC testing peptides. The cancer-specific/associated antigen sequences have

CC cytostatic activity, and can be used for promoting cancer cell apoptosis.
CC The method can be used for identifying candidates that are cancer-
CC specific or cancer-associated antigens for use in the diagnosis and
CC treatment of cancer. The method involves the use of a site of
CC deglycosylated amino acids in the cancer cells, and so confers a cancer-
CC specific or highly cancer-associated immunogenicity or marker function to
CC the peptide and avoiding self-recognition. The peptides are further not
CC intracellularly expressed, but are located on the cell surfaces
CC (predictably secreted or released into pericellular fluids) in sufficient
CC numbers, and so are sufficiently accessible for targeting T cells; and
CC are present at the earlier stages of cancer progression as well as during
CC later stages; and are retained on the surface of the cancer cells for a
CC time sufficient for the therapeutic T cells to find their target and
CC retain the bound T cells for a time sufficient to affect cancer cell
CC death. ADP51697 to ADP51771 represent amino acid sequence used in the
CC exemplification of the present invention
XX
SQ Sequence 6 AA;
Query Match 25.0%; Score 6; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 NNNSS 21
DB 1 NNNSS 6
RESULT 2
ADV54659
ID ADV54659 standard; peptide; 22 AA.
XX
AC ADV54659;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 2156.
XX
KW diagnosis; cancer; obesity; diabetes; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIRV-) VTB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 2156; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for

CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a G-protein coupled receptor peptide
 CC combo.
 CC
 XX
 SQ

Sequence 22 AA;

Query Match 25.0%; Score 6; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 21
 DB 8 NNNNS 13

RESULT 3

ADV55655
 ID ADV55655 standard; peptide; 22 AA.

AC ADV55655;

XX 10-MAR-2005 (first entry)

XX G protein coupled receptor peptide SEQ ID NO 3153.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX Unidentified.

XX WO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW

PA (UYGB-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.

XX Example; SEQ ID NO 3153; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers

CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a G-protein coupled receptor peptide
 CC combo.
 CC
 XX
 SQ

Sequence 22 AA;

Query Match 25.0%; Score 6; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNNS 21
 DB 8 NNNNS 13

RESULT 4

AAW99457

ID AAW99457 standard; protein; 23 AA.

XX AAW99457;

XX 08-JUN-1999 (first entry)

XX C.albicans alpha-INTip 1st cation binding site-derived peptide.

XX Integrin-like motif; vaccine; immune response; antibody; inhibition;
 KW adhesion; endothelial cell; pathogenesis; infection.

XX Synthetic.

OS Candida albicans.

XX US5886151-A.

XX 23-MAR-1999.

XX 03-MAY-1996; 96US-00642846.

PR 03-MAY-1996; 96US-00642846.

XX (MINU) UNIV MINNESOTA.

XX Tao N, Kendrick K, Gale CA, Hostetter MK, Bendel CM;

XX WPI; 1999-242618/20.

XX New isolated Candida albicans protein with integrin-like motifs.

XX Claim 1; Col 33; 21pp; English.

XX Peptides AAW99456-W99461 are derived from a Candida albicans protein with
 CC integrin-like motifs, alpha-INP1. This sequence represents a peptide
 CC derived from the first cation binding site of alpha-INP1. The peptides
 CC can be used for producing vaccines for stimulating an immune response.
 CC The antibodies can inhibit the adhesion of C.albicans to cells,
 CC particularly endothelial cells. This blocking activity of the adhesion to
 CC cells can reduce or prevent subsequent events in the pathogenesis of
 CC invasive candidal infection

XX Sequence 23 AA;

Query Match 25.0%; Score 6; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 48;

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TNNNNS 20
Db       5 TNNNNS 10
        |||||
RESULT 5
AAE19801
ID  AAE19801 standard; peptide; 23 AA.
XX
AC  AAE19801;
XX
DT  18-JUN-2002 (first entry)
XX
DE  First cation-binding site peptide.
XX
KW  Integrin-like protein; alphaIntlp; gene; fungicide; contraceptive; HIV;
KW  human immunodeficiency virus; vaccine; cholera.
XX
OS  Unidentified.
XX
PN  US6346411-B1.
XX
PD  12-FEB-2002.
XX
PF  08-MAR-1999; 99US-00264604.
XX
PR  03-MAY-1996; 96US-00642846.
XX
PA  (MINU ) UNIV MINNESOTA.
XX
PI  Hostetter MK, Gale CA, Bendel CM, Tao N;
XX
DR  WPI; 2002-224995/28.
XX
PT  Polynucleotide encoding Candida albicans protein with integrin-like
PT  motifs and protein, useful as vaccines and for raising antibodies for
PT  inhibiting adhesion of pathogen to cells preferably epithelial cells.
XX
PS  Example; Col 17; 25pp; English.
XX
CC  The present invention relates to an isolated polynucleotide encoding
CC  Candida albicans protein with integrin-like motifs. Candida albicans
CC  protein is utilised in vaccines (for gastrointestinal pathogens like
CC  cholera) and as antigens to prepare anti-peptide antibodies, which are
CC  utilised in inhibiting adhesion of C. albicans to cells preferably
CC  epithelial cells. In the genitourinary tract, expression of spermicides
CC  by S. cerevisiae transformed with the C. albicans integrin-like gene on
CC  an extrachromosomal plasmid could provide a cheap and infrequent method
CC  of contraception. Also, synthesis of protein-based antiretroviral agents
CC  could help to reduce transmission of human immunodeficiency virus (HIV)
CC  in the birth canal. The present sequence is first cation-binding site
CC  peptide used in the exemplification of the invention
XX
SQ  Sequence 23 AA;

Query Match      25.0%; Score 6; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TNNNNS 20
Db       5 TNNNNS 10
        |||||
RESULT 6
ADM33266
ID  ADM33266 standard; peptide; 23 AA.
XX
AC  ADM33266;
XX
DT  03-JUN-2004 (first entry)
XX

```

```

XX DE Candida albicans integrin-like protein epitope seqid 4.
XX KW fungicide; vaccine; cell adhesion inhibitor; integrin-like motif;
XX KW integrin-like protein; alphaIntlp; EF-hand divalent cation binding site;
XX KW transmembrane domain; RGD tripeptide; I domain;
XX KW gastrointestinal pathogen; cholera; epitope.
XX OS Candida albicans.
XX PN US2003082680-A1.
XX PD 01-MAY-2003.
XX PF 15-OCT-2001; 2001US-00978343.
XX PR 03-MAY-1996; 96US-00642846.
XX PR 08-MAR-1999; 99US-00264604.
XX PA (MINU ) UNIV MINNESOTA.
XX XX Hostetter MK, Gale CA, Kendrick K;
XX PI WPI; 2003-743894/70.
XX DR
XX PT New isolated and purified integrin-like protein of Candida albicans,
XX PT alpha Intlp, useful for raising antibodies to alpha Intlp protein for
XX PT inhibiting adhesion of C. albicans to epithelial cells.
XX PS Claim 16; SEQ ID NO 4; 25pp; English.
XX XX
CC  The invention describes an isolated and purified Candida albicans protein
CC  (I) with integrin-like motifs (alphaIntlp) comprising an I domain, two EF
CC  -hand divalent cation binding sites, a sequence sufficient to encode a
CC  transmembrane domain, an internal RGD tripeptide, and a carboxy-terminal
CC  sequence with a single tyrosine residue. Antibodies to (I) are useful for
CC  inhibiting adhesion of C. albicans to cells, e.g. human epithelial cells,
CC  which comprises contacting the C. albicans blastospores with antibodies
CC  to (I) or its fragments or by contacting the cells with antibodies to a
CC  peptide comprising integrin-like motifs containing an I domain, two EF-
CC  hand divalent cation binding sites, a sequence sufficient to form a
CC  transmembrane domain, an internal RGD tripeptide and a carboxy-terminal
CC  sequence having a single tyrosine residue. An extrachromosomal plasmid of
CC  Saccharomyces cerevisiae containing non-native DNA encoding (I) is useful
CC  for delivering a gene product to a subject. A vaccine comprising (I) or a
CC  (I) peptide may be used to provide a source of vaccine antigen for
CC  gastrointestinal pathogens, e.g. cholera. This is the amino acid sequence
CC  of a Candida albicans integrin-like protein (alphaIntlp) epitope
CC  encompassing the first cation binding site.
XX
SQ  Sequence 23 AA;

Query Match      25.0%; Score 6; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TNNNNS 20
Db       5 TNNNNS 10
        |||||
RESULT 7
AAW00431
ID  AAW00431 standard; peptide; 5 AA.
XX
AC  AAW00431;
XX
DT  29-AUG-1996 (first entry)
XX
DE  Interleukin-6 antagonist peptide.
XX
KW  IL-6; antagonist; autoimmune disease.
XX

```

OS Synthetic.
 XX JP07324097-A.
 XX
 XX 12-DEC-1995.
 XX
 XX 30-MAY-1994; 94JP-00117259.
 XX
 XX 30-MAY-1994; 94JP-00117259.
 XX
 XX (DAIIL) DAICEL CHEM IND LTD.
 XX (FUJI) FUJISAWA PHARM CO LTD.
 XX
 XX WPI; 1996-065476/07.
 XX
 XX Interleukin 6 antagonist - useful for treating autoimmune diseases.
 XX
 XX Claim 4, 6; Page 2, 3; 19pp; Japanese.
 XX
 XX New IL-6 antagonists are provided which are of formula X-W-Y, in which X
 CC is H or an amino-protecting group, Y is OH or a carboxy- protecting
 CC group, and W is a peptide containing all or part of the sequence as given
 CC in AA000401, AA000402, AA000403 or AA000404, where any free mercapto
 CC groups in the sequence are optionally protected. The present sequence is
 CC a specifically preferred partial sequence of AA000403 and is itself
 CC claimed as a new chemical entity. The IL-6 antagonists are useful for
 CC treating autoimmune diseases
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 20.8%; Score 5; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 NSSFY 23
 DB 1 NSSFY 5
 |||||
 RESULT 8
 AAP71426
 ID AAP71426 standard; protein; 7 AA.
 XX
 XX AC AAP71426;
 XX
 XX 25-MAR-2003 (revised)
 DT 03-MAY-1991 (first entry)
 XX
 XX Immunomodulator peptide DR-7 inhibits HIV-T4 interaction.
 XX
 XX AIDS; T4 cell receptor; immunomodulation.
 KW
 XX Synthetic.
 OS
 XX WO8703601-A.
 PN
 XX 18-JUN-1987.
 PD
 XX 08-DEC-1986; 86WO-FR000425.
 PF
 XX 06-DEC-1985; 85FR-00018155.
 PR
 XX (INSP) INST PASTEUR.
 PA (AUFR/) AUFRAY C.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 XX Auffray C, Montagnier L, Klatzmann D, Charron D;
 PI
 XX WPI; 1987-177935/25.
 DR
 XX New peptide derivs. contg. specified exposed tetra:peptide sequences -
 PT inhibiting interaction of AIDS virus with T4 cell receptors.
 XX

PS Claim 8; Page 49; 57pp; French.
 XX
 XX The peptide is a specific example of a peptide comprising the
 CC tetrapeptide motif RFDS preceded by either Ala, Val or Leu and followed
 CC by an Asp residue. The peptide comprises 6-30 amino acid residues. It
 CC interferes with interaction between the AIDS virus and T4 receptors on
 CC lymphocytes. The peptide also has immuno- modulatory activity. It is
 CC useful in diagnosis to detect antibodies to the region of the viral
 CC genome containing the RFDS sequence. See also AAP71422-5 and AAP71427-
 CC P71437. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 20.8%; Score 5; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LRFDS 5
 DB 1 LRFDS 5
 |||||
 RESULT 9
 AAW11529
 ID AAW11529 standard; peptide; 8 AA.
 XX
 XX AC AAW11529;
 XX
 XX 22-APR-1997 (first entry)
 DT
 XX Interleukin-6 antagonist 2.
 DE
 XX Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease; skin;
 KW intestine; systemic lupus erythematosus; chronic rheumatism.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 8
 FT /note= "amidated"
 FT
 XX JP08311098-A.
 PN
 XX 26-NOV-1996.
 PD
 XX 22-MAY-1995; 95JP-00146742.
 PF
 XX 22-MAY-1995; 95JP-00146742.
 PR
 XX (DAIIL) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 XX WPI; 1997-061811/06.
 DR
 XX Interleukin-6 antagonistic peptide(s) comprising arginine - useful for
 PT treating autoimmune, renal, skin and intestinal diseases.
 PT
 XX Example 2; Page 11; 20pp; Japanese.
 PS
 XX The present peptide is a specific example of new interleukin-6
 CC antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino acids
 CC or an amino group protecting group; Y is 1-5 amino acids, a carboxyl
 CC group protecting group or an amide; A is preferably Arg having an opt.
 CC protected guanidino group but can be any amino acid; D is Arg having an
 CC opt. protected guanidino group and B is preferably a Leu residue but can
 CC be any amino acid, including non-natural amino acids, opt. having a
 CC protected side-chain. The peptides are useful for treating autoimmune
 CC diseases (e.g. systemic lupus erythematosus or chronic rheumatism),
 CC renal, skin and intestinal diseases
 XX
 XX Sequence 8 AA;
 SQ

```

Query Match      20.8%; Score 5; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 19 NSSFY 23
Db 1 NSSFY 5

RESULT 10
AAW11528
ID AAW11528 standard; peptide; 9 AA.
XX
AC AAW11528;
XX
DT 22-APR-1997 (first entry)
XX
DE Interleukin-6 antagonist 1.
XX
KW Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease; skin;
KW intestine; systemic lupus erythematosus; chronic rheumatism.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /notes="amidated"
XX
PN JP08311098-A.
XX
PD 26-NOV-1996.
XX
PF 22-MAY-1995; 95JP-00146742.
XX
PR 22-MAY-1995; 95JP-00146742.
XX
PA (DAIL ) DAICEL CHEM IND LTD.
PA (FUJI ) FUJISAWA PHARM CO LTD.
XX
XX WPI; 1997-061811/06.
XX
XX Interleukin-6 antagonistic peptide(s) comprising arginine - useful for
XX treating autoimmune, renal, skin and intestinal diseases.
XX
XX Example 1; Page 11; 20pp; Japanese.
XX
XX The present peptide is a specific example of new interleukin-6
XX antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino acids
XX or an amino group protecting group; Y is 1-5 amino acids, a carboxyl
XX group protecting group or an amide; A is preferably Arg having an opt.
XX protected guanidino group but can be any amino acid; D is Arg having an
XX opt. protected guanidino group and B is preferably a Leu residue but can
XX be any amino acid, including non-natural amino acids, opt. having a
XX protected side-chain. The peptides are useful for treating autoimmune
XX diseases (e.g. systemic lupus erythematosus or chronic rheumatism),
XX renal, skin and intestinal diseases
XX
SQ Sequence 9 AA;
Query Match      20.8%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 19 NSSFY 23
Db 2 NSSFY 6

RESULT 11
AAY47083
ID AAY47083 standard; peptide; 9 AA.
XX
XX AAY47083;
AC

Query Match      20.8%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 9 SIFEQ 13
Db 1 SIFEQ 5

Query Match      20.8%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 9 SIFEQ 13
Db 1 SIFEQ 5

RESULT 12
ABP12131
ID ABP12131 standard; peptide; 9 AA.
XX
AC ABP12131;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)

```

```

XX 01-DEC-1999 (first entry)
DT
XX Immunogenic peptide having a human leukocyte antigen binding motif #1694.
DE
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
PD
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US005039.
PR 13-MAR-1998; 98WO-US005039.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment and
XX diagnosis of cancers and viral diseases.
XX
XX Claim 1; Page 93; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also known
XX as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
XX can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
XX or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
XX the antigen from which the peptide is derived. Cytotoxic T lymphocytes
XX (CTLs) which destroy antigen-bearing cells are normally induced by an
XX antigen in the form of a peptide fragment bound to a HLA molecule, rather
XX than the intact foreign antigen itself, and are particularly important in
XX tumour rejection and in fighting viral infections. The peptides are
XX therefore useful therapeutically to treat or prevent viral infections and
XX cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
XX and C, AIDS, and renal carcinoma. They can be administered as vaccines to
XX elicit an immune response in individuals susceptible or otherwise at risk
XX of viral infection or cancer, or used to treat chronic or acute
XX conditions. They are also useful diagnostically, and can be used to
XX induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
XX the peptide e.g. to produce CTLs ex vivo for infusion back into a
XX patient. The polynucleotides encoding the immunogenic peptides are also
XX useful therapeutically and for immunisation as above
XX
SQ Sequence 9 AA;

```


XX HIV A02 super motif env peptide #188.
DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027766.
XX
XX 05-OCT-1999; 99US-00412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
PI
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PT
XX
XX Claim 32; Page 117; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 9 AA;
SQ
Query Match 20.8%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 NNNS 20
DB 3 NNNS 7
RESULT 13
ABB94781
ID ABB94781 standard; peptide; 9 AA.
XX
AC ABB94781;
XX
XX 17-JUN-2002 (first entry)
DT
XX CTL epitope HLA peptide SEQ ID NO:310.
DE
XX

KW Human; 158P1H4; chromosome 8q22q23, 158P1F4; chromosome 8q23; cancer;
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;
XX human leukocyte antigen; helper T lymphocyte; HTL.
OS Homo sapiens.
OS Synthetic.
XX WO200216598-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026411.
XX
XX 22-AUG-2000; 2000US-0227098P.
PR
XX 10-APR-2001; 2001US-0282739P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Challita-Eid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Paris M, Ge W, Jakobovits A;
PI
XX WPI; 2002-269357/31.
XX
XX Monitoring 158P1H4 gene products in biological sample from patient who
PT has or is suspected of having cancer, useful for treating cancer,
PT comprises identifying presence of aberrant 158P1H4 gene products in
PT biological sample.
XX
XX Claim 64; Page 152; 209pp; English.
XX
XX The present invention describes a method for monitoring 158P1H4 gene
CC products in a biological sample from a patient who has or is suspected of
CC having cancer. The method comprises determining the status of 158P1H4
CC gene products in a tissue sample from an individual, comparing the status
CC to the status of 158P1H4 gene products in a normal sample, and
CC identifying the presence of aberrant 158P1H4 gene products in the sample.
CC 158P1H4 sequences have cytostatic activity and can be used in vaccine
CC production. 158P1H4 polynucleotides may be used in monitoring genetic
CC abnormalities. The 158P1H4 proteins may be used in assessing the status
CC of 158P1H4 gene products in normal versus cancerous tissues and so
CC elucidating the malignant phenotype, in generating and characterising
CC domain-specific antibodies, for identifying agents or cellular factors
CC that bind to 158P1H4 or its particular domain, and for generating cancer
CC vaccines. Antibodies against 158P1H4 are useful in diagnostic and
CC prognostic assays, in treating patients with cancer, in generating
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and
CC as immunological reagents for detecting 158P1H4-expressing cells. The
CC antibodies are particularly useful in bladder cancer diagnostic and
CC prognostic assays, and imaging methodologies. The 158P1H4 gene has been
CC located to chromosome 8q22-q23, and the 158P1F4 gene also described in
CC the present invention has been located to chromosome 8q23. ABL50400 to
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 9 AA;
SQ
Query Match 20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
DB 5 DSQTK 9
RESULT 14
ABB94700
ID ABB94700 standard; peptide; 9 AA.
XX
XX ABB94700;
AC
XX
XX 17-JUN-2002 (first entry)
DT
XX

DE CTL epitope HLA peptide SEQ ID NO:229.
XX Human; 158PIH4; chromosome 8q220q23, 158PIF4; chromosome 8q23; cancer;
KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;
KW human leukocyte antigen; helper T lymphocyte; HTL.
XX Homo sapiens.
OS Synthetic.
XX WO200216598-A2.
XX 28-FEB-2002.
XX 22-AUG-2001; 2001WO-US026411.
XX 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX (AGEN-) AGENSYS INC.
XX Challita-Bid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Faris M, Ge W, Jakobovits A;
XX WPI; 2002-269357/31.
XX Monitoring 158PIH4 gene products in biological sample from patient who
PT has or is suspected of having cancer, useful for treating cancer,
PT comprises identifying presence of aberrant 158PIH4 gene products in
PT biological sample.
PS Claim 64; Page 149; 209pp; English.
XX The present invention describes a method for monitoring 158PIH4 gene
CC products in a biological sample from a patient who has or is suspected of
CC having cancer. The method comprises determining the status of 158PIH4
CC gene products in a tissue sample from an individual, comparing the status
CC to the status of 158PIH4 gene products in a normal sample, and
CC identifying the presence of aberrant 158PIH4 gene products in the sample.
CC 158PIH4 sequences have cytostatic activity and can be used in vaccine
CC production. 158PIH4 polynucleotides may be used in monitoring genetic
CC abnormalities. The 158PIH4 proteins may be used in assessing the status
CC of 158PIH4 gene products in normal versus cancerous tissues and so
CC elucidating the malignant phenotype, in generating and characterising
CC domain-specific antibodies, for identifying agents or cellular factors
CC that bind to 158PIH4 or its particular domain, and for generating cancer
CC vaccines. Antibodies against 158PIH4 are useful in diagnostic and
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and
CC as immunological reagents for detecting 158PIH4-expressing cells. The
CC antibodies are particularly useful in bladder cancer diagnostic and
CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been
CC located to chromosome 8q22-q23, and the 158PIF4 gene also described in
CC the present invention has been located to chromosome 8q23. ABL50400 to
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the
CC exemplification of the present invention
XX Sequence 9 AA;
SQ Query Match 20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
|||||
Db 5 DSQTK 9
RESULT 15
ABB94890
ID ABB94890 standard; peptide; 9 AA.
XX
AC ABB94890;
XX

DT 17-JUN-2002 (first entry)
XX CTL epitope HLA peptide SEQ ID NO:419.
DE Human; 158PIH4; chromosome 8q220q23, 158PIF4; chromosome 8q23; cancer;
XX bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;
KW human leukocyte antigen; helper T lymphocyte; HTL.
XX Homo sapiens.
OS Synthetic.
XX WO200216598-A2.
XX 28-FEB-2002.
XX 22-AUG-2001; 2001WO-US026411.
XX 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX (AGEN-) AGENSYS INC.
XX Challita-Bid PM, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Faris M, Ge W, Jakobovits A;
XX WPI; 2002-269357/31.
XX Monitoring 158PIH4 gene products in biological sample from patient who
PT has or is suspected of having cancer, useful for treating cancer,
PT comprises identifying presence of aberrant 158PIH4 gene products in
PT biological sample.
XX Claim 64; Page 156; 209pp; English.
XX The present invention describes a method for monitoring 158PIH4 gene
CC products in a biological sample from a patient who has or is suspected of
CC having cancer. The method comprises determining the status of 158PIH4
CC gene products in a tissue sample from an individual, comparing the status
CC to the status of 158PIH4 gene products in a normal sample, and
CC identifying the presence of aberrant 158PIH4 gene products in the sample.
CC 158PIH4 sequences have cytostatic activity and can be used in vaccine
CC production. 158PIH4 polynucleotides may be used in monitoring genetic
CC abnormalities. The 158PIH4 proteins may be used in assessing the status
CC of 158PIH4 gene products in normal versus cancerous tissues and so
CC elucidating the malignant phenotype, in generating and characterising
CC domain-specific antibodies, for identifying agents or cellular factors
CC that bind to 158PIH4 or its particular domain, and for generating cancer
CC vaccines. Antibodies against 158PIH4 are useful in diagnostic and
CC prognostic assays, in treating patients with cancer, in generating
CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses, and
CC as immunological reagents for detecting 158PIH4-expressing cells. The
CC antibodies are particularly useful in bladder cancer diagnostic and
CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been
CC located to chromosome 8q22-q23, and the 158PIF4 gene also described in
CC the present invention has been located to chromosome 8q23. ABL50400 to
CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the
CC exemplification of the present invention
XX Sequence 9 AA;
SQ Query Match 20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
|||||
Db 1 DSQTK 5
Search completed: January 20, 2006, 17:54:47
Job time : 101 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:52:55 ; Search time 22 Seconds
(without alignments)
90.192 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24

Sequence: 1 LRFDSQTSIFPEQETNNNSFYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 247600

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/FCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	25.0	23	1	US-08-642-846-4
2	6	25.0	23	2	US-09-264-604-4
3	6	25.0	23	2	US-09-378-343-4
4	6	25.0	23	5	US-09-599-652-4
5	5	20.8	17	1	US-08-729-152-32
6	5	20.8	21	2	US-09-962-756-501
7	5	20.8	23	1	US-08-486-953A-48
8	5	20.8	23	2	US-08-204-052-48
9	5	20.8	23	2	US-09-967-869A-1
10	4	16.7	4	1	US-07-834-848-3
11	4	16.7	4	1	US-08-251-027-10
12	4	16.7	4	1	US-08-747-137-33
13	4	16.7	4	2	US-10-353-174-33
14	4	16.7	5	1	US-07-834-848-7
15	4	16.7	5	1	US-07-834-848-10
16	4	16.7	5	2	US-09-164-021-11
17	4	16.7	5	2	US-09-608-892-68
18	4	16.7	5	2	US-09-519-703-11
19	4	16.7	5	2	US-09-623-548A-1080
20	4	16.7	5	2	US-09-657-276-1080
21	4	16.7	6	1	US-07-620-426B-18
22	4	16.7	6	1	US-07-662-007B-18
23	4	16.7	6	1	US-07-824-247-18
24	4	16.7	6	2	US-08-470-204A-18
25	4	16.7	6	2	US-09-721-108-133
26	4	16.7	6	2	US-09-579-894-20
27	4	16.7	7	1	US-08-486-721A-7
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 32, Appl
					Sequence 501, App
					Sequence 48, Appl
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 68, Appl
					Sequence 11, Appl
					Sequence 1080, Ap
					Sequence 18, Appl
					Sequence 18, Appl
					Sequence 18, Appl
					Sequence 133, App
					Sequence 20, Appl
					Sequence 7, Appli

Sequence 9, Appli	7	1	US-08-253-751-9	4	16.7
Sequence 9, Appli	7	1	US-08-453-925-9	4	16.7
Sequence 51, Appl	7	1	US-08-478-315-51	4	16.7
Sequence 7, Appli	7	2	US-08-403-253A-7	4	16.7
Sequence 51, Appl	7	2	US-09-019-793A-51	4	16.7
Sequence 80, Appl	7	2	US-09-914-259-80	4	16.7
Sequence 7, Appli	7	2	US-08-435-816A-7	4	16.7
Sequence 132, App	7	2	US-09-721-108-132	4	16.7
Sequence 61, Appl	7	2	US-09-192-854-61	4	16.7
Sequence 92, Appl	7	2	US-09-601-326-92	4	16.7
Sequence 99, Appl	7	2	US-09-511-939-99	4	16.7
Sequence 7, Appli	7	2	US-09-350-202-7	4	16.7
Sequence 7, Appli	7	2	US-08-592-711-7	4	16.7
Sequence 7, Appli	7	2	US-09-349-915B-7	4	16.7
Sequence 8, Appli	8	1	US-08-057-184-8	4	16.7
Sequence 31, Appl	8	1	US-08-097-938-31	4	16.7
Sequence 31, Appl	8	1	US-08-476-000-31	4	16.7
Sequence 6, Appli	8	1	US-08-486-721A-6	4	16.7
Sequence 31, Appl	8	1	US-08-472-840-31	4	16.7
Sequence 31, Appl	8	1	US-08-476-976-31	4	16.7
Sequence 31, Appl	8	2	US-08-474-410-31	4	16.7
Sequence 31, Appl	8	2	US-08-486-673B-31	4	16.7
Sequence 131, App	8	2	US-09-721-108-131	4	16.7
Sequence 144, App	8	2	US-09-601-729-144	4	16.7
Sequence 503, App	8	2	US-09-303-518D-503	4	16.7
Sequence 2, Appli	9	2	US-08-776-404B-2	4	16.7
Sequence 130, App	9	2	US-09-721-108-130	4	16.7
Sequence 131, App	9	2	US-09-285-912A-131	4	16.7
Sequence 132, App	9	2	US-09-285-912A-132	4	16.7
Sequence 8, Appli	10	1	US-08-045-261-8	4	16.7
Sequence 149, App	10	1	US-08-480-190-149	4	16.7
Sequence 149, App	10	1	US-08-488-379-149	4	16.7
Sequence 26, Appl	10	1	US-08-428-257A-26	4	16.7
Sequence 149, App	10	2	US-08-475-399A-149	4	16.7
Sequence 129, App	10	2	US-09-721-108-129	4	16.7
Sequence 157, App	10	2	US-09-601-729-157	4	16.7
Sequence 149, App	10	2	US-08-077-255A-149	4	16.7
Sequence 55, Appl	10	2	US-09-644-456B-55	4	16.7
Sequence 1, Appli	10	2	US-10-101-812-1	4	16.7
Sequence 149, App	10	4	PCR-US93-07545-149	4	16.7
Sequence 10, Appl	11	1	US-08-411-727-10	4	16.7
Sequence 18, Appl	11	1	US-08-411-727-18	4	16.7
Sequence 43, Appl	11	1	US-08-040-548-43	4	16.7
Sequence 43, Appl	11	1	US-08-466-344-43	4	16.7
Sequence 58, Appl	11	2	US-08-893-853-58	4	16.7
Sequence 93, Appl	11	2	US-08-491-954-93	4	16.7
Sequence 109, App	11	2	US-09-113-921-109	4	16.7
Sequence 109, App	11	2	US-09-451-067-109	4	16.7
Sequence 128, App	11	2	US-09-721-108-128	4	16.7
Patent No. 5200183	11	6	5200183-15	4	16.7
Patent No. 5206152	11	6	5206152-12	4	16.7
Sequence 1, Appli	12	1	US-08-057-184-1	4	16.7
Sequence 100, App	12	1	US-08-480-190-100	4	16.7
Sequence 111, App	12	1	US-08-480-190-111	4	16.7
Sequence 187, App	12	1	US-08-480-190-187	4	16.7
Sequence 100, App	12	1	US-08-488-379-100	4	16.7
Sequence 111, App	12	1	US-08-488-379-111	4	16.7
Sequence 187, App	12	1	US-08-488-379-187	4	16.7
Sequence 13, Appl	12	2	US-09-003-903-13	4	16.7
Sequence 27, Appl	12	2	US-08-481-968A-27	4	16.7
Sequence 27, Appl	12	2	US-08-154-712B-27	4	16.7
Sequence 100, App	12	2	US-08-475-399A-100	4	16.7
Sequence 111, App	12	2	US-08-475-399A-111	4	16.7
Sequence 187, App	12	2	US-08-475-399A-187	4	16.7
Sequence 3, Appli	12	2	US-09-744-900-3	4	16.7
Sequence 100, App	12	2	US-09-721-108-100	4	16.7
Sequence 127, App	12	2	US-08-077-255A-127	4	16.7
Sequence 111, App	12	2	US-08-077-255A-111	4	16.7
Sequence 187, App	12	2	US-08-077-255A-187	4	16.7
Sequence 27, Appl	12	2	PCT-US93-07545-27	4	16.7
Sequence 100, App	12	4	PCT-US93-07545-100	4	16.7
Sequence 111, App	12	4	PCT-US93-07545-111	4	16.7
Sequence 187, App	12	4	PCT-US93-07545-187	4	16.7

101	4	16.7	13	1	US-08-057-184-2	Sequence 2, Appli	174	4	16.7	17	1	US-08-488-379-98	Sequence 98, Appl
102	4	16.7	13	1	US-08-346-293-16	Sequence 16, Appl	175	4	16.7	17	1	US-08-488-379-108	Sequence 108, App
103	4	16.7	13	1	US-08-248-839C-45	Sequence 45, Appl	176	4	16.7	17	1	US-08-488-379-109	Sequence 109, App
104	4	16.7	13	1	US-08-321-670-10	Sequence 10, Appl	177	4	16.7	17	2	US-09-556-877-143	Sequence 143, App
105	4	16.7	13	2	US-08-836-075A-157	Sequence 157, App	178	4	16.7	17	2	US-09-620-412C-143	Sequence 143, App
106	4	16.7	13	2	US-09-194-285-56	Sequence 56, Appl	179	4	16.7	17	2	US-08-475-399A-97	Sequence 97, Appl
107	4	16.7	13	2	US-09-721-108-126	Sequence 126, App	180	4	16.7	17	2	US-08-475-399A-98	Sequence 98, Appl
108	4	16.7	13	2	US-09-519-959-2	Sequence 2, Appli	181	4	16.7	17	2	US-08-475-399A-108	Sequence 108, App
109	4	16.7	14	1	US-08-346-293-17	Sequence 17, Appl	182	4	16.7	17	2	US-08-475-399A-109	Sequence 109, App
110	4	16.7	14	1	US-08-176-126B-5	Sequence 5, Appli	183	4	16.7	17	2	US-09-598-419-143	Sequence 143, App
111	4	16.7	14	1	US-08-290-448A-92	Sequence 92, Appl	184	4	16.7	17	2	US-09-721-108-122	Sequence 122, App
112	4	16.7	14	1	US-08-290-448A-92	Sequence 92, Appl	185	4	16.7	17	2	US-08-077-255A-97	Sequence 97, Appl
113	4	16.7	14	1	US-08-175-069A-92	Sequence 92, Appl	186	4	16.7	17	2	US-08-077-255A-98	Sequence 98, Appl
114	4	16.7	14	1	US-08-480-190-110	Sequence 110, App	187	4	16.7	17	2	US-08-077-255A-108	Sequence 108, App
115	4	16.7	14	1	US-08-669-435-5	Sequence 5, Appli	188	4	16.7	17	2	US-08-077-255A-109	Sequence 109, App
116	4	16.7	14	1	US-08-488-379-110	Sequence 110, App	189	4	16.7	17	2	US-10-204-664A-3	Sequence 3, Appli
117	4	16.7	14	1	US-08-372-100C-8	Sequence 8, Appli	190	4	16.7	17	4	PCT-US93-07545-97	Sequence 97, Appl
118	4	16.7	14	2	US-08-331-625A-33	Sequence 33, Appl	191	4	16.7	17	4	PCT-US93-07545-98	Sequence 98, Appl
119	4	16.7	14	2	US-08-865-511B-8	Sequence 8, Appli	192	4	16.7	17	4	PCT-US93-07545-108	Sequence 108, App
120	4	16.7	14	2	US-09-231-159-10	Sequence 10, Appl	193	4	16.7	17	4	PCT-US93-07545-109	Sequence 109, App
121	4	16.7	14	2	US-08-611-307-10	Sequence 10, Appl	194	4	16.7	18	1	US-08-383-753-66	Sequence 66, Appl
122	4	16.7	14	2	US-08-461-939B-92	Sequence 92, Appl	195	4	16.7	18	1	US-08-480-190-106	Sequence 106, App
123	4	16.7	14	2	US-08-464-000-92	Sequence 92, Appl	196	4	16.7	18	1	US-08-480-190-107	Sequence 107, App
124	4	16.7	14	2	US-09-494-151-33	Sequence 33, Appl	197	4	16.7	18	1	US-08-586-772-66	Sequence 66, Appl
125	4	16.7	14	2	US-08-475-399A-110	Sequence 110, App	198	4	16.7	18	1	US-08-488-379-106	Sequence 106, App
126	4	16.7	14	2	US-08-506-436-8	Sequence 8, Appli	199	4	16.7	18	1	US-08-488-379-107	Sequence 107, App
127	4	16.7	14	2	US-09-972-484-33	Sequence 33, Appl	200	4	16.7	18	1	US-08-649-991-48	Sequence 48, Appl
128	4	16.7	14	2	US-09-721-108-125	Sequence 125, App	201	4	16.7	18	1	US-08-649-991-50	Sequence 50, Appl
129	4	16.7	14	2	US-08-077-255A-110	Sequence 110, App	202	4	16.7	18	1	US-08-649-991-51	Sequence 51, Appl
130	4	16.7	14	2	US-08-928-074-10	Sequence 10, Appl	203	4	16.7	18	1	US-08-959-512-66	Sequence 66, Appl
131	4	16.7	14	4	PCT-US93-07545-110	Sequence 110, App	204	4	16.7	18	2	US-09-513-983-66	Sequence 66, Appl
132	4	16.7	14	4	PCT-US94-14431A-5	Sequence 5, Appli	205	4	16.7	18	2	US-08-630-915A-172	Sequence 172, App
133	4	16.7	14	4	PCT-US95-17085-8	Sequence 8, Appli	206	4	16.7	18	2	US-08-475-399A-106	Sequence 106, App
134	4	16.7	15	1	US-08-471-780C-73	Sequence 73, Appl	207	4	16.7	18	2	US-08-475-399A-107	Sequence 107, App
135	4	16.7	15	1	US-08-467-282B-73	Sequence 73, Appl	208	4	16.7	18	2	US-09-721-108-121	Sequence 121, App
136	4	16.7	15	1	US-08-480-190-99	Sequence 99, Appl	209	4	16.7	18	2	US-08-077-255A-106	Sequence 106, App
137	4	16.7	15	1	US-08-471-282A-73	Sequence 73, Appl	210	4	16.7	18	2	US-08-077-255A-107	Sequence 107, App
138	4	16.7	15	1	US-08-466-710C-73	Sequence 73, Appl	211	4	16.7	18	2	US-09-879-937-172	Sequence 172, App
139	4	16.7	15	1	US-08-488-379-99	Sequence 99, Appl	212	4	16.7	18	2	US-10-394-980-29	Sequence 29, Appl
140	4	16.7	15	2	US-08-468-739C-73	Sequence 73, Appl	213	4	16.7	18	2	US-09-869-003-20	Sequence 20, Appl
141	4	16.7	15	2	US-08-481-968A-17	Sequence 17, Appl	214	4	16.7	18	4	PCT-US93-07545-106	Sequence 106, App
142	4	16.7	15	2	US-08-154-712B-17	Sequence 17, Appl	215	4	16.7	18	4	PCT-US93-07545-107	Sequence 107, App
143	4	16.7	15	2	US-08-475-399A-99	Sequence 99, Appl	216	4	16.7	19	1	US-08-480-190-94	Sequence 94, Appl
144	4	16.7	15	2	US-09-205-258-986	Sequence 986, App	217	4	16.7	19	1	US-08-480-190-95	Sequence 95, Appl
145	4	16.7	15	2	US-09-157-689-50	Sequence 50, Appl	218	4	16.7	19	1	US-08-480-190-96	Sequence 96, Appl
146	4	16.7	15	2	US-09-157-689-51	Sequence 51, Appl	219	4	16.7	19	1	US-08-480-190-105	Sequence 105, App
147	4	16.7	15	2	US-09-157-689-52	Sequence 52, Appl	220	4	16.7	19	1	US-08-488-379-94	Sequence 94, Appl
148	4	16.7	15	2	US-09-721-108-124	Sequence 124, App	221	4	16.7	19	1	US-08-488-379-95	Sequence 95, Appl
149	4	16.7	15	2	US-08-077-255A-99	Sequence 99, Appl	222	4	16.7	19	1	US-08-488-379-96	Sequence 96, Appl
150	4	16.7	15	2	US-09-947-925A-17	Sequence 17, Appl	223	4	16.7	19	1	US-08-488-379-105	Sequence 105, App
151	4	16.7	15	2	US-09-293-769A-73	Sequence 73, Appl	224	4	16.7	19	2	US-08-865-511B-22	Sequence 22, Appl
152	4	16.7	15	2	US-09-953-510-50	Sequence 50, Appl	225	4	16.7	19	2	US-08-865-511B-23	Sequence 23, Appl
153	4	16.7	15	2	US-09-953-510-51	Sequence 51, Appl	226	4	16.7	19	2	US-08-475-399A-94	Sequence 94, Appl
154	4	16.7	15	2	US-09-953-510-52	Sequence 52, Appl	227	4	16.7	19	2	US-08-475-399A-95	Sequence 95, Appl
155	4	16.7	15	2	US-10-004-860-986	Sequence 986, App	228	4	16.7	19	2	US-08-475-399A-96	Sequence 96, Appl
156	4	16.7	15	4	PCT-US93-07545-99	Sequence 99, Appl	229	4	16.7	19	2	US-08-475-399A-105	Sequence 105, App
157	4	16.7	16	1	US-07-794-288B-204	Sequence 204, App	230	4	16.7	19	2	US-09-721-108-120	Sequence 120, App
158	4	16.7	16	1	US-08-480-190-171	Sequence 171, App	231	4	16.7	19	2	US-08-077-255A-94	Sequence 94, Appl
159	4	16.7	16	1	US-08-488-379-171	Sequence 171, App	232	4	16.7	19	2	US-08-077-255A-95	Sequence 95, Appl
160	4	16.7	16	2	US-09-155-613A-9	Sequence 9, Appli	233	4	16.7	19	2	US-08-077-255A-96	Sequence 96, Appl
161	4	16.7	16	2	US-08-475-399A-171	Sequence 171, App	234	4	16.7	19	2	US-08-077-255A-105	Sequence 105, App
162	4	16.7	16	2	US-08-851-567B-18	Sequence 18, Appl	235	4	16.7	19	2	US-09-688-017-203	Sequence 203, App
163	4	16.7	16	2	US-09-721-108-123	Sequence 123, App	236	4	16.7	19	4	PCT-US93-07545-94	Sequence 94, Appl
164	4	16.7	16	2	US-08-077-255A-171	Sequence 171, App	237	4	16.7	19	4	PCT-US93-07545-95	Sequence 95, Appl
165	4	16.7	16	2	US-09-618-577-33	Sequence 33, Appl	238	4	16.7	19	4	PCT-US93-07545-96	Sequence 96, Appl
166	4	16.7	16	2	US-09-055-505-33	Sequence 33, Appl	239	4	16.7	19	4	PCT-US93-07545-105	Sequence 105, App
167	4	16.7	16	2	US-09-013-077A-3	Sequence 3, Appli	240	4	16.7	20	1	US-08-043-760-1	Sequence 1, Appli
168	4	16.7	16	4	PCT-US93-07545-171	Sequence 171, App	241	4	16.7	20	1	US-07-798-776-10	Sequence 10, Appl
169	4	16.7	17	1	US-08-480-190-97	Sequence 97, Appl	242	4	16.7	20	1	US-08-218-025A-41	Sequence 41, Appl
170	4	16.7	17	1	US-08-480-190-98	Sequence 98, Appl	243	4	16.7	20	1	US-08-218-025A-42	Sequence 42, Appl
171	4	16.7	17	1	US-08-480-190-108	Sequence 108, App	244	4	16.7	20	1	US-08-360-049-1	Sequence 1, Appli
172	4	16.7	17	1	US-08-480-190-109	Sequence 109, App	245	4	16.7	20	1	US-08-480-190-93	Sequence 93, Appl
173	4	16.7	17	1	US-08-488-379-97	Sequence 97, Appl	246	4	16.7	20	1	US-08-480-190-104	Sequence 104, App

247	4	16.7	20	1	US-08-480-190-244	Sequence 244, App	320	4	16.7	22	2	US-08-470-106-30	Sequence 30, Appl
248	4	16.7	20	1	US-08-411-726-4	Sequence 4, Appli	321	4	16.7	22	2	US-09-028-937-30	Sequence 30, Appl
249	4	16.7	20	1	US-08-488-379-93	Sequence 93, Appl	322	4	16.7	22	2	US-08-913-951-92	Sequence 92, Appl
250	4	16.7	20	1	US-08-488-379-104	Sequence 104, App	323	4	16.7	22	2	US-08-475-399A-43	Sequence 43, Appl
251	4	16.7	20	1	US-08-488-379-244	Sequence 244, App	324	4	16.7	22	2	US-08-475-399A-102	Sequence 102, App
252	4	16.7	20	1	US-08-934-915-89	Sequence 89, Appl	325	4	16.7	22	2	US-08-851-567B-70	Sequence 70, Appl
253	4	16.7	20	1	US-08-934-915-153	Sequence 153, App	326	4	16.7	22	2	US-09-402-181B-92	Sequence 92, Appl
254	4	16.7	20	1	US-08-372-100C-2	Sequence 2, Appli	327	4	16.7	22	2	US-09-721-456-92	Sequence 92, Appl
255	4	16.7	20	1	US-08-372-100C-3	Sequence 3, Appli	328	4	16.7	22	2	US-08-077-255A-43	Sequence 43, Appl
256	4	16.7	20	1	US-08-251-288A-10	Sequence 10, Appl	329	4	16.7	22	2	US-08-077-255A-102	Sequence 102, App
257	4	16.7	20	2	US-09-298-819A-10	Sequence 10, Appl	330	4	16.7	22	2	US-08-187-873-8	Sequence 8, Appli
258	4	16.7	20	2	US-08-865-511B-2	Sequence 2, Appli	331	4	16.7	22	4	PCT-US93-07545-43	Sequence 43, Appl
259	4	16.7	20	2	US-08-865-511B-3	Sequence 3, Appli	332	4	16.7	22	4	PCT-US93-07545-102	Sequence 102, App
260	4	16.7	20	2	US-09-586-563C-10	Sequence 10, Appl	333	4	16.7	23	1	US-08-480-190-101	Sequence 101, App
261	4	16.7	20	2	US-09-586-562C-10	Sequence 10, Appl	334	4	16.7	23	1	US-08-480-190-195	Sequence 195, App
262	4	16.7	20	2	US-08-475-399A-93	Sequence 93, Appl	335	4	16.7	23	1	US-08-493-235-37	Sequence 37, Appl
263	4	16.7	20	2	US-08-475-399A-104	Sequence 104, App	336	4	16.7	23	1	US-08-528-057-29	Sequence 29, Appl
264	4	16.7	20	2	US-08-475-399A-244	Sequence 244, App	337	4	16.7	23	1	US-08-486-953A-43	Sequence 43, Appl
265	4	16.7	20	2	US-08-506-436-2	Sequence 2, Appli	338	4	16.7	23	1	US-08-486-953A-44	Sequence 44, Appl
266	4	16.7	20	2	US-08-506-436-3	Sequence 3, Appli	339	4	16.7	23	1	US-08-679-405-7	Sequence 7, Appli
267	4	16.7	20	2	US-09-721-108-119	Sequence 119, App	340	4	16.7	23	1	US-08-488-379-101	Sequence 101, App
268	4	16.7	20	2	US-08-077-255A-93	Sequence 93, Appl	341	4	16.7	23	1	US-08-488-379-195	Sequence 195, App
269	4	16.7	20	2	US-08-077-255A-104	Sequence 104, App	342	4	16.7	23	1	US-08-842-793-7	Sequence 7, Appli
270	4	16.7	20	2	US-08-077-255A-244	Sequence 244, App	343	4	16.7	23	1	US-08-031-538-55	Sequence 55, Appl
271	4	16.7	20	2	US-09-623-548A-302	Sequence 302, App	344	4	16.7	23	2	US-08-609-236-3	Sequence 3, Appli
272	4	16.7	20	2	US-09-657-276-302	Sequence 302, App	345	4	16.7	23	2	US-08-475-399A-101	Sequence 101, App
273	4	16.7	20	4	PCT-US93-07545-93	Sequence 93, Appl	346	4	16.7	23	2	US-08-475-399A-195	Sequence 195, App
274	4	16.7	20	4	PCT-US93-07545-104	Sequence 104, App	347	4	16.7	23	2	US-08-077-255A-101	Sequence 101, App
275	4	16.7	20	4	PCT-US93-07545-244	Sequence 244, App	348	4	16.7	23	2	US-08-077-255A-195	Sequence 195, App
276	4	16.7	20	4	PCT-US95-17085-2	Sequence 2, Appli	349	4	16.7	23	2	US-09-285-912A-65	Sequence 65, Appl
277	4	16.7	20	4	PCT-US95-17085-3	Sequence 3, Appli	350	4	16.7	23	2	US-09-285-912A-109	Sequence 109, App
278	4	16.7	21	1	US-08-480-190-92	Sequence 92, Appl	351	4	16.7	23	2	US-08-204-052-43	Sequence 43, Appl
279	4	16.7	21	1	US-08-480-190-103	Sequence 103, App	352	4	16.7	23	2	US-08-204-052-44	Sequence 44, Appl
280	4	16.7	21	1	US-08-488-379-92	Sequence 92, Appl	353	4	16.7	23	2	PCT-US93-07545-101	Sequence 101, App
281	4	16.7	21	1	US-08-488-379-103	Sequence 103, App	354	4	16.7	23	4	PCT-US93-07545-195	Sequence 195, App
282	4	16.7	21	2	US-08-423-646A-34	Sequence 34, Appl	355	4	16.7	23	4	PCT-US96-11458-7	Sequence 7, Appli
283	4	16.7	21	2	US-08-423-646A-35	Sequence 35, Appl	356	4	16.7	24	2	US-08-725-459B-34	Sequence 34, Appl
284	4	16.7	21	2	US-08-423-646A-36	Sequence 36, Appl	357	4	16.7	24	2	US-09-270-767-36880	Sequence 36880, A
285	4	16.7	21	2	US-08-475-399A-92	Sequence 92, Appl	358	4	16.7	24	2	US-09-270-767-52097	Sequence 52097, A
286	4	16.7	21	2	US-08-475-399A-103	Sequence 103, App	359	4	16.7	25	1	US-08-145-708A-20	Sequence 20, Appl
287	4	16.7	21	2	US-09-721-108-118	Sequence 118, App	360	4	16.7	25	1	US-08-406-347A-12	Sequence 12, Appl
288	4	16.7	21	2	US-09-721-108-119	Sequence 119, App	361	4	16.7	25	1	US-08-331-454-20	Sequence 20, Appl
289	4	16.7	21	2	US-09-721-108-150	Sequence 150, App	362	4	16.7	25	2	US-09-314-268-4	Sequence 4, Appli
290	4	16.7	21	2	US-09-721-108-151	Sequence 151, App	363	4	16.7	25	2	US-08-905-054B-10	Sequence 10, Appl
291	4	16.7	21	2	US-09-721-108-152	Sequence 152, App	364	4	16.7	25	2	US-09-716-129-133	Sequence 133, App
292	4	16.7	21	2	US-09-721-108-153	Sequence 153, App	365	4	16.7	25	2	US-09-258-031C-1	Sequence 1, Appli
293	4	16.7	21	2	US-09-721-108-154	Sequence 154, App	366	4	16.7	25	4	PCT-US92-07813-10	Sequence 10, Appl
294	4	16.7	21	2	US-09-721-108-155	Sequence 155, App	367	3	12.5	3	1	US-08-251-027-4	Sequence 4, Appli
295	4	16.7	21	2	US-09-721-108-156	Sequence 156, App	368	3	12.5	3	1	US-08-305-768-26	Sequence 26, Appl
296	4	16.7	21	2	US-09-721-108-157	Sequence 157, App	369	3	12.5	3	1	US-08-871-163-26	Sequence 26, Appl
297	4	16.7	21	2	US-09-721-108-158	Sequence 158, App	370	3	12.5	3	2	US-08-767-903-26	Sequence 26, Appl
298	4	16.7	21	2	US-09-721-108-159	Sequence 159, App	371	3	12.5	3	4	PCT-US95-11724-26	Sequence 26, Appl
299	4	16.7	21	2	US-09-721-108-160	Sequence 160, App	372	3	12.5	4	1	US-08-285-777-2	Sequence 2, Appli
300	4	16.7	21	2	US-09-721-108-161	Sequence 161, App	373	3	12.5	4	1	US-08-457-605-2	Sequence 2, Appli
301	4	16.7	21	2	US-09-721-108-162	Sequence 162, App	374	3	12.5	4	1	US-08-305-768-30	Sequence 30, Appl
302	4	16.7	21	2	US-08-077-255A-92	Sequence 92, Appl	375	3	12.5	4	1	US-08-305-768-29	Sequence 29, Appl
303	4	16.7	21	2	US-08-077-255A-103	Sequence 103, App	376	3	12.5	4	1	US-08-372-262-4	Sequence 4, Appli
304	4	16.7	21	2	US-09-270-767-58351	Sequence 58351, A	377	3	12.5	4	1	US-08-456-424-8	Sequence 8, Appli
305	4	16.7	21	2	US-09-270-767-59315	Sequence 59315, A	378	3	12.5	4	1	US-08-456-424-9	Sequence 9, Appli
306	4	16.7	21	2	US-09-962-756-562	Sequence 562, App	379	3	12.5	4	1	US-08-456-424-13	Sequence 13, Appl
307	4	16.7	21	2	US-09-962-756-643	Sequence 643, App	380	3	12.5	4	1	US-08-456-424-14	Sequence 14, Appl
308	4	16.7	21	2	US-09-962-756-650	Sequence 650, App	381	3	12.5	4	1	US-08-456-424-24	Sequence 24, Appl
309	4	16.7	21	2	US-09-962-756-1746	Sequence 1746, App	382	3	12.5	4	1	US-08-456-424-25	Sequence 25, Appl
310	4	16.7	21	4	PCT-US93-07545-92	Sequence 92, Appl	383	3	12.5	4	1	US-08-456-424-95	Sequence 95, Appl
311	4	16.7	21	4	PCT-US93-07545-103	Sequence 103, App	384	3	12.5	4	1	US-08-456-424-96	Sequence 96, Appl
312	4	16.7	22	1	US-07-681-701-3	Sequence 3, Appli	385	3	12.5	4	1	US-08-871-163-29	Sequence 29, Appl
313	4	16.7	22	1	US-08-480-190-43	Sequence 43, Appl	386	3	12.5	4	1	US-08-871-163-30	Sequence 30, Appl
314	4	16.7	22	1	US-08-480-190-102	Sequence 102, App	387	3	12.5	4	2	US-08-947-965-63	Sequence 63, Appl
315	4	16.7	22	1	US-08-493-235-36	Sequence 36, Appl	388	3	12.5	4	2	US-08-767-903-29	Sequence 29, Appl
316	4	16.7	22	1	US-08-488-379-43	Sequence 43, Appl	389	3	12.5	4	2	US-08-767-903-30	Sequence 30, Appl
317	4	16.7	22	1	US-08-488-379-102	Sequence 102, App	390	3	12.5	4	2	US-08-974-549A-169	Sequence 169, App
318	4	16.7	22	2	US-08-318-794-30	Sequence 30, Appl	391	3	12.5	4	2	US-09-066-481-14	Sequence 14, Appl
319	4	16.7	22	2	US-08-974-549A-92	Sequence 92, Appl	392	3	12.5	4	2	US-09-336-447A-44	Sequence 44, Appl

393	3	12.5	4	2	US-08-862-871-8	Sequence 8, Appli	466	3	12.5	5	2	US-09-089-645A-38	Sequence 38, Appli
394	3	12.5	4	2	US-09-248-093-9	Sequence 9, Appli	467	3	12.5	5	2	US-09-082-514-29	Sequence 29, Appli
395	3	12.5	4	2	US-09-430-702-8	Sequence 8, Appli	468	3	12.5	5	2	US-09-398-193-26	Sequence 26, Appli
396	3	12.5	4	2	US-09-402-181B-169	Sequence 169, App	469	3	12.5	5	2	US-09-061-768A-28	Sequence 28, Appli
397	3	12.5	4	2	US-09-721-456-169	Sequence 169, App	470	3	12.5	5	2	US-09-263-975-21	Sequence 21, Appli
398	3	12.5	4	2	US-09-721-870-126	Sequence 126, App	471	3	12.5	5	2	US-09-081-707-6	Sequence 6, Appli
399	3	12.5	4	2	US-09-721-870-128	Sequence 128, App	472	3	12.5	5	2	US-08-472-929-2	Sequence 2, Appli
400	3	12.5	4	2	US-09-721-870-152	Sequence 152, App	473	3	12.5	5	2	US-09-541-965A-1	Sequence 1, Appli
401	3	12.5	4	2	US-09-664-595A-18	Sequence 18, Appli	474	3	12.5	5	2	US-08-466-163B-63	Sequence 63, Appli
402	3	12.5	4	2	US-10-132-920B-54	Sequence 54, Appli	475	3	12.5	5	2	US-09-503-998-36	Sequence 36, Appli
403	3	12.5	4	2	US-09-952-267B-44	Sequence 44, Appli	476	3	12.5	5	2	US-09-503-998-37	Sequence 37, Appli
404	3	12.5	4	2	US-09-211-715-18	Sequence 18, Appli	477	3	12.5	5	2	US-09-503-998-38	Sequence 38, Appli
405	3	12.5	4	2	US-09-211-715-20	Sequence 20, Appli	478	3	12.5	5	2	US-09-588-921-6	Sequence 6, Appli
406	3	12.5	4	2	US-09-722-377-79	Sequence 79, Appli	479	3	12.5	5	2	US-09-544-791-1	Sequence 1, Appli
407	3	12.5	4	2	US-09-700-696C-51	Sequence 51, Appli	480	3	12.5	5	2	US-09-430-702-9	Sequence 9, Appli
408	3	12.5	4	2	US-09-693-746-43	Sequence 43, Appli	481	3	12.5	5	2	US-09-373-694-36	Sequence 36, Appli
409	3	12.5	4	2	US-09-693-746-44	Sequence 44, Appli	482	3	12.5	5	2	US-09-373-694-37	Sequence 37, Appli
410	3	12.5	4	2	US-09-693-746-134	Sequence 134, App	483	3	12.5	5	2	US-09-373-694-38	Sequence 38, Appli
411	3	12.5	4	2	US-09-693-746-147	Sequence 147, App	484	3	12.5	5	2	US-09-544-789-1	Sequence 1, Appli
412	3	12.5	4	2	US-08-325-457-2	Sequence 2, Appli	485	3	12.5	5	2	US-09-129-192C-21	Sequence 21, Appli
413	3	12.5	4	2	US-09-817-198C-6	Sequence 6, Appli	486	3	12.5	5	2	US-09-588-822-6	Sequence 6, Appli
414	3	12.5	4	2	US-10-084-825-8	Sequence 8, Appli	487	3	12.5	5	2	US-09-436-874-21	Sequence 21, Appli
415	3	12.5	4	2	US-09-547-789-15	Sequence 15, Appli	488	3	12.5	5	2	US-09-205-258-858	Sequence 858, App
416	3	12.5	4	4	PCT-US95-11724-29	Sequence 29, Appli	489	3	12.5	5	2	US-08-634-332A-68	Sequence 68, Appli
417	3	12.5	4	4	PCT-US95-11724-30	Sequence 30, Appli	490	3	12.5	5	2	US-09-627-851B-6	Sequence 6, Appli
418	3	12.5	4	6	5169835-44	Patent No. 5169835	491	3	12.5	5	2	US-09-387-715-7	Sequence 7, Appli
419	3	12.5	5	1	US-07-901-717-3	Sequence 3, Appli	492	3	12.5	5	2	US-09-387-715-53	Sequence 53, Appli
420	3	12.5	5	1	US-08-014-979-116	Sequence 116, App	493	3	12.5	5	2	US-09-939-481-36	Sequence 36, Appli
421	3	12.5	5	1	US-08-014-979-117	Sequence 117, App	494	3	12.5	5	2	US-09-939-481-37	Sequence 37, Appli
422	3	12.5	5	1	US-08-014-979-118	Sequence 118, App	495	3	12.5	5	2	US-09-939-481-38	Sequence 38, Appli
423	3	12.5	5	1	US-08-014-979-119	Sequence 119, App	496	3	12.5	5	2	US-09-721-870-153	Sequence 153, App
424	3	12.5	5	1	US-08-014-979-120	Sequence 120, App	497	3	12.5	5	2	US-09-721-870-154	Sequence 154, App
425	3	12.5	5	1	US-08-305-768-31	Sequence 31, Appli	498	3	12.5	5	2	US-09-764-246-28	Sequence 28, Appli
426	3	12.5	5	1	US-08-064-111C-9	Sequence 9, Appli	499	3	12.5	5	2	US-09-802-096-63	Sequence 63, Appli
427	3	12.5	5	1	US-08-371-505-1	Sequence 1, Appli	500	3	12.5	5	2	US-09-802-077-63	Sequence 63, Appli
428	3	12.5	5	1	US-08-405-200-8	Sequence 8, Appli	501	3	12.5	5	2	US-09-566-047-107	Sequence 107, App
429	3	12.5	5	1	US-08-405-200-9	Sequence 9, Appli	502	3	12.5	5	2	US-09-211-715-224	Sequence 224, App
430	3	12.5	5	1	US-08-615-888-2	Sequence 2, Appli	503	3	12.5	5	2	US-09-608-892-40	Sequence 40, Appli
431	3	12.5	5	1	US-08-460-343B-15	Sequence 15, Appli	504	3	12.5	5	2	US-09-608-892-41	Sequence 41, Appli
432	3	12.5	5	1	US-08-460-343B-48	Sequence 48, Appli	505	3	12.5	5	2	US-10-346-927-36	Sequence 36, Appli
433	3	12.5	5	1	US-08-398-028B-15	Sequence 15, Appli	506	3	12.5	5	2	US-10-346-927-37	Sequence 37, Appli
434	3	12.5	5	1	US-08-398-028B-48	Sequence 48, Appli	507	3	12.5	5	2	US-10-346-927-38	Sequence 38, Appli
435	3	12.5	5	1	US-08-511-662-11	Sequence 11, Appli	508	3	12.5	5	2	US-09-623-548A-1079	Sequence 1079, Ap
436	3	12.5	5	1	US-08-504-265B-15	Sequence 15, Appli	509	3	12.5	5	2	US-09-623-548A-1179	Sequence 1179, Ap
437	3	12.5	5	1	US-08-504-265B-48	Sequence 48, Appli	510	3	12.5	5	2	US-09-051-395-7	Sequence 7, Appli
438	3	12.5	5	1	US-08-966-389-2	Sequence 2, Appli	511	3	12.5	5	2	US-09-759-484-1	Sequence 13, Appli
439	3	12.5	5	1	US-07-950-571A-5	Sequence 5, Appli	512	3	12.5	5	2	US-10-070-217-13	Sequence 21, Appli
440	3	12.5	5	1	US-08-292-968-29	Sequence 29, Appli	513	3	12.5	5	2	US-10-062-623B-21	Sequence 21, Appli
441	3	12.5	5	1	US-09-103-509-2	Sequence 2, Appli	514	3	12.5	5	2	US-10-062-623B-22	Sequence 22, Appli
442	3	12.5	5	1	US-08-871-163-31	Sequence 31, Appli	515	3	12.5	5	2	US-09-657-276-1079	Sequence 1079, Ap
443	3	12.5	5	1	US-09-102-644-2	Sequence 2, Appli	516	3	12.5	5	2	US-09-657-276-1179	Sequence 1179, Ap
444	3	12.5	5	1	US-08-679-865-21	Sequence 21, Appli	517	3	12.5	5	2	US-10-004-860-858	Sequence 858, App
445	3	12.5	5	1	US-08-680-876-21	Sequence 21, Appli	518	3	12.5	5	2	US-09-925-179-63	Sequence 63, Appli
446	3	12.5	5	1	US-08-467-974-29	Sequence 29, Appli	519	3	12.5	5	4	PCT-US95-11724-31	Sequence 31, Appli
447	3	12.5	5	1	US-08-232-539D-50	Sequence 50, Appli	520	3	12.5	5	4	PCT-US96-12632-11	Sequence 11, Appli
448	3	12.5	5	1	US-08-467-536-29	Sequence 29, Appli	521	3	12.5	5	6	5217869-49	Patent No. 5217869
449	3	12.5	5	1	US-08-211-312-2	Sequence 2, Appli	522	3	12.5	5	6	5217869-63	Patent No. 5217869
450	3	12.5	5	1	US-09-218-032-2	Sequence 2, Appli	523	3	12.5	6	1	US-08-285-777-18	Sequence 18, Appli
451	3	12.5	5	2	US-08-915-189-36	Sequence 36, Appli	524	3	12.5	6	1	US-08-285-777-19	Sequence 19, Appli
452	3	12.5	5	2	US-08-915-189-37	Sequence 37, Appli	525	3	12.5	6	1	US-08-285-777-20	Sequence 20, Appli
453	3	12.5	5	2	US-08-915-189-38	Sequence 38, Appli	526	3	12.5	6	1	US-08-180-209B-6	Sequence 6, Appli
454	3	12.5	5	2	US-08-467-976-29	Sequence 29, Appli	527	3	12.5	6	1	US-08-305-768-9	Sequence 9, Appli
455	3	12.5	5	2	US-08-767-903-31	Sequence 31, Appli	528	3	12.5	6	1	US-08-305-768-14	Sequence 14, Appli
456	3	12.5	5	2	US-08-972-760-36	Sequence 36, Appli	529	3	12.5	6	1	US-08-305-768-15	Sequence 15, Appli
457	3	12.5	5	2	US-08-972-760-37	Sequence 37, Appli	530	3	12.5	6	1	US-08-305-768-16	Sequence 16, Appli
458	3	12.5	5	2	US-08-972-760-38	Sequence 38, Appli	531	3	12.5	6	1	US-08-305-768-17	Sequence 17, Appli
459	3	12.5	5	2	US-08-472-285-2	Sequence 2, Appli	532	3	12.5	6	1	US-08-305-768-18	Sequence 18, Appli
460	3	12.5	5	2	US-08-466-151-63	Sequence 63, Appli	533	3	12.5	6	1	US-08-305-768-19	Sequence 19, Appli
461	3	12.5	5	2	US-08-894-173-26	Sequence 26, Appli	534	3	12.5	6	1	US-08-305-768-20	Sequence 20, Appli
462	3	12.5	5	2	US-08-981-122-63	Sequence 63, Appli	535	3	12.5	6	1	US-08-305-768-21	Sequence 21, Appli
463	3	12.5	5	2	US-08-882-046-107	Sequence 107, App	536	3	12.5	6	1	US-08-305-768-22	Sequence 22, Appli
464	3	12.5	5	2	US-09-089-645A-36	Sequence 36, Appli	537	3	12.5	6	1	US-08-305-768-23	Sequence 23, Appli
465	3	12.5	5	2	US-09-089-645A-37	Sequence 37, Appli	538	3	12.5	6	1	US-08-305-768-24	Sequence 24, Appli

539	3	12.5	6	1	US-08-385-745-6	Sequence 6, Appli	612	3	12.5	6	2	US-08-767-903-32	Sequence 32, Appl
540	3	12.5	6	1	US-07-789-184-165	Sequence 165, App	613	3	12.5	6	2	US-08-767-903-33	Sequence 33, Appl
541	3	12.5	6	1	US-08-537-069-1	Sequence 1, Appli	614	3	12.5	6	2	US-08-767-903-34	Sequence 34, Appl
542	3	12.5	6	1	US-08-537-069-2	Sequence 2, Appli	615	3	12.5	6	2	US-08-767-903-35	Sequence 35, Appl
543	3	12.5	6	1	US-08-537-069-3	Sequence 3, Appli	616	3	12.5	6	2	US-08-767-903-36	Sequence 36, Appl
544	3	12.5	6	1	US-08-537-069-4	Sequence 4, Appli	617	3	12.5	6	2	US-08-767-903-37	Sequence 37, Appl
545	3	12.5	6	1	US-08-537-069-5	Sequence 5, Appli	618	3	12.5	6	2	US-08-767-903-38	Sequence 38, Appl
546	3	12.5	6	1	US-08-537-069-6	Sequence 6, Appli	619	3	12.5	6	2	US-08-767-903-42	Sequence 42, Appl
547	3	12.5	6	1	US-08-537-069-7	Sequence 7, Appli	620	3	12.5	6	2	US-08-767-903-43	Sequence 43, Appl
548	3	12.5	6	1	US-08-537-069-8	Sequence 8, Appli	621	3	12.5	6	2	US-08-767-903-44	Sequence 44, Appl
549	3	12.5	6	1	US-08-537-069-9	Sequence 9, Appli	622	3	12.5	6	2	US-08-767-903-45	Sequence 45, Appl
550	3	12.5	6	1	US-08-537-069-10	Sequence 10, Appl	623	3	12.5	6	2	US-08-767-903-46	Sequence 46, Appl
551	3	12.5	6	1	US-08-537-069-11	Sequence 11, Appl	624	3	12.5	6	2	US-08-767-903-47	Sequence 47, Appl
552	3	12.5	6	1	US-08-537-069-12	Sequence 12, Appl	625	3	12.5	6	2	US-08-473-489A-165	Sequence 165, App
553	3	12.5	6	1	US-08-537-069-13	Sequence 13, Appl	626	3	12.5	6	2	US-08-466-151-61	Sequence 61, Appl
554	3	12.5	6	1	US-08-405-200-4	Sequence 4, Appli	627	3	12.5	6	2	US-08-812-586-19	Sequence 19, Appl
555	3	12.5	6	1	US-08-475-263-165	Sequence 165, App	628	3	12.5	6	2	US-08-485-695-165	Sequence 165, App
556	3	12.5	6	1	US-09-012-343-2	Sequence 2, Appli	629	3	12.5	6	2	US-09-074-658-40	Sequence 40, Appl
557	3	12.5	6	1	US-08-485-886-165	Sequence 165, App	630	3	12.5	6	2	US-09-196-934-13	Sequence 13, Appl
558	3	12.5	6	1	US-08-477-362-165	Sequence 165, App	631	3	12.5	6	2	US-08-018-760-165	Sequence 165, App
559	3	12.5	6	1	US-08-477-134-165	Sequence 165, App	632	3	12.5	6	2	US-09-001-984C-35	Sequence 35, Appl
560	3	12.5	6	1	US-08-871-163-9	Sequence 9, Appli	633	3	12.5	6	2	US-09-026-904-24	Sequence 24, Appl
561	3	12.5	6	1	US-08-871-163-14	Sequence 14, Appl	634	3	12.5	6	2	US-09-081-707-9	Sequence 9, Appli
562	3	12.5	6	1	US-08-871-163-15	Sequence 15, Appl	635	3	12.5	6	2	US-08-485-388-6	Sequence 6, Appli
563	3	12.5	6	1	US-08-871-163-16	Sequence 16, Appl	636	3	12.5	6	2	US-08-474-853-6	Sequence 6, Appli
564	3	12.5	6	1	US-08-871-163-17	Sequence 17, Appl	637	3	12.5	6	2	US-08-466-163B-61	Sequence 61, Appl
565	3	12.5	6	1	US-08-871-163-18	Sequence 18, Appl	638	3	12.5	6	2	US-09-187-859-855	Sequence 855, App
566	3	12.5	6	1	US-08-871-163-19	Sequence 19, Appl	639	3	12.5	6	2	US-09-187-859-870	Sequence 870, App
567	3	12.5	6	1	US-08-871-163-20	Sequence 20, Appl	640	3	12.5	6	2	US-09-166-205B-6	Sequence 6, Appli
568	3	12.5	6	1	US-08-871-163-21	Sequence 21, Appl	641	3	12.5	6	2	US-09-463-129B-2	Sequence 2, Appli
569	3	12.5	6	1	US-08-871-163-22	Sequence 22, Appl	642	3	12.5	6	2	US-09-588-921-9	Sequence 9, Appli
570	3	12.5	6	1	US-08-871-163-23	Sequence 23, Appl	643	3	12.5	6	2	US-09-305-927-265	Sequence 265, App
571	3	12.5	6	1	US-08-871-163-24	Sequence 24, Appl	644	3	12.5	6	2	US-09-305-927-280	Sequence 280, App
572	3	12.5	6	1	US-08-871-163-32	Sequence 32, Appl	645	3	12.5	6	2	US-09-170-769A-15	Sequence 15, Appl
573	3	12.5	6	1	US-08-871-163-33	Sequence 33, Appl	646	3	12.5	6	2	US-09-301-593-64	Sequence 64, Appl
574	3	12.5	6	1	US-08-871-163-34	Sequence 34, Appl	647	3	12.5	6	2	US-09-430-702-10	Sequence 10, Appl
575	3	12.5	6	1	US-08-871-163-35	Sequence 35, Appl	648	3	12.5	6	2	US-09-641-803-13	Sequence 13, Appl
576	3	12.5	6	1	US-08-871-163-36	Sequence 36, Appl	649	3	12.5	6	2	US-09-588-822-9	Sequence 9, Appli
577	3	12.5	6	1	US-08-871-163-37	Sequence 37, Appl	650	3	12.5	6	2	US-09-396-347F-35	Sequence 35, Appl
578	3	12.5	6	1	US-08-871-163-38	Sequence 38, Appl	651	3	12.5	6	2	US-09-394-455-46	Sequence 46, Appl
579	3	12.5	6	1	US-08-871-163-42	Sequence 42, Appl	652	3	12.5	6	2	US-08-634-332A-42	Sequence 42, Appl
580	3	12.5	6	1	US-08-871-163-43	Sequence 43, Appl	653	3	12.5	6	2	US-09-535-832A-20	Sequence 20, Appl
581	3	12.5	6	1	US-08-871-163-44	Sequence 44, Appl	654	3	12.5	6	2	US-09-214-307A-14	Sequence 14, Appl
582	3	12.5	6	1	US-08-871-163-45	Sequence 45, Appl	655	3	12.5	6	2	US-09-627-851B-9	Sequence 9, Appli
583	3	12.5	6	1	US-08-871-163-46	Sequence 46, Appl	656	3	12.5	6	2	US-09-387-715-49	Sequence 49, Appl
584	3	12.5	6	1	US-08-871-163-47	Sequence 47, Appl	657	3	12.5	6	2	US-09-839-542B-855	Sequence 855, App
585	3	12.5	6	1	US-08-726-306A-145	Sequence 145, App	658	3	12.5	6	2	US-09-839-542B-870	Sequence 870, App
586	3	12.5	6	1	US-08-232-539D-48	Sequence 48, Appl	659	3	12.5	6	2	US-09-264-516A-265	Sequence 265, App
587	3	12.5	6	1	US-08-482-228-14	Sequence 14, Appl	660	3	12.5	6	2	US-09-264-516A-280	Sequence 280, App
588	3	12.5	6	1	US-08-482-228-17	Sequence 17, Appl	661	3	12.5	6	2	US-09-632-570-33	Sequence 33, Appl
589	3	12.5	6	1	US-08-482-228-18	Sequence 18, Appl	662	3	12.5	6	2	US-09-721-870-155	Sequence 155, App
590	3	12.5	6	1	US-08-482-228-90	Sequence 90, Appl	663	3	12.5	6	2	US-09-721-870-163	Sequence 163, App
591	3	12.5	6	1	US-08-482-228-170	Sequence 170, App	664	3	12.5	6	2	US-09-721-870-164	Sequence 164, App
592	3	12.5	6	1	US-08-867-941-40	Sequence 40, Appl	665	3	12.5	6	2	US-09-721-108-203	Sequence 203, App
593	3	12.5	6	1	US-09-127-574-48	Sequence 48, Appl	666	3	12.5	6	2	US-09-387-671-24	Sequence 24, Appl
594	3	12.5	6	1	US-08-751-767A-76	Sequence 76, Appl	667	3	12.5	6	2	US-09-234-395-241	Sequence 241, App
595	3	12.5	6	2	US-08-482-528-14	Sequence 14, Appl	668	3	12.5	6	2	US-09-234-395-256	Sequence 256, App
596	3	12.5	6	2	US-08-482-528-17	Sequence 17, Appl	669	3	12.5	6	2	US-09-305-928-231	Sequence 231, App
597	3	12.5	6	2	US-08-482-528-18	Sequence 18, Appl	670	3	12.5	6	2	US-09-305-928-256	Sequence 256, App
598	3	12.5	6	2	US-08-482-528-90	Sequence 90, Appl	671	3	12.5	6	2	US-09-802-096-61	Sequence 61, Appl
599	3	12.5	6	2	US-08-482-528-170	Sequence 170, App	672	3	12.5	6	2	US-09-802-077-61	Sequence 61, Appl
600	3	12.5	6	2	US-08-767-903-9	Sequence 9, Appli	673	3	12.5	6	2	US-09-845-225-24	Sequence 24, Appl
601	3	12.5	6	2	US-08-767-903-14	Sequence 14, Appl	674	3	12.5	6	2	US-09-693-746-65	Sequence 65, Appl
602	3	12.5	6	2	US-08-767-903-15	Sequence 15, Appl	675	3	12.5	6	2	US-09-693-746-66	Sequence 66, Appl
603	3	12.5	6	2	US-08-767-903-16	Sequence 16, Appl	676	3	12.5	6	2	US-09-912-414-1	Sequence 1, Appli
604	3	12.5	6	2	US-08-767-903-17	Sequence 17, Appl	677	3	12.5	6	2	US-09-623-548A-1180	Sequence 1180, Ap
605	3	12.5	6	2	US-08-767-903-18	Sequence 18, Appl	678	3	12.5	6	2	US-09-623-548A-1186	Sequence 1186, Ap
606	3	12.5	6	2	US-08-767-903-19	Sequence 19, Appl	679	3	12.5	6	2	US-09-641-802-13	Sequence 13, Appl
607	3	12.5	6	2	US-08-767-903-20	Sequence 20, Appl	680	3	12.5	6	2	US-09-651-685-24	Sequence 24, Appl
608	3	12.5	6	2	US-08-767-903-21	Sequence 21, Appl	681	3	12.5	6	2	US-10-054-968-14	Sequence 14, Appl
609	3	12.5	6	2	US-08-767-903-22	Sequence 22, Appl	682	3	12.5	6	2	US-09-657-276-1180	Sequence 1180, Ap
610	3	12.5	6	2	US-08-767-903-23	Sequence 23, Appl	683	3	12.5	6	2	US-09-657-276-1186	Sequence 1186, Ap
611	3	12.5	6	2	US-08-767-903-24	Sequence 24, Appl	684	3	12.5	6	2	US-09-641-801-13	Sequence 13, Appl

685	3	12.5	6	2	US-10-394-980-256	Sequence 256, App	758	3	12.5	7	2	US-08-935-100-35	Sequence 35, Appl
686	3	12.5	6	2	US-09-791-524A-101	Sequence 101, App	759	3	12.5	7	2	US-08-974-549A-130	Sequence 130, App
687	3	12.5	6	2	US-09-925-179-61	Sequence 61, Appl	760	3	12.5	7	2	US-08-974-549A-133	Sequence 133, App
688	3	12.5	6	2	US-10-281-652-13	Sequence 13, Appl	761	3	12.5	7	2	US-09-147-933-14	Sequence 14, Appl
689	3	12.5	6	2	US-09-688-017-36	Sequence 36, Appl	762	3	12.5	7	2	US-09-147-933-18	Sequence 18, Appl
690	3	12.5	6	2	US-10-006-869-855	Sequence 855, App	763	3	12.5	7	2	US-09-147-933-26	Sequence 26, Appl
691	3	12.5	6	2	US-10-006-869-870	Sequence 870, App	764	3	12.5	7	2	US-09-258-754-236	Sequence 236, App
692	3	12.5	6	4	PCI-US94-02629-6	Sequence 6, Appl	765	3	12.5	7	2	US-09-258-754-384	Sequence 384, App
693	3	12.5	6	4	PCI-US95-03236-28	Sequence 28, Appl	766	3	12.5	7	2	US-08-826-133-1	Sequence 1, Appl
694	3	12.5	6	4	PCI-US95-11724-9	Sequence 9, Appl	767	3	12.5	7	2	US-09-562-897-16	Sequence 16, Appl
695	3	12.5	6	4	PCI-US95-11724-14	Sequence 14, Appl	768	3	12.5	7	2	US-09-042-107-236	Sequence 236, App
696	3	12.5	6	4	PCI-US95-11724-15	Sequence 15, Appl	769	3	12.5	7	2	US-09-042-107-384	Sequence 384, App
697	3	12.5	6	4	PCI-US95-11724-16	Sequence 16, Appl	770	3	12.5	7	2	US-08-706-344C-16	Sequence 16, Appl
698	3	12.5	6	4	PCI-US95-11724-17	Sequence 17, Appl	771	3	12.5	7	2	US-08-478-316-47	Sequence 47, Appl
699	3	12.5	6	4	PCI-US95-11724-18	Sequence 18, Appl	772	3	12.5	7	2	US-08-478-316-48	Sequence 48, Appl
700	3	12.5	6	4	PCI-US95-11724-19	Sequence 19, Appl	773	3	12.5	7	2	US-08-478-316-49	Sequence 49, Appl
701	3	12.5	6	4	PCI-US95-11724-20	Sequence 20, Appl	774	3	12.5	7	2	US-08-478-316-50	Sequence 50, Appl
702	3	12.5	6	4	PCI-US95-11724-21	Sequence 21, Appl	775	3	12.5	7	2	US-08-478-316-51	Sequence 51, Appl
703	3	12.5	6	4	PCI-US95-11724-22	Sequence 22, Appl	776	3	12.5	7	2	US-08-932-082-8	Sequence 8, Appl
704	3	12.5	6	4	PCI-US95-11724-23	Sequence 23, Appl	777	3	12.5	7	2	US-09-323-571-22	Sequence 22, Appl
705	3	12.5	6	4	PCI-US95-11724-24	Sequence 24, Appl	778	3	12.5	7	2	US-09-081-707-13	Sequence 13, Appl
706	3	12.5	6	6	5169835-47	Patent No. 5169835	779	3	12.5	7	2	US-09-214-095D-32	Sequence 32, Appl
707	3	12.5	7	1	US-07-715-183C-14	Sequence 14, Appl	780	3	12.5	7	2	US-09-214-095D-35	Sequence 35, Appl
708	3	12.5	7	1	US-07-945-982-7	Sequence 7, Appl	781	3	12.5	7	2	US-09-045-920-10	Sequence 10, Appl
709	3	12.5	7	1	US-08-285-777-21	Sequence 21, Appl	782	3	12.5	7	2	US-09-397-238A-15	Sequence 15, Appl
710	3	12.5	7	1	US-08-285-777-22	Sequence 22, Appl	783	3	12.5	7	2	US-08-486-673B-8	Sequence 8, Appl
711	3	12.5	7	1	US-08-372-455-7	Sequence 7, Appl	784	3	12.5	7	2	US-09-069-821-18	Sequence 18, Appl
712	3	12.5	7	1	US-08-372-455-7	Sequence 7, Appl	785	3	12.5	7	2	US-09-455-679-45	Sequence 45, Appl
713	3	12.5	7	1	US-08-279-906A-1	Sequence 1, Appl	786	3	12.5	7	2	US-09-227-357-366	Sequence 366, App
714	3	12.5	7	1	US-08-097-938-8	Sequence 8, Appl	787	3	12.5	7	2	US-09-400-653A-2	Sequence 2, Appl
715	3	12.5	7	1	US-08-200-900A-30	Sequence 30, Appl	788	3	12.5	7	2	US-09-187-859-857	Sequence 857, App
716	3	12.5	7	1	US-08-537-069-14	Sequence 14, Appl	789	3	12.5	7	2	US-09-187-859-872	Sequence 872, App
717	3	12.5	7	1	US-08-273-474-4	Sequence 4, Appl	790	3	12.5	7	2	US-09-187-859-1833	Sequence 1833, Ap
718	3	12.5	7	1	US-08-273-474-35	Sequence 35, Appl	791	3	12.5	7	2	US-09-187-859-1863	Sequence 1863, Ap
719	3	12.5	7	1	US-08-405-200-33	Sequence 33, Appl	792	3	12.5	7	2	US-09-187-859-2121	Sequence 2121, Ap
720	3	12.5	7	1	US-08-476-000-8	Sequence 8, Appl	793	3	12.5	7	2	US-09-187-859-2141	Sequence 2141, Ap
721	3	12.5	7	1	US-08-486-721A-5	Sequence 5, Appl	794	3	12.5	7	2	US-09-187-859-2189	Sequence 2189, Ap
722	3	12.5	7	1	US-08-486-721A-8	Sequence 8, Appl	795	3	12.5	7	2	US-09-187-859-2219	Sequence 2219, Ap
723	3	12.5	7	1	US-08-486-721A-11	Sequence 11, Appl	796	3	12.5	7	2	US-09-187-859-2863	Sequence 2863, Ap
724	3	12.5	7	1	US-08-486-721A-12	Sequence 12, Appl	797	3	12.5	7	2	US-09-187-859-2926	Sequence 2926, Ap
725	3	12.5	7	1	US-08-486-721A-13	Sequence 13, Appl	798	3	12.5	7	2	US-09-187-859-3805	Sequence 3805, Ap
726	3	12.5	7	1	US-08-486-721A-14	Sequence 14, Appl	799	3	12.5	7	2	US-09-110-822-7	Sequence 7, Appl
727	3	12.5	7	1	US-08-299-567-2	Sequence 2, Appl	800	3	12.5	7	2	US-09-019-793A-47	Sequence 47, Appl
728	3	12.5	7	1	US-08-472-840-8	Sequence 8, Appl	801	3	12.5	7	2	US-09-019-793A-48	Sequence 48, Appl
729	3	12.5	7	1	US-08-392-973A-34	Sequence 34, Appl	802	3	12.5	7	2	US-09-019-793A-49	Sequence 49, Appl
730	3	12.5	7	1	US-08-377-432-29	Sequence 29, Appl	803	3	12.5	7	2	US-09-019-793A-50	Sequence 50, Appl
731	3	12.5	7	1	US-08-866-845-1	Sequence 1, Appl	804	3	12.5	7	2	US-09-248-061B-2	Sequence 2, Appl
732	3	12.5	7	1	US-08-340-283-183	Sequence 183, App	805	3	12.5	7	2	US-09-588-921-13	Sequence 13, Appl
733	3	12.5	7	1	US-08-476-976-8	Sequence 8, Appl	806	3	12.5	7	2	US-09-479-479-5	Sequence 5, Appl
734	3	12.5	7	1	US-08-871-163-39	Sequence 39, Appl	807	3	12.5	7	2	US-09-297-851-5	Sequence 5, Appl
735	3	12.5	7	1	US-08-871-163-40	Sequence 40, Appl	808	3	12.5	7	2	US-09-305-927-267	Sequence 267, App
736	3	12.5	7	1	US-08-702-105A-22	Sequence 22, Appl	809	3	12.5	7	2	US-09-305-927-282	Sequence 282, App
737	3	12.5	7	1	US-08-968-676-68	Sequence 68, Appl	810	3	12.5	7	2	US-09-212-868-1	Sequence 1, Appl
738	3	12.5	7	1	US-08-946-241B-11	Sequence 11, Appl	811	3	12.5	7	2	US-09-430-702-11	Sequence 11, Appl
739	3	12.5	7	1	US-08-672-345C-32	Sequence 32, Appl	812	3	12.5	7	2	US-09-496-118B-10	Sequence 10, Appl
740	3	12.5	7	1	US-08-672-345C-35	Sequence 35, Appl	813	3	12.5	7	2	US-09-588-822-13	Sequence 13, Appl
741	3	12.5	7	1	US-08-053-451B-173	Sequence 173, App	814	3	12.5	7	2	US-09-446-301A-7	Sequence 7, Appl
742	3	12.5	7	1	US-08-482-228-30	Sequence 30, Appl	815	3	12.5	7	2	US-08-900-241-29	Sequence 29, Appl
743	3	12.5	7	1	US-08-814-806-5	Sequence 5, Appl	816	3	12.5	7	2	US-08-900-241-29	Sequence 29, Appl
744	3	12.5	7	2	US-09-071-877-10	Sequence 10, Appl	817	3	12.5	7	2	US-09-394-455-36	Sequence 36, Appl
745	3	12.5	7	2	US-08-482-528-30	Sequence 30, Appl	818	3	12.5	7	2	US-09-281-495-5	Sequence 5, Appl
746	3	12.5	7	2	US-08-767-903-39	Sequence 39, Appl	819	3	12.5	7	2	US-09-627-851B-13	Sequence 13, Appl
747	3	12.5	7	2	US-08-767-903-40	Sequence 40, Appl	820	3	12.5	7	2	US-09-326-806-7	Sequence 7, Appl
748	3	12.5	7	2	US-08-702-110A-22	Sequence 22, Appl	821	3	12.5	7	2	US-09-293-854-5	Sequence 5, Appl
749	3	12.5	7	2	US-08-474-410-8	Sequence 11, Appl	822	3	12.5	7	2	US-09-822-270-4	Sequence 4, Appl
750	3	12.5	7	2	US-09-309-053-11	Sequence 16, Appl	823	3	12.5	7	2	US-09-552-802B-48	Sequence 48, Appl
751	3	12.5	7	2	US-08-836-480-16	Sequence 16, Appl	824	3	12.5	7	2	US-08-407-620A-5	Sequence 5, Appl
752	3	12.5	7	2	US-08-377-781A-16	Sequence 16, Appl	825	3	12.5	7	2	US-09-839-542B-857	Sequence 857, App
753	3	12.5	7	2	US-09-173-941-48	Sequence 48, Appl	826	3	12.5	7	2	US-09-839-542B-872	Sequence 872, App
754	3	12.5	7	2	US-09-173-941-51	Sequence 51, Appl	827	3	12.5	7	2	US-09-839-542B-1833	Sequence 1833, Ap
755	3	12.5	7	2	US-09-173-941-52	Sequence 52, Appl	828	3	12.5	7	2	US-09-839-542B-1863	Sequence 1863, Ap
756	3	12.5	7	2	US-08-435-568A-20	Sequence 20, Appl	829	3	12.5	7	2	US-09-839-542B-2121	Sequence 2121, Ap
757	3	12.5	7	2	US-08-935-100-4	Sequence 4, Appl	830	3	12.5	7	2	US-09-839-542B-2141	Sequence 2141, Ap

977 3 12.5 8 1 US-08-279-906A-11
978 3 12.5 8 1 US-08-032-846-36
979 3 12.5 8 1 US-08-405-200-32
980 3 12.5 8 1 US-08-406-347A-11
981 3 12.5 8 1 US-08-688-675-7
982 3 12.5 8 1 US-08-040-548-42
983 3 12.5 8 1 US-08-466-344-42
984 3 12.5 8 1 US-08-259-550A-51
985 3 12.5 8 1 US-08-475-213-4
986 3 12.5 8 1 US-08-676-125A-1
987 3 12.5 8 1 US-08-508-664-20
988 3 12.5 8 1 US-08-922-267A-70
989 3 12.5 8 1 US-08-704-655-13
990 3 12.5 8 1 US-08-906-925-3
991 3 12.5 8 1 US-08-541-780-17
992 3 12.5 8 1 US-08-630-645-5
993 3 12.5 8 1 US-09-016-366A-65
994 3 12.5 8 1 US-08-350-260A-467
995 3 12.5 8 1 US-08-350-260A-468
996 3 12.5 8 1 US-08-350-260A-478
997 3 12.5 8 1 US-08-350-260A-526
998 3 12.5 8 1 US-08-978-404B-57
999 3 12.5 8 1 US-08-978-404B-67
1000 3 12.5 8 1 US-08-837-593-10

ALIGNMENTS

RESULT 1
US-08-642-846-4
; Sequence 4, Application US/08642846
; Patent No. 586151
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; APPLICANT: GALE, CHERYL A.
; APPLICANT: BENDEL, CATHERINE M.
; APPLICANT: TAO, NIAN-JUN
; APPLICANT: KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00280101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-642-846-4

Sequence 11, Appl
Sequence 36, Appl
Sequence 32, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 51, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 70, Appl
Sequence 13, Appl
Sequence 3, Appl
Sequence 17, Appl
Sequence 5, Appl
Sequence 65, Appl
Sequence 467, Appl
Sequence 468, Appl
Sequence 478, Appl
Sequence 526, Appl
Sequence 57, Appl
Sequence 67, Appl
Sequence 10, Appl

Query Match 25.0%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNS 20
| | | | |
Db 5 TNNNNS 10

RESULT 2
US-09-264-604-4
; Sequence 4, Application US/09264604
; Patent No. 634611
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; APPLICANT: GALE, CHERYL A.
; APPLICANT: BENDEL, CATHERINE M.
; APPLICANT: TAO, NIAN-JUN
; APPLICANT: KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00280101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-264-604-4

Query Match 25.0%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNNS 20
| | | | |
Db 5 TNNNNS 10

RESULT 3
US-09-978-343-4
; Sequence 4, Application US/09978343
; Patent No. 6774219
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.

GALE, CHERYL A.
BENDEL, CATHERINE M.
TAO, NIAN-JUN
KENDRICK, KATHLEEN
TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,343
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/642,846
FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00280101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-978-343-4

Query Match 25.0%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20
|||||
DB 5 TNNNS 10

RESULT 4
US-09-599-652-4
Sequence 4, Application US/09599652
Patent No. RE37741
GENERAL INFORMATION:
APPLICANT: HOSTETTER, MARGARET K.
APPLICANT: GALE, CHERYL A.
APPLICANT: BENDEL, CATHERINE M.
APPLICANT: TAO, NIAN-JUN
APPLICANT: KENDRICK, KATHLEEN
TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
TITLE OF INVENTION: 12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,652
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/642,846
FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00280101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-599-652-4

Query Match 25.0%; Score 6; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNNS 20
|||||
DB 5 TNNNS 10

RESULT 5
US-08-729-152-32
Sequence 32, Application US/08729152
Patent No. 5871739
GENERAL INFORMATION:
APPLICANT: Incue, Eri
TITLE OF INVENTION: Pharmaceutical Composition
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: Southern Building, Suite 700, 805 Fifteenth
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,152
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291993/1995
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
INFORMATION FOR SEQ ID NO: 32:

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-729-152-32

Query Match 20.8%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFEQE 14
Db 9 IFEQE 13

RESULT 6
US-09-962-756-501
; Sequence 501, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 501
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-501

Query Match 20.8%; Score 5; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 NSSFY 23
Db 8 NSSFY 12

RESULT 7
US-08-486-953A-48
; Sequence 48, Application US/08486953A
; Patent No. 5849290
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP

; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,953A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,052
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/223002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/428-0200
; TELEFAX: 617/428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-953A-48

Query Match 20.8%; Score 5; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFEQE 14
Db 19 IFEQE 23

RESULT 8
US-08-204-052-48
; Sequence 48, Application US/08204052
; Patent No. 6723893
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,052
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,980
; FILING DATE: 26-FEB-1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/223001
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-052-48

Query Match 20.8%; Score 5; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFEQE 14
Db 19 IFEQE 23

RESULT 9
US-09-967-869A-1
Sequence 1, Application US/09967869A
Patent No. 6919204
GENERAL INFORMATION:
APPLICANT: WOLFFE, Alan P.
APPLICANT: URNOV, Evdod
APPLICANT: LAI, Albert
APPLICANT: RASCHKE, Eva
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION USING LOCALIZATION
FILE REFERENCE: 8325-0019 / S19
CURRENT APPLICATION NUMBER: US/09/967,869A
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: segment from
OTHER INFORMATION: Drosophila MBD-like sequence
US-09-967-869A-1

Query Match 20.8%; Score 5; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NNNSS 21
Db 7 NNNSS 11

RESULT 10
US-07-834-848-3
Sequence 3, Application US/07834848
Patent No. 5436221
GENERAL INFORMATION:
APPLICANT: KITAGUCHI, HIROSHI
APPLICANT: KOMAZAWA, HIROYUKI
APPLICANT: KOJIMA, MASAYOSHI
APPLICANT: MORI, HIDETO
APPLICANT: NISHIKAWA, NAOYUKI
APPLICANT: SATOH, HIDEAKI
APPLICANT: ORIKASA, ATSUSHI
APPLICANT: ONO, MITSUNORI

APPLICANT: AZUMA, ICHIRO
APPLICANT: SAIKI, IKUO
TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
STREET: 2100 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,848
FILING DATE: 19920213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Biggart, Waddell A.
REGISTRATION NUMBER: 24,961
REFERENCE/DOCKET NUMBER: Q28480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-834-848-3

Query Match 16.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
Db 1 RFDS 4

RESULT 11
US-08-251-027-10
Sequence 10, Application US/08251027
Patent No. 5519005
GENERAL INFORMATION:
APPLICANT: Lider, Ofer
APPLICANT: Greenspoon, No. 5519005m
APPLICANT: Hershkoviz, Rami
APPLICANT: Alon, Ronen
TITLE OF INVENTION: A METHOD OF INHIBITION OF CELLULAR AND
TITLE OF INVENTION: MOLECULAR LEVEL BIOLOGICAL INTERACTIONS UTILIZING
TITLE OF INVENTION: NON-PEPTIDIC SURROGATES OF THE ARG-GLY-ASP SEQUENCE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5519005thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,027

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,848
FILING DATE: 19920213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Biggart, Waddell A.
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER: Q28480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-834-848-7

Query Match 16.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
Db 2 RFDS 5

RESULT 15

US-07-834-848-10
Sequence 10, Application US/07834848
Patent No. 5436221
GENERAL INFORMATION:
APPLICANT: KITAGUCHI, HIROSHI
APPLICANT: KOMAZAWA, HIROYUKI
APPLICANT: KOJIMA, MASAYOSHI
APPLICANT: MORI, HIDEYO
APPLICANT: NISHIKAWA, NAOTYUKI
APPLICANT: SATOH, HIDEAKI
APPLICANT: ORIKASA, ATSUSHI
APPLICANT: ONO, MITSUNORI
APPLICANT: AZUMA, ICHIRO
APPLICANT: SAIKI, IKUO
TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
STREET: 2100 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,848
FILING DATE: 19920213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Biggart, Waddell A.
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER: Q28480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060

TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-834-848-10

Query Match 16.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
Db 2 RFDS 5

Search completed: January 20, 2006, 17:56:44
Job time : 29 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:53:00 ; Search time 58 Seconds
(without alignments)
172.895 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24

Sequence: 1 LRFDSQTSIFEQETNNNSFYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412413

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	25.0	23	3	US-09-378-343-4
2	5	20.8	9	3	US-09-935-384-41
3	5	20.8	9	3	US-09-935-384-131
4	5	20.8	9	3	US-09-935-384-229
5	5	20.8	9	3	US-09-935-384-310
6	5	20.8	9	3	US-09-935-384-419
7	5	20.8	9	3	US-09-935-384-529
8	5	20.8	9	3	US-09-935-384-616
9	5	20.8	9	5	US-10-808-187-1154
10	5	20.8	9	5	US-10-705-459-307
11	5	20.8	9	5	US-10-807-807-1154
12	5	20.8	10	3	US-09-935-384-368
13	5	20.8	10	3	US-09-935-384-661
14	5	20.8	12	3	US-09-982-172-186
15	5	20.8	12	3	US-09-982-172-245
16	5	20.8	12	4	US-10-378-173-67
17	5	20.8	16	4	US-10-239-313A-590
18	5	20.8	16	4	US-10-312-732A-18
19	5	20.8	18	4	US-10-225-567A-1150
20	5	20.8	18	4	US-10-225-567A-1588
21	5	20.8	21	3	US-09-962-756-501
22	5	20.8	21	4	US-10-253-471-501
23	5	20.8	21	4	US-10-253-493-501
24	5	20.8	23	3	US-09-967-869A-1
25	5	20.8	23	6	US-11-045-828-1
26	5	20.8	25	4	US-10-416-249-377
27	4	16.7	4	4	US-10-128-590-73
28	4	16.7	4	4	US-10-353-174-33
29	4	16.7	4	4	US-10-128-587A-73
30	4	16.7	4	4	US-10-128-578B-65
31	4	16.7	4	4	US-10-391-393-122
32	4	16.7	4	5	US-10-769-565-6
33	4	16.7	4	5	US-10-780-003-50
34	4	16.7	4	5	US-10-781-933-3
35	4	16.7	4	6	US-11-006-372-33
36	4	16.7	4	5	US-10-197-954-59
37	4	16.7	4	5	US-10-841-056-68
38	4	16.7	4	5	US-10-841-121-68
39	4	16.7	4	5	US-10-760-085-59
40	4	16.7	4	5	US-10-759-731A-89
41	4	16.7	4	5	US-10-939-309-98
42	4	16.7	4	5	US-10-841-049-68
43	4	16.7	4	5	US-11-066-697-1080
44	4	16.7	4	6	US-09-897-107-102
45	4	16.7	4	6	US-10-702-765-133
46	4	16.7	4	6	US-11-025-608-4
47	4	16.7	4	7	US-08-592-711-7
48	4	16.7	4	7	US-09-845-667-51
49	4	16.7	4	7	US-09-192-854-61
50	4	16.7	4	7	US-09-183-055-7
51	4	16.7	4	7	US-09-968-561A-99
52	4	16.7	4	7	US-09-350-202-7
53	4	16.7	4	7	US-09-968-744A-99
54	4	16.7	4	7	US-09-968-561A-99
55	4	16.7	4	7	US-10-104-019-51
56	4	16.7	4	7	US-10-104-019-51
57	4	16.7	4	7	US-10-428-826-92
58	4	16.7	4	7	US-10-080-608A-80
59	4	16.7	4	7	US-10-390-330-7
60	4	16.7	4	7	US-10-371-067-10
61	4	16.7	4	7	US-10-702-765-132
62	4	16.7	4	7	US-10-327-598-716
63	4	16.7	4	7	US-11-115-682-99
64	4	16.7	4	8	US-10-127-691-31
65	4	16.7	4	8	US-10-140-164-9
66	4	16.7	4	8	US-10-140-164-39
67	4	16.7	4	8	US-10-073-133A-9
68	4	16.7	4	8	US-10-462-452-459
69	4	16.7	4	8	US-10-367-580-192
70	4	16.7	4	8	US-10-367-593-192
71	4	16.7	4	8	US-10-367-594-192
72	4	16.7	4	8	US-10-367-654-192
73	4	16.7	4	8	US-10-367-658-192
74	4	16.7	4	8	US-10-367-668-192
75	4	16.7	4	8	US-10-601-953-571
76	4	16.7	4	8	US-10-601-953-571
77	4	16.7	4	8	US-10-380-196A-7
78	4	16.7	4	8	US-10-702-765-131
79	4	16.7	4	8	US-10-322-266-444
80	4	16.7	4	8	US-10-322-266-460
81	4	16.7	4	8	US-10-367-674-192
82	4	16.7	4	8	US-10-841-471-9
83	4	16.7	4	8	US-10-786-850-32
84	4	16.7	4	8	US-10-643-627-31
85	4	16.7	4	8	US-10-498-468A-14
86	4	16.7	4	8	US-10-820-067A-171
87	4	16.7	4	9	US-08-821-739A-49
88	4	16.7	4	9	US-08-821-739A-53
89	4	16.7	4	9	US-09-935-384-32
90	4	16.7	4	9	US-09-935-384-46
91	4	16.7	4	9	US-09-935-384-133
92	4	16.7	4	9	US-09-935-384-147
93	4	16.7	4	9	US-09-935-384-450
94	4	16.7	4	9	US-09-935-384-535
95	4	16.7	4	9	US-09-935-384-634
96	4	16.7	4	9	US-09-935-384-633
97	4	16.7	4	9	US-10-203-754A-6
98	4	16.7	4	9	US-10-105-232-167
99	4	16.7	4	9	US-10-189-437-154
100	4	16.7	4	9	US-10-702-765-130

Sequence 33, Appl
Sequence 73, Appl
Sequence 65, Appl
Sequence 122, Appl
Sequence 6, Appl
Sequence 50, Appl
Sequence 3, Appl
Sequence 33, Appl
Sequence 59, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 98, Appl
Sequence 98, Appl
Sequence 1080, App
Sequence 102, App
Sequence 133, App
Sequence 4, Appl
Sequence 7, Appl
Sequence 51, Appl
Sequence 61, Appl
Sequence 7, Appl
Sequence 99, Appl
Sequence 99, Appl
Sequence 99, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 92, Appl
Sequence 80, Appl
Sequence 7, Appl
Sequence 10, Appl
Sequence 132, App
Sequence 716, App
Sequence 99, Appl
Sequence 31, Appl
Sequence 9, Appl
Sequence 39, Appl
Sequence 459, App
Sequence 192, App
Sequence 192, App
Sequence 192, App
Sequence 192, App
Sequence 192, App
Sequence 588, App
Sequence 571, App
Sequence 7, Appl
Sequence 131, App
Sequence 444, App
Sequence 460, App
Sequence 192, App
Sequence 9, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 14, Appl
Sequence 171, App
Sequence 49, Appl
Sequence 53, Appl
Sequence 32, Appl
Sequence 46, Appl
Sequence 133, App
Sequence 147, App
Sequence 450, App
Sequence 535, App
Sequence 614, App
Sequence 633, App
Sequence 6, Appl
Sequence 167, App
Sequence 154, App
Sequence 130, App

101	4	16.7	9	4	US-10-715-417-44	Sequence 44, Appl	174	4	16.7	13	4	US-10-182-033-18	Sequence 18, Appl
102	4	16.7	9	4	US-10-657-022-585	Sequence 585, App	175	4	16.7	13	4	US-10-378-173-104	Sequence 104, App
103	4	16.7	9	4	US-10-354-090-44	Sequence 44, Appl	176	4	16.7	13	4	US-10-469-304-67	Sequence 67, Appl
104	4	16.7	9	5	US-10-808-187-2369	Sequence 2369, Ap	177	4	16.7	13	4	US-10-469-304-68	Sequence 68, Appl
105	4	16.7	9	5	US-10-680-557-1	Sequence 1, Appl	178	4	16.7	13	4	US-10-469-304-69	Sequence 69, Appl
106	4	16.7	9	5	US-10-807-807-2369	Sequence 2369, Ap	179	4	16.7	13	4	US-10-469-304-70	Sequence 70, Appl
107	4	16.7	9	5	US-10-498-468A-1	Sequence 1, Appl	180	4	16.7	13	4	US-10-469-304-71	Sequence 71, Appl
108	4	16.7	9	5	US-10-498-468A-6	Sequence 6, Appl	181	4	16.7	13	4	US-10-469-304-71	Sequence 71, Appl
109	4	16.7	9	5	US-10-498-468A-7	Sequence 7, Appl	182	4	16.7	13	4	US-10-702-765-126	Sequence 126, App
110	4	16.7	9	5	US-10-498-468A-8	Sequence 8, Appl	183	4	16.7	13	4	US-10-469-145-9	Sequence 9, Appl
111	4	16.7	9	5	US-10-498-468A-12	Sequence 12, Appl	184	4	16.7	13	4	US-10-468-496-1189	Sequence 1189, Ap
112	4	16.7	9	5	US-10-498-468A-13	Sequence 13, Appl	185	4	16.7	13	4	US-10-468-496-1190	Sequence 1190, Ap
113	4	16.7	9	5	US-10-860-050-167	Sequence 167, App	186	4	16.7	13	4	US-10-468-496-1191	Sequence 1191, Ap
114	4	16.7	10	3	US-09-572-404B-1176	Sequence 1176, Ap	187	4	16.7	13	5	US-10-822-173-56	Sequence 1192, Ap
115	4	16.7	10	3	US-09-935-384-163	Sequence 163, App	188	4	16.7	13	5	US-10-903-213-56	Sequence 56, Appl
116	4	16.7	10	3	US-09-935-384-289	Sequence 289, App	189	4	16.7	13	5	US-10-498-468A-15	Sequence 56, Appl
117	4	16.7	10	3	US-09-935-384-366	Sequence 366, App	190	4	16.7	13	5	US-10-948-707-1232	Sequence 15, Appl
118	4	16.7	10	3	US-09-935-384-587	Sequence 587, App	191	4	16.7	13	5	US-10-948-707-1232	Sequence 1232, Ap
119	4	16.7	10	4	US-10-101-812-1	Sequence 1, Appl	192	4	16.7	14	3	US-09-972-484-33	Sequence 33, Appl
120	4	16.7	10	4	US-10-101-662A-1	Sequence 1, Appl	193	4	16.7	14	3	US-09-988-493-264	Sequence 264, App
121	4	16.7	10	4	US-10-133-210-259	Sequence 259, App	194	4	16.7	14	3	US-09-991-225-24	Sequence 24, Appl
122	4	16.7	10	4	US-10-287-670-1	Sequence 1, Appl	194	4	16.7	14	3	US-09-991-225-25	Sequence 25, Appl
123	4	16.7	10	4	US-10-200-708-322	Sequence 322, App	195	4	16.7	14	3	US-09-991-225-42	Sequence 42, Appl
124	4	16.7	10	4	US-10-200-708-597	Sequence 597, App	196	4	16.7	14	3	US-09-991-225-43	Sequence 43, Appl
125	4	16.7	10	4	US-10-462-452-399	Sequence 399, App	197	4	16.7	14	3	US-09-991-225-44	Sequence 44, Appl
126	4	16.7	10	4	US-10-462-452-413	Sequence 413, App	198	4	16.7	14	4	US-10-097-065-553	Sequence 553, App
127	4	16.7	10	4	US-10-462-452-421	Sequence 421, App	199	4	16.7	14	4	US-10-120-604-27	Sequence 27, Appl
128	4	16.7	10	4	US-10-462-452-434	Sequence 434, App	200	4	16.7	14	4	US-10-120-604-28	Sequence 28, Appl
129	4	16.7	10	4	US-10-430-685-180	Sequence 180, App	201	4	16.7	14	4	US-10-120-604-70	Sequence 70, Appl
130	4	16.7	10	4	US-10-430-685-183	Sequence 183, App	202	4	16.7	14	4	US-10-120-604-71	Sequence 71, Appl
131	4	16.7	10	4	US-10-430-685-193	Sequence 193, App	203	4	16.7	14	4	US-10-120-604-86	Sequence 86, Appl
132	4	16.7	10	4	US-10-430-685-231	Sequence 231, App	204	4	16.7	14	4	US-10-120-604-87	Sequence 87, Appl
133	4	16.7	10	4	US-10-601-953-527	Sequence 527, App	205	4	16.7	14	4	US-10-219-834-117	Sequence 117, App
134	4	16.7	10	4	US-10-601-953-541	Sequence 541, App	206	4	16.7	14	4	US-10-219-834-122	Sequence 122, App
135	4	16.7	10	4	US-10-601-953-549	Sequence 549, App	207	4	16.7	14	4	US-10-239-311A-638	Sequence 638, App
136	4	16.7	10	4	US-10-601-953-562	Sequence 562, App	208	4	16.7	14	4	US-10-082-014-96	Sequence 96, Appl
137	4	16.7	10	4	US-10-702-765-129	Sequence 129, App	209	4	16.7	14	4	US-10-239-423-24	Sequence 24, Appl
138	4	16.7	10	4	US-10-322-266-400	Sequence 400, App	210	4	16.7	14	4	US-10-372-076-97	Sequence 97, Appl
139	4	16.7	10	4	US-10-322-266-414	Sequence 414, App	211	4	16.7	14	4	US-10-372-876-553	Sequence 553, App
140	4	16.7	10	4	US-10-322-266-422	Sequence 422, App	212	4	16.7	14	4	US-10-369-405-24	Sequence 24, Appl
141	4	16.7	10	4	US-10-322-266-435	Sequence 435, App	213	4	16.7	14	4	US-10-369-405-25	Sequence 25, Appl
142	4	16.7	10	4	US-10-777-053-294	Sequence 294, App	214	4	16.7	14	4	US-10-369-405-42	Sequence 42, Appl
143	4	16.7	10	4	US-10-715-417-51	Sequence 51, Appl	215	4	16.7	14	4	US-10-369-405-43	Sequence 43, Appl
144	4	16.7	10	4	US-10-715-417-52	Sequence 52, Appl	216	4	16.7	14	4	US-10-369-405-44	Sequence 44, Appl
145	4	16.7	10	4	US-10-715-417-59	Sequence 59, Appl	217	4	16.7	14	4	US-10-361-208-159	Sequence 159, App
146	4	16.7	10	4	US-10-327-598-707	Sequence 707, App	218	4	16.7	14	4	US-10-702-765-125	Sequence 125, App
147	4	16.7	10	4	US-10-837-217-294	Sequence 294, App	219	4	16.7	14	4	US-10-746-442-10	Sequence 10, Appl
148	4	16.7	10	4	US-10-354-090-51	Sequence 51, Appl	220	4	16.7	14	4	US-10-732-862A-111	Sequence 111, App
149	4	16.7	10	4	US-10-354-090-52	Sequence 52, Appl	221	4	16.7	14	4	US-10-677-074-97	Sequence 97, Appl
150	4	16.7	10	4	US-10-859-933-1	Sequence 59, Appl	222	4	16.7	14	5	US-10-926-386-37	Sequence 37, Appl
151	4	16.7	10	5	US-11-027-273-1	Sequence 1, Appl	223	4	16.7	14	5	US-10-926-386-38	Sequence 38, Appl
152	4	16.7	10	6	US-09-988-493-67	Sequence 1, Appl	224	4	16.7	14	6	US-11-070-456-27	Sequence 27, Appl
153	4	16.7	11	3	US-10-262-435-109	Sequence 67, Appl	225	4	16.7	14	6	US-11-070-456-27	Sequence 27, Appl
154	4	16.7	11	4	US-10-239-313A-281	Sequence 0, Appl	226	4	16.7	14	6	US-11-070-456-28	Sequence 28, Appl
155	4	16.7	11	4	US-10-086-208-109	Sequence 281, App	227	4	16.7	14	6	US-11-070-456-70	Sequence 70, Appl
156	4	16.7	11	4	US-10-702-765-128	Sequence 109, App	228	4	16.7	14	6	US-11-070-456-71	Sequence 71, Appl
157	4	16.7	11	4	US-10-808-187-1532	Sequence 128, App	229	4	16.7	14	6	US-11-070-456-86	Sequence 86, Appl
158	4	16.7	11	5	US-10-808-187-1532	Sequence 1532, Ap	230	4	16.7	14	6	US-11-070-456-87	Sequence 87, Appl
159	4	16.7	11	5	US-10-705-459-332	Sequence 332, App	231	4	16.7	15	3	US-09-947-925A-17	Sequence 17, Appl
160	4	16.7	11	5	US-10-705-459-332	Sequence 332, App	232	4	16.7	15	3	US-09-947-925A-18	Sequence 18, Appl
161	4	16.7	11	5	US-10-479-933-12	Sequence 12, Appl	233	4	16.7	15	3	US-09-768-779A-18	Sequence 50, Appl
162	4	16.7	11	5	US-10-807-807-1532	Sequence 1532, Ap	234	4	16.7	15	3	US-09-953-510-50	Sequence 51, Appl
163	4	16.7	11	5	US-10-807-807-1625	Sequence 1625, Ap	235	4	16.7	15	3	US-09-953-510-51	Sequence 51, Appl
164	4	16.7	12	3	US-09-947-925A-27	Sequence 27, Appl	236	4	16.7	15	3	US-09-953-510-52	Sequence 52, Appl
165	4	16.7	12	3	US-09-991-225-23	Sequence 23, Appl	237	4	16.7	15	3	US-09-919-603-21	Sequence 21, Appl
166	4	16.7	12	4	US-10-369-405-23	Sequence 23, Appl	238	4	16.7	15	3	US-09-882-774-11	Sequence 11, Appl
167	4	16.7	12	4	US-10-702-765-127	Sequence 127, App	239	4	16.7	15	3	US-09-726-470A-224	Sequence 224, App
168	4	16.7	12	5	US-10-746-547-3	Sequence 3, Appl	240	4	16.7	15	3	US-09-991-225-60	Sequence 60, Appl
169	4	16.7	12	5	US-10-275-652-44	Sequence 44, Appl	241	4	16.7	15	3	US-09-991-225-72	Sequence 72, Appl
170	4	16.7	13	3	US-09-851-138-157	Sequence 157, App	242	4	16.7	15	3	US-09-933-767-986	Sequence 986, App
171	4	16.7	13	3	US-09-782-130-13	Sequence 13, Appl	243	4	16.7	15	3	US-09-953-413-51	Sequence 51, Appl
172	4	16.7	13	3	US-09-782-130-14	Sequence 14, Appl	244	4	16.7	15	3	US-09-953-413-52	Sequence 52, Appl
173	4	16.7	13	4	US-10-219-834-121	Sequence 121, App	245	4	16.7	15	4	US-10-004-860-986	Sequence 986, App

247	4	16.7	15	4	US-10-023-282-986	Sequence 986, App	320	4	16.7	17	5	US-10-807-807-1053	Sequence 1053, App
248	4	16.7	15	4	US-10-291-480-18	Sequence 18, App	321	4	16.7	17	5	US-10-860-050-153	Sequence 153, App
249	4	16.7	15	4	US-10-225-567A-2046	Sequence 2046, App	322	4	16.7	17	5	US-10-860-050-166	Sequence 166, App
250	4	16.7	15	4	US-10-147-255-50	Sequence 50, App	323	4	16.7	17	5	US-10-860-050-207	Sequence 207, App
251	4	16.7	15	4	US-10-147-255-51	Sequence 51, App	324	4	16.7	17	5	US-10-860-050-398	Sequence 398, App
252	4	16.7	15	4	US-10-147-255-52	Sequence 52, App	325	4	16.7	18	3	US-09-879-957-1172	Sequence 172, App
253	4	16.7	15	4	US-10-294-891-42	Sequence 42, App	326	4	16.7	18	4	US-10-105-232-397	Sequence 397, App
254	4	16.7	15	4	US-10-369-405-60	Sequence 60, App	327	4	16.7	18	4	US-10-082-014-105	Sequence 105, App
255	4	16.7	15	4	US-10-369-405-72	Sequence 72, App	328	4	16.7	18	4	US-10-189-437-384	Sequence 384, App
256	4	16.7	15	4	US-10-702-765-124	Sequence 124, App	329	4	16.7	18	4	US-10-372-076-106	Sequence 106, App
257	4	16.7	15	4	US-10-416-249-312	Sequence 312, App	330	4	16.7	18	4	US-10-394-980-29	Sequence 29, App
258	4	16.7	15	4	US-10-416-249-577	Sequence 577, App	331	4	16.7	18	4	US-10-702-765-1121	Sequence 121, App
259	4	16.7	15	4	US-10-441-952A-243	Sequence 243, App	332	4	16.7	18	4	US-10-685-898-84	Sequence 84, App
260	4	16.7	15	5	US-10-695-155-50	Sequence 50, App	333	4	16.7	18	4	US-10-732-862A-120	Sequence 120, App
261	4	16.7	15	5	US-10-695-155-51	Sequence 51, App	334	4	16.7	18	4	US-10-677-074-106	Sequence 106, App
262	4	16.7	15	5	US-10-695-155-52	Sequence 52, App	335	4	16.7	18	4	US-10-807-856-112	Sequence 172, App
263	4	16.7	15	5	US-10-695-155-109	Sequence 109, App	336	4	16.7	18	5	US-10-808-041-2	Sequence 2, App
264	4	16.7	15	5	US-10-695-155-110	Sequence 110, App	337	4	16.7	18	5	US-10-732-813-16	Sequence 16, App
265	4	16.7	15	5	US-10-695-155-111	Sequence 111, App	338	4	16.7	18	5	US-10-473-882-66	Sequence 66, App
266	4	16.7	15	5	US-10-742-469-128	Sequence 128, App	339	4	16.7	18	5	US-10-952-557-29	Sequence 29, App
267	4	16.7	15	5	US-10-751-826-73	Sequence 73, App	340	4	16.7	18	3	US-10-860-050-397	Sequence 397, App
268	4	16.7	15	5	US-10-732-813-15	Sequence 15, App	341	4	16.7	19	3	US-09-864-761-42095	Sequence 42095, A
269	4	16.7	15	5	US-10-920-313-42	Sequence 42, App	342	4	16.7	19	4	US-10-309-764-144	Sequence 144, App
270	4	16.7	15	5	US-10-771-242-243	Sequence 243, App	343	4	16.7	19	4	US-10-452-024-34	Sequence 34, App
271	4	16.7	15	5	US-10-503-706-84	Sequence 84, App	344	4	16.7	19	4	US-10-403-938-31	Sequence 31, App
272	4	16.7	15	5	US-10-503-706-85	Sequence 85, App	345	4	16.7	19	4	US-10-702-765-120	Sequence 120, App
273	4	16.7	15	5	US-10-503-706-86	Sequence 86, App	346	4	16.7	19	5	US-10-808-041-1	Sequence 1, App
274	4	16.7	15	5	US-10-503-706-87	Sequence 87, App	347	4	16.7	19	5	US-10-938-243-441	Sequence 441, App
275	4	16.7	16	3	US-09-813-333-20	Sequence 20, App	348	4	16.7	19	5	US-10-862-195-2065	Sequence 2065, App
276	4	16.7	16	3	US-09-539-382-40	Sequence 40, App	349	4	16.7	19	5	US-10-862-195-2092	Sequence 2092, App
277	4	16.7	16	3	US-09-013-077A-3	Sequence 3, App	350	4	16.7	19	6	US-11-021-928A-328	Sequence 328, App
278	4	16.7	16	4	US-10-156-820-9	Sequence 9, App	351	4	16.7	19	6	US-11-131-054-203	Sequence 203, App
279	4	16.7	16	4	US-10-044-703-20	Sequence 20, App	352	4	16.7	19	6	US-11-131-042-203	Sequence 203, App
280	4	16.7	16	4	US-10-067-790-40	Sequence 40, App	353	4	16.7	20	2	US-08-677-599B-5	Sequence 5, App
281	4	16.7	16	4	US-10-067-892-40	Sequence 40, App	354	4	16.7	20	3	US-09-993-808-115	Sequence 115, App
282	4	16.7	16	4	US-10-067-893-40	Sequence 40, App	355	4	16.7	20	3	US-09-995-860-115	Sequence 115, App
283	4	16.7	16	4	US-10-225-567A-1004	Sequence 1004, App	356	4	16.7	20	3	US-09-995-791-115	Sequence 115, App
284	4	16.7	16	4	US-10-225-567A-1093	Sequence 1093, App	357	4	16.7	20	3	US-09-833-245-397	Sequence 397, App
285	4	16.7	16	4	US-10-153-244-318	Sequence 318, App	358	4	16.7	20	3	US-09-739-466C-24	Sequence 24, App
286	4	16.7	16	4	US-10-153-244-332	Sequence 332, App	359	4	16.7	20	4	US-10-094-407A-38	Sequence 38, App
287	4	16.7	16	4	US-10-224-123-35	Sequence 35, App	360	4	16.7	20	4	US-10-012-952A-207	Sequence 207, App
288	4	16.7	16	4	US-10-239-313A-317	Sequence 317, App	361	4	16.7	20	4	US-10-280-066-432	Sequence 432, App
289	4	16.7	16	4	US-10-105-232-399	Sequence 399, App	362	4	16.7	20	4	US-10-309-764-145	Sequence 145, App
290	4	16.7	16	4	US-10-312-732A-17	Sequence 17, App	363	4	16.7	20	4	US-10-309-764-146	Sequence 146, App
291	4	16.7	16	4	US-10-189-437-386	Sequence 386, App	364	4	16.7	20	4	US-10-414-583-22	Sequence 22, App
292	4	16.7	16	4	US-10-262-794A-18	Sequence 18, App	365	4	16.7	20	4	US-10-414-583-64	Sequence 64, App
293	4	16.7	16	4	US-10-239-103-20	Sequence 20, App	366	4	16.7	20	4	US-10-452-024-33	Sequence 33, App
294	4	16.7	16	4	US-10-702-765-123	Sequence 123, App	367	4	16.7	20	4	US-10-702-765-119	Sequence 119, App
295	4	16.7	16	5	US-10-738-034-3	Sequence 3, App	368	4	16.7	20	4	US-10-440-390-84	Sequence 84, App
296	4	16.7	16	5	US-10-652-779-63	Sequence 63, App	369	4	16.7	20	4	US-10-321-798-115	Sequence 115, App
297	4	16.7	16	5	US-10-862-195-1773	Sequence 1773, App	370	4	16.7	20	5	US-10-776-013-330	Sequence 330, App
298	4	16.7	16	5	US-10-860-050-399	Sequence 399, App	371	4	16.7	20	5	US-10-690-276-250	Sequence 250, App
299	4	16.7	16	6	US-11-025-608-10	Sequence 10, App	372	4	16.7	20	5	US-10-690-276-639	Sequence 698, App
300	4	16.7	16	6	US-11-031-911-4	Sequence 4, App	373	4	16.7	20	5	US-10-862-195-418	Sequence 419, App
301	4	16.7	17	3	US-09-841-132-143	Sequence 143, App	374	4	16.7	20	6	US-11-066-697-302	Sequence 4, App
302	4	16.7	17	4	US-10-133-210-261	Sequence 261, App	375	4	16.7	21	3	US-09-864-761-38455	Sequence 38455, A
303	4	16.7	17	4	US-10-225-567A-1067	Sequence 1067, App	376	4	16.7	21	3	US-09-894-967A-35	Sequence 34, App
304	4	16.7	17	4	US-10-225-567A-1159	Sequence 1159, App	377	4	16.7	21	3	US-09-894-967A-35	Sequence 35, App
305	4	16.7	17	4	US-10-147-910-5	Sequence 5, App	378	4	16.7	21	3	US-09-894-967A-35	Sequence 36, App
306	4	16.7	17	4	US-10-239-313A-293	Sequence 293, App	379	4	16.7	21	3	US-09-894-967A-36	Sequence 36, App
307	4	16.7	17	4	US-10-105-232-153	Sequence 153, App	380	4	16.7	21	3	US-09-962-756-562	Sequence 562, App
308	4	16.7	17	4	US-10-105-232-166	Sequence 166, App	381	4	16.7	21	3	US-09-962-756-643	Sequence 643, App
309	4	16.7	17	4	US-10-105-232-207	Sequence 207, App	382	4	16.7	21	3	US-09-962-756-650	Sequence 650, App
310	4	16.7	17	4	US-10-105-232-398	Sequence 398, App	383	4	16.7	21	3	US-09-962-756-1746	Sequence 1746, App
311	4	16.7	17	4	US-10-189-437-140	Sequence 140, App	384	4	16.7	21	4	US-10-062-710-176	Sequence 176, App
312	4	16.7	17	4	US-10-189-437-153	Sequence 153, App	385	4	16.7	21	4	US-10-105-232-396	Sequence 396, App
313	4	16.7	17	4	US-10-189-437-194	Sequence 194, App	386	4	16.7	21	4	US-10-189-437-383	Sequence 383, App
314	4	16.7	17	4	US-10-189-437-385	Sequence 385, App	387	4	16.7	21	4	US-10-253-471-562	Sequence 562, App
315	4	16.7	17	4	US-10-702-765-122	Sequence 122, App	388	4	16.7	21	4	US-10-253-471-643	Sequence 643, App
316	4	16.7	17	5	US-10-695-155-155	Sequence 155, App	389	4	16.7	21	4	US-10-253-471-650	Sequence 650, App
317	4	16.7	17	5	US-10-872-153-143	Sequence 143, App	390	4	16.7	21	4	US-10-253-471-1746	Sequence 1746, App
318	4	16.7	17	5	US-10-808-187-1053	Sequence 1053, App	391	4	16.7	21	4	US-10-253-493-562	Sequence 562, App
319	4	16.7	17	5	US-10-862-195-993	Sequence 993, App	392	4	16.7	21	4	US-10-253-493-643	Sequence 643, App

393	4	16.7	21	4	US-10-253-493-650	Sequence 650, App	466	3	12.5	4	3	US-09-817-199A-8	Sequence 8, Appli
394	4	16.7	21	4	US-10-253-493-1746	Sequence 1746, Ap	467	3	12.5	4	3	US-09-817-199A-6	Sequence 6, Appli
395	4	16.7	21	4	US-10-396-551-1	Sequence 1, Appli	468	3	12.5	4	3	US-09-902-556-5	Sequence 5, Appli
396	4	16.7	21	4	US-10-396-551-13	Sequence 13, Appl	469	3	12.5	4	3	US-09-952-267-44	Sequence 44, Appl
397	4	16.7	21	4	US-10-702-765-118	Sequence 118, App	470	3	12.5	4	3	US-09-809-638-725	Sequence 725, App
398	4	16.7	21	4	US-10-702-765-149	Sequence 149, App	471	3	12.5	4	3	US-09-793-451-721	Sequence 721, App
399	4	16.7	21	4	US-10-702-765-150	Sequence 150, App	472	3	12.5	4	3	US-09-793-451-723	Sequence 723, App
400	4	16.7	21	4	US-10-702-765-151	Sequence 151, App	473	3	12.5	4	3	US-09-793-451-725	Sequence 725, App
401	4	16.7	21	4	US-10-702-765-152	Sequence 152, App	474	3	12.5	4	4	US-10-199-805-1	Sequence 1, Appli
402	4	16.7	21	4	US-10-702-765-153	Sequence 153, App	475	3	12.5	4	4	US-10-084-825-8	Sequence 8, Appli
403	4	16.7	21	4	US-10-702-765-154	Sequence 154, App	476	3	12.5	4	4	US-10-132-920B-54	Sequence 54, Appl
404	4	16.7	21	4	US-10-702-765-155	Sequence 155, App	477	3	12.5	4	4	US-10-285-045-15	Sequence 15, Appl
405	4	16.7	21	4	US-10-702-765-156	Sequence 156, App	478	3	12.5	4	4	US-10-284-660-15	Sequence 15, Appl
406	4	16.7	21	4	US-10-702-765-157	Sequence 157, App	479	3	12.5	4	4	US-10-283-423-43	Sequence 43, Appl
407	4	16.7	21	4	US-10-702-765-158	Sequence 158, App	480	3	12.5	4	4	US-10-283-423-44	Sequence 44, Appl
408	4	16.7	21	4	US-10-702-765-159	Sequence 159, App	481	3	12.5	4	4	US-10-283-423-44	Sequence 44, Appl
409	4	16.7	21	4	US-10-702-765-160	Sequence 160, App	482	3	12.5	4	4	US-10-283-423-134	Sequence 134, App
410	4	16.7	21	4	US-10-702-765-161	Sequence 161, App	483	3	12.5	4	4	US-10-283-423-147	Sequence 147, App
411	4	16.7	21	4	US-10-702-765-162	Sequence 162, App	484	3	12.5	4	4	US-10-197-927-22	Sequence 22, Appl
412	4	16.7	21	4	US-10-641-340-3	Sequence 3, Appli	485	3	12.5	4	4	US-10-213-821-43	Sequence 43, Appl
413	4	16.7	21	5	US-10-479-166-18	Sequence 18, Appl	486	3	12.5	4	4	US-10-213-821-44	Sequence 44, Appl
414	4	16.7	21	5	US-10-808-187-1373	Sequence 1373, Ap	487	3	12.5	4	4	US-10-213-821-147	Sequence 134, App
415	4	16.7	21	5	US-10-807-807-1373	Sequence 1373, Ap	488	3	12.5	4	4	US-10-213-821-147	Sequence 134, App
416	4	16.7	21	5	US-10-748-033-9	Sequence 9, Appli	489	3	12.5	4	4	US-10-237-467-13	Sequence 13, Appl
417	4	16.7	21	5	US-10-860-050-396	Sequence 396, App	490	3	12.5	4	4	US-10-309-627-5	Sequence 5, Appli
418	4	16.7	22	2	US-08-677-599B-4	Sequence 4, Appli	491	3	12.5	4	4	US-10-283-722-721	Sequence 721, App
419	4	16.7	22	3	US-09-991-548-30	Sequence 30, Appl	492	3	12.5	4	4	US-10-283-722-723	Sequence 723, App
420	4	16.7	22	3	US-10-044-692-92	Sequence 92, Appl	493	3	12.5	4	4	US-10-283-722-725	Sequence 725, App
421	4	16.7	22	4	US-10-044-539-92	Sequence 92, Appl	494	3	12.5	4	4	US-10-325-810-169	Sequence 169, App
422	4	16.7	22	4	US-10-325-810-92	Sequence 92, Appl	495	3	12.5	4	4	US-10-407-079-18	Sequence 18, Appl
423	4	16.7	22	4	US-10-262-794A-70	Sequence 70, Appl	496	3	12.5	4	4	US-10-407-079-20	Sequence 20, Appl
424	4	16.7	22	4	US-10-763-049-8	Sequence 8, Appli	497	3	12.5	4	4	US-10-093-460-34	Sequence 34, Appl
425	4	16.7	22	5	US-10-877-124-92	Sequence 92, Appl	498	3	12.5	4	4	US-10-283-903-721	Sequence 721, App
426	4	16.7	22	5	US-10-877-022-92	Sequence 92, Appl	499	3	12.5	4	4	US-10-283-903-723	Sequence 723, App
427	4	16.7	22	5	US-10-877-146-92	Sequence 92, Appl	500	3	12.5	4	4	US-10-013-312-1291	Sequence 1291, Ap
428	4	16.7	23	4	US-10-057-789-196	Sequence 196, App	501	3	12.5	4	4	US-10-419-380-5	Sequence 5, Appli
429	4	16.7	23	4	US-10-212-628-196	Sequence 196, App	502	3	12.5	4	4	US-10-306-631-55	Sequence 55, Appl
430	4	16.7	23	4	US-10-105-232-202	Sequence 202, App	503	3	12.5	4	4	US-10-285-824-5	Sequence 5, Appli
431	4	16.7	23	4	US-10-189-437-189	Sequence 189, App	504	3	12.5	4	4	US-10-363-208-50	Sequence 50, Appl
432	4	16.7	23	5	US-10-990-767-39	Sequence 39, Appl	505	3	12.5	4	4	US-10-363-208-52	Sequence 52, Appl
433	4	16.7	23	5	US-10-860-050-202	Sequence 202, App	506	3	12.5	4	4	US-10-435-751-54	Sequence 54, Appl
434	4	16.7	24	3	US-09-892-877-279	Sequence 279, App	507	3	12.5	4	4	US-10-438-181A-54	Sequence 54, Appl
435	4	16.7	24	3	US-09-948-783-291	Sequence 291, App	508	3	12.5	4	4	US-10-422-571-62	Sequence 62, Appl
436	4	16.7	24	4	US-10-385-415-82	Sequence 82, Appl	509	3	12.5	4	4	US-10-693-802-1	Sequence 1, Appli
437	4	16.7	24	4	US-10-424-599-246265	Sequence 246265,	510	3	12.5	4	4	US-10-313-972-64	Sequence 64, Appl
438	4	16.7	24	4	US-10-601-656-60	Sequence 60, Appl	511	3	12.5	4	4	US-10-736-048-43	Sequence 43, Appl
439	4	16.7	24	5	US-10-479-166-19	Sequence 19, Appl	512	3	12.5	4	4	US-10-736-048-44	Sequence 44, Appl
440	4	16.7	24	5	US-10-777-893-63	Sequence 73, Appl	513	3	12.5	4	4	US-10-736-048-134	Sequence 134, App
441	4	16.7	24	5	US-10-873-015-73	Sequence 73, Appl	514	3	12.5	4	4	US-10-736-048-147	Sequence 147, App
442	4	16.7	25	3	US-09-864-761-38929	Sequence 38929, A	515	3	12.5	4	4	US-10-463-782A-44	Sequence 44, Appl
443	4	16.7	25	3	US-09-258-031B-1	Sequence 1, Appli	516	3	12.5	4	4	US-10-641-633-44	Sequence 44, Appl
444	4	16.7	25	4	US-10-062-710-51	Sequence 51, Appl	517	3	12.5	4	4	US-10-764-390-28	Sequence 28, Appl
445	4	16.7	25	4	US-10-239-313A-292	Sequence 292, App	518	3	12.5	4	4	US-10-764-390-30	Sequence 30, Appl
446	4	16.7	25	4	US-10-239-313A-695	Sequence 695, App	519	3	12.5	4	4	US-10-764-390-37	Sequence 37, Appl
447	4	16.7	25	4	US-10-008-524A-4	Sequence 4, Appli	520	3	12.5	4	4	US-10-764-390-38	Sequence 38, Appl
448	4	16.7	25	4	US-10-632-983-133	Sequence 133, App	521	3	12.5	4	4	US-10-764-390-39	Sequence 39, Appl
449	4	16.7	25	4	US-10-416-249-42	Sequence 42, Appl	522	3	12.5	4	5	US-10-877-124-169	Sequence 169, App
450	4	16.7	25	4	US-10-416-249-355	Sequence 354, App	523	3	12.5	4	5	US-10-877-022-169	Sequence 169, App
451	4	16.7	25	4	US-10-416-249-454	Sequence 454, App	524	3	12.5	4	5	US-10-807-635-15	Sequence 15, Appl
452	4	16.7	25	4	US-10-263-367-9	Sequence 9, Appli	525	3	12.5	4	5	US-10-808-187-810	Sequence 810, App
453	4	16.7	25	4	US-10-601-656-61	Sequence 61, Appl	526	3	12.5	4	5	US-10-808-187-1266	Sequence 1266, Ap
454	4	16.7	25	4	US-10-327-598-238	Sequence 238, App	527	3	12.5	4	5	US-10-877-146-169	Sequence 169, App
455	4	16.7	25	4	US-10-327-598-241	Sequence 241, App	528	3	12.5	4	5	US-10-920-788-51	Sequence 51, Appl
456	4	16.7	25	4	US-10-327-598-242	Sequence 242, App	529	3	12.5	4	5	US-10-936-138-15	Sequence 15, Appl
457	4	16.7	25	4	US-10-327-598-243	Sequence 243, App	530	3	12.5	4	5	US-10-949-419-15	Sequence 15, Appl
458	4	16.7	25	4	US-10-327-598-244	Sequence 244, App	531	3	12.5	4	5	US-10-884-355A-29	Sequence 29, Appl
459	4	16.7	25	5	US-10-873-015-74	Sequence 74, Appl	532	3	12.5	4	5	US-10-884-355A-30	Sequence 30, Appl
460	3	12.5	3	4	US-10-363-208-42	Sequence 42, Appl	533	3	12.5	4	5	US-10-992-334-2	Sequence 2, Appli
461	3	12.5	3	5	US-10-884-355A-46	Sequence 26, Appl	534	3	12.5	4	5	US-10-924-367A-2	Sequence 2, Appli
462	3	12.5	4	2	US-08-325-457-2	Sequence 2, Appli	535	3	12.5	4	5	US-10-872-768-44	Sequence 44, Appl
463	3	12.5	4	3	US-09-248-093-9	Sequence 9, Appli	536	3	12.5	4	5	US-10-872-769-44	Sequence 44, Appl
464	3	12.5	4	3	US-09-740-026A-8	Sequence 8, Appli	537	3	12.5	4	5	US-10-892-402-137	Sequence 137, App
465	3	12.5	4	3	US-09-924-099-8	Sequence 8, Appli	538	3	12.5	4	5	US-10-892-402-141	Sequence 141, App

539	3	12.5	4	5	US-10-892-402-145	Sequence 145, App	612	3	12.5	5	5	US-10-796-719-121	Sequence 121, App
540	3	12.5	4	5	US-10-650-467-126	Sequence 126, App	613	3	12.5	5	5	US-10-874-923-129	Sequence 129, App
541	3	12.5	4	5	US-10-650-467-128	Sequence 128, App	614	3	12.5	5	5	US-10-760-085-23	Sequence 23, Appl
542	3	12.5	4	5	US-10-650-467-152	Sequence 152, App	615	3	12.5	5	5	US-10-726-332-103	Sequence 103, App
543	3	12.5	4	5	US-10-807-807-810	Sequence 810, App	616	3	12.5	5	5	US-10-884-355A-31	Sequence 31, Appl
544	3	12.5	4	5	US-10-807-807-1266	Sequence 1266, App	617	3	12.5	5	5	US-10-968-237-63	Sequence 63, Appl
545	3	12.5	4	6	US-11-083-611-111	Sequence 111, App	618	3	12.5	5	5	US-10-773-032-69	Sequence 69, Appl
546	3	12.5	4	6	US-11-117-746-8	Sequence 8, Appl	619	3	12.5	5	5	US-10-773-032-69	Sequence 318, App
547	3	12.5	4	6	US-11-117-746-6	Sequence 6, Appl	620	3	12.5	5	5	US-10-773-032-351	Sequence 351, App
548	3	12.5	4	6	US-11-043-964-8	Sequence 8, Appl	621	3	12.5	5	5	US-10-773-032-382	Sequence 382, App
549	3	12.5	5	3	US-09-802-077-63	Sequence 63, Appl	622	3	12.5	5	5	US-10-773-032-383	Sequence 383, App
550	3	12.5	5	3	US-09-802-096-63	Sequence 63, Appl	623	3	12.5	5	5	US-10-773-032-419	Sequence 419, App
551	3	12.5	5	3	US-09-764-246-28	Sequence 28, Appl	624	3	12.5	5	5	US-10-886-779-5	Sequence 5, Appl
552	3	12.5	5	3	US-09-884-681-21	Sequence 21, Appl	625	3	12.5	5	5	US-10-759-731A-80	Sequence 80, Appl
553	3	12.5	5	3	US-09-939-481-36	Sequence 36, Appl	626	3	12.5	5	5	US-10-479-933-4	Sequence 4, Appl
554	3	12.5	5	3	US-09-939-481-37	Sequence 37, Appl	627	3	12.5	5	5	US-10-715-810-19	Sequence 19, Appl
555	3	12.5	5	3	US-09-939-481-38	Sequence 38, Appl	628	3	12.5	5	5	US-10-715-810-34	Sequence 34, Appl
556	3	12.5	5	3	US-09-982-172-179	Sequence 179, App	629	3	12.5	5	5	US-10-715-810-98	Sequence 98, Appl
557	3	12.5	5	3	US-09-751-100B-26	Sequence 26, Appl	630	3	12.5	5	5	US-10-939-309-89	Sequence 89, Appl
558	3	12.5	5	3	US-09-925-179-63	Sequence 63, Appl	631	3	12.5	5	5	US-10-650-467-153	Sequence 153, App
559	3	12.5	5	3	US-09-387-715-7	Sequence 7, Appl	632	3	12.5	5	5	US-10-650-467-154	Sequence 154, App
560	3	12.5	5	3	US-09-387-715-53	Sequence 53, Appl	633	3	12.5	5	5	US-10-946-647-1103	Sequence 1103, App
561	3	12.5	5	3	US-09-759-484-1	Sequence 1, Appl	634	3	12.5	5	5	US-10-841-049-40	Sequence 40, Appl
562	3	12.5	5	3	US-09-933-767-858	Sequence 858, App	635	3	12.5	5	5	US-10-841-049-41	Sequence 41, Appl
563	3	12.5	5	4	US-10-014-485A-72	Sequence 72, Appl	636	3	12.5	5	6	US-11-029-331-13	Sequence 13, Appl
564	3	12.5	5	4	US-10-014-485A-84	Sequence 84, Appl	637	3	12.5	5	6	US-11-066-697-1079	Sequence 1079, App
565	3	12.5	5	4	US-10-099-895-19	Sequence 19, Appl	638	3	12.5	5	6	US-11-066-697-1179	Sequence 1179, App
566	3	12.5	5	4	US-10-004-860-858	Sequence 858, App	639	3	12.5	5	6	US-11-113-006-21	Sequence 21, Appl
567	3	12.5	5	4	US-10-174-105A-72	Sequence 72, Appl	640	3	12.5	5	6	US-11-113-006-22	Sequence 22, Appl
568	3	12.5	5	4	US-10-174-105A-84	Sequence 84, Appl	641	3	12.5	6	2	US-08-881-509-27	Sequence 27, Appl
569	3	12.5	5	4	US-10-237-850-36	Sequence 36, Appl	642	3	12.5	6	3	US-09-802-077-61	Sequence 61, Appl
570	3	12.5	5	4	US-10-237-850-37	Sequence 37, Appl	643	3	12.5	6	3	US-09-802-096-61	Sequence 61, Appl
571	3	12.5	5	4	US-10-237-850-38	Sequence 38, Appl	644	3	12.5	6	3	US-09-748-038B-22	Sequence 22, Appl
572	3	12.5	5	4	US-10-023-282-858	Sequence 858, App	645	3	12.5	6	3	US-09-748-038B-23	Sequence 23, Appl
573	3	12.5	5	4	US-10-206-693-147	Sequence 147, App	646	3	12.5	6	3	US-09-301-593-64	Sequence 64, Appl
574	3	12.5	5	4	US-10-062-623A-21	Sequence 21, Appl	647	3	12.5	6	3	US-09-845-667-38	Sequence 38, Appl
575	3	12.5	5	4	US-10-062-623A-22	Sequence 22, Appl	648	3	12.5	6	3	US-09-821-819A-3	Sequence 3, Appl
576	3	12.5	5	4	US-10-197-954-23	Sequence 23, Appl	649	3	12.5	6	3	US-09-990-762-66	Sequence 66, Appl
577	3	12.5	5	4	US-10-127-288-21	Sequence 21, Appl	650	3	12.5	6	3	US-09-234-395-241	Sequence 241, App
578	3	12.5	5	4	US-10-364-842-7	Sequence 7, Appl	651	3	12.5	6	3	US-09-234-395-256	Sequence 256, App
579	3	12.5	5	4	US-10-364-842-53	Sequence 53, Appl	652	3	12.5	6	3	US-09-897-107-98	Sequence 98, Appl
580	3	12.5	5	4	US-10-293-580-21	Sequence 21, Appl	653	3	12.5	6	3	US-09-897-107-100	Sequence 100, App
581	3	12.5	5	4	US-10-243-836-2	Sequence 2, Appl	654	3	12.5	6	3	US-09-305-928-241	Sequence 241, App
582	3	12.5	5	4	US-10-436-826-2	Sequence 2, Appl	655	3	12.5	6	3	US-09-305-928-256	Sequence 256, App
583	3	12.5	5	4	US-10-436-549-69	Sequence 69, App	656	3	12.5	6	3	US-09-823-829-39	Sequence 39, Appl
584	3	12.5	5	4	US-10-436-549-318	Sequence 318, App	657	3	12.5	6	3	US-09-823-829-40	Sequence 40, Appl
585	3	12.5	5	4	US-10-436-549-351	Sequence 351, App	658	3	12.5	6	3	US-09-823-829-61	Sequence 61, Appl
586	3	12.5	5	4	US-10-436-549-382	Sequence 382, App	659	3	12.5	6	3	US-09-727-963A-5	Sequence 5, Appl
587	3	12.5	5	4	US-10-436-549-383	Sequence 383, App	660	3	12.5	6	3	US-09-727-963A-18	Sequence 18, Appl
588	3	12.5	5	4	US-10-436-549-419	Sequence 419, App	661	3	12.5	6	3	US-09-727-963A-56	Sequence 56, Appl
589	3	12.5	5	4	US-10-363-208-51	Sequence 51, Appl	662	3	12.5	6	3	US-09-727-963A-65	Sequence 65, Appl
590	3	12.5	5	4	US-10-363-208-53	Sequence 53, Appl	663	3	12.5	6	3	US-09-727-963A-68	Sequence 68, Appl
591	3	12.5	5	4	US-10-181-937-55	Sequence 55, Appl	664	3	12.5	6	3	US-09-727-963A-33	Sequence 33, Appl
592	3	12.5	5	4	US-10-416-090-46	Sequence 46, App	665	3	12.5	6	3	US-09-878-603-24	Sequence 24, Appl
593	3	12.5	5	4	US-10-320-730A-2	Sequence 2, Appl	666	3	12.5	6	3	US-09-264-516A-265	Sequence 265, App
594	3	12.5	5	4	US-10-320-730A-3	Sequence 3, Appl	667	3	12.5	6	3	US-09-264-516A-280	Sequence 280, App
595	3	12.5	5	4	US-10-742-344-2	Sequence 2, Appl	668	3	12.5	6	3	US-09-912-414-1	Sequence 1, Appl
596	3	12.5	5	4	US-10-731-921-5	Sequence 5, Appl	669	3	12.5	6	3	US-09-962-863-6	Sequence 6, Appl
597	3	12.5	5	4	US-10-716-204-28	Sequence 28, Appl	670	3	12.5	6	3	US-09-858-852A-66	Sequence 66, Appl
598	3	12.5	5	4	US-10-773-229-7	Sequence 7, Appl	671	3	12.5	6	3	US-09-925-179-61	Sequence 61, Appl
599	3	12.5	5	4	US-10-677-093-53	Sequence 53, Appl	672	3	12.5	6	3	US-09-387-715-49	Sequence 49, Appl
600	3	12.5	5	4	US-10-712-425-69	Sequence 69, Appl	673	3	12.5	6	3	US-09-791-524-101	Sequence 101, App
601	3	12.5	5	4	US-10-712-425-318	Sequence 318, App	674	3	12.5	6	3	US-09-833-245-599	Sequence 599, App
602	3	12.5	5	4	US-10-712-425-331	Sequence 351, App	675	3	12.5	6	4	US-10-024-632-27	Sequence 27, App
603	3	12.5	5	4	US-10-712-425-382	Sequence 382, App	676	3	12.5	6	4	US-10-157-240-2	Sequence 2, Appl
604	3	12.5	5	4	US-10-712-425-383	Sequence 383, App	677	3	12.5	6	4	US-10-006-869-855	Sequence 855, App
605	3	12.5	5	4	US-10-712-425-419	Sequence 419, App	678	3	12.5	6	4	US-10-006-869-870	Sequence 870, App
606	3	12.5	5	5	US-10-841-056-40	Sequence 40, Appl	679	3	12.5	6	4	US-10-281-652-13	Sequence 13, Appl
607	3	12.5	5	5	US-10-841-056-41	Sequence 41, Appl	680	3	12.5	6	4	US-10-141-357-265	Sequence 265, App
608	3	12.5	5	5	US-10-841-121-40	Sequence 40, Appl	681	3	12.5	6	4	US-10-141-357-280	Sequence 280, App
609	3	12.5	5	5	US-10-841-121-41	Sequence 41, Appl	682	3	12.5	6	4	US-10-054-968-14	Sequence 14, Appl
610	3	12.5	5	5	US-10-766-735-121	Sequence 121, App	683	3	12.5	6	4	US-10-311-111-2	Sequence 2, Appl
611	3	12.5	5	5	US-10-823-964A-17	Sequence 17, Appl	684	3	12.5	6	4	US-10-159-006-64	Sequence 64, Appl

685	3	12.5	6	4	US-10-283-423-65	Sequence 65, Appl	758	3	12.5	6	5	US-10-938-249-36	Sequence 36, Appl
686	3	12.5	6	4	US-10-283-423-66	Sequence 66, Appl	759	3	12.5	6	5	US-10-691-330-13	Sequence 13, Appl
687	3	12.5	6	4	US-10-364-842-49	Sequence 49, Appl	760	3	12.5	6	5	US-10-699-114-205	Sequence 205, App
688	3	12.5	6	4	US-10-188-608-31	Sequence 31, Appl	761	3	12.5	6	5	US-10-699-114-218	Sequence 218, App
689	3	12.5	6	4	US-10-188-608-32	Sequence 32, Appl	762	3	12.5	6	5	US-10-699-114-219	Sequence 219, App
690	3	12.5	6	4	US-10-213-821-65	Sequence 65, Appl	763	3	12.5	6	5	US-10-699-114-278	Sequence 278, App
691	3	12.5	6	4	US-10-213-821-66	Sequence 66, Appl	764	3	12.5	6	5	US-10-699-114-279	Sequence 279, App
692	3	12.5	6	4	US-10-348-232-46	Sequence 46, Appl	765	3	12.5	6	5	US-10-699-114-438	Sequence 438, App
693	3	12.5	6	4	US-10-348-232-134	Sequence 134, App	766	3	12.5	6	5	US-10-699-114-439	Sequence 439, App
694	3	12.5	6	4	US-10-441-626-33	Sequence 33, Appl	767	3	12.5	6	5	US-10-699-114-561	Sequence 561, App
695	3	12.5	6	4	US-10-436-826-33	Sequence 33, Appl	768	3	12.5	6	5	US-10-699-114-613	Sequence 613, App
696	3	12.5	6	4	US-10-441-625-33	Sequence 33, Appl	769	3	12.5	6	5	US-10-699-114-1022	Sequence 1022, Ap
697	3	12.5	6	4	US-10-414-524-89	Sequence 89, Appl	770	3	12.5	6	5	US-10-699-114-1045	Sequence 1045, Ap
698	3	12.5	6	4	US-10-407-079-26	Sequence 26, Appl	771	3	12.5	6	5	US-10-699-114-1046	Sequence 1046, Ap
699	3	12.5	6	4	US-10-395-032-885	Sequence 855, App	772	3	12.5	6	5	US-10-486-595-10	Sequence 10, Appl
700	3	12.5	6	4	US-10-395-032-870	Sequence 870, App	773	3	12.5	6	5	US-10-884-355A-9	Sequence 9, Appl
701	3	12.5	6	4	US-10-378-173-211	Sequence 211, App	774	3	12.5	6	5	US-10-884-355A-14	Sequence 14, Appl
702	3	12.5	6	4	US-10-394-980-256	Sequence 256, App	775	3	12.5	6	5	US-10-884-355A-15	Sequence 15, Appl
703	3	12.5	6	4	US-10-363-208-54	Sequence 54, Appl	776	3	12.5	6	5	US-10-884-355A-16	Sequence 16, Appl
704	3	12.5	6	4	US-10-363-208-56	Sequence 56, Appl	777	3	12.5	6	5	US-10-884-355A-17	Sequence 17, Appl
705	3	12.5	6	4	US-10-328-953-34	Sequence 34, Appl	778	3	12.5	6	5	US-10-884-355A-18	Sequence 18, Appl
706	3	12.5	6	4	US-10-367-580-304	Sequence 304, App	779	3	12.5	6	5	US-10-884-355A-24	Sequence 24, Appl
707	3	12.5	6	4	US-10-367-593-304	Sequence 304, App	780	3	12.5	6	5	US-10-884-355A-32	Sequence 32, Appl
708	3	12.5	6	4	US-10-367-594-304	Sequence 304, App	781	3	12.5	6	5	US-10-884-355A-33	Sequence 33, Appl
709	3	12.5	6	4	US-10-367-654-304	Sequence 304, App	782	3	12.5	6	5	US-10-884-355A-34	Sequence 34, Appl
710	3	12.5	6	4	US-10-367-658-304	Sequence 304, App	783	3	12.5	6	5	US-10-884-355A-35	Sequence 35, Appl
711	3	12.5	6	4	US-10-367-668-304	Sequence 304, App	784	3	12.5	6	5	US-10-884-355A-36	Sequence 36, Appl
712	3	12.5	6	4	US-10-702-765-203	Sequence 203, App	785	3	12.5	6	5	US-10-884-355A-37	Sequence 37, Appl
713	3	12.5	6	4	US-10-736-048-65	Sequence 65, Appl	786	3	12.5	6	5	US-10-884-355A-38	Sequence 38, Appl
714	3	12.5	6	4	US-10-736-048-66	Sequence 66, Appl	787	3	12.5	6	5	US-10-884-355A-42	Sequence 42, Appl
715	3	12.5	6	4	US-10-367-674-304	Sequence 304, App	788	3	12.5	6	5	US-10-884-355A-43	Sequence 43, Appl
716	3	12.5	6	4	US-10-801-994-66	Sequence 66, Appl	789	3	12.5	6	5	US-10-884-355A-44	Sequence 44, Appl
717	3	12.5	6	4	US-10-398-932-2	Sequence 2, Appl	790	3	12.5	6	5	US-10-884-355A-45	Sequence 45, Appl
718	3	12.5	6	4	US-10-699-088-205	Sequence 205, App	791	3	12.5	6	5	US-10-884-355A-46	Sequence 46, Appl
719	3	12.5	6	4	US-10-699-088-218	Sequence 218, App	792	3	12.5	6	5	US-10-884-355A-47	Sequence 47, Appl
720	3	12.5	6	4	US-10-699-088-219	Sequence 219, App	793	3	12.5	6	5	US-10-915-233-66	Sequence 61, Appl
721	3	12.5	6	4	US-10-699-088-278	Sequence 278, App	794	3	12.5	6	5	US-10-968-237-61	Sequence 61, Appl
722	3	12.5	6	4	US-10-699-088-279	Sequence 279, App	795	3	12.5	6	5	US-10-880-922-36	Sequence 66, Appl
723	3	12.5	6	4	US-10-699-088-438	Sequence 438, App	796	3	12.5	6	5	US-10-880-922-36	Sequence 36, Appl
724	3	12.5	6	4	US-10-699-088-439	Sequence 439, App	797	3	12.5	6	5	US-10-950-010-446	Sequence 446, App
725	3	12.5	6	4	US-10-699-088-561	Sequence 561, App	798	3	12.5	6	5	US-10-806-924-74	Sequence 74, App
726	3	12.5	6	4	US-10-699-088-613	Sequence 613, App	799	3	12.5	6	5	US-10-806-924-97	Sequence 97, Appl
727	3	12.5	6	4	US-10-699-088-1022	Sequence 1022, Ap	800	3	12.5	6	5	US-10-806-924-98	Sequence 98, Appl
728	3	12.5	6	4	US-10-699-088-1045	Sequence 1045, Ap	801	3	12.5	6	5	US-10-806-924-168	Sequence 168, App
729	3	12.5	6	4	US-10-699-088-1046	Sequence 1046, Ap	802	3	12.5	6	5	US-10-806-924-181	Sequence 181, App
730	3	12.5	6	4	US-10-786-850-43	Sequence 43, Appl	803	3	12.5	6	5	US-10-806-924-182	Sequence 182, App
731	3	12.5	6	4	US-10-786-850-48	Sequence 48, Appl	804	3	12.5	6	5	US-10-806-924-241	Sequence 241, App
732	3	12.5	6	5	US-10-859-548-6	Sequence 6, Appl	805	3	12.5	6	5	US-10-806-924-242	Sequence 242, App
733	3	12.5	6	5	US-10-486-605-11	Sequence 11, Appl	806	3	12.5	6	5	US-10-806-924-401	Sequence 401, App
734	3	12.5	6	5	US-10-699-113-111	Sequence 11, App	807	3	12.5	6	5	US-10-806-924-402	Sequence 402, App
735	3	12.5	6	5	US-10-699-113-134	Sequence 134, App	808	3	12.5	6	5	US-10-806-924-524	Sequence 524, App
736	3	12.5	6	5	US-10-699-113-135	Sequence 135, App	809	3	12.5	6	5	US-10-806-924-576	Sequence 576, App
737	3	12.5	6	5	US-10-699-113-205	Sequence 205, App	810	3	12.5	6	5	US-10-931-260-272	Sequence 272, App
738	3	12.5	6	5	US-10-699-113-218	Sequence 218, App	811	3	12.5	6	5	US-10-496-869-10	Sequence 10, Appl
739	3	12.5	6	5	US-10-699-113-219	Sequence 219, App	812	3	12.5	6	5	US-10-650-467-155	Sequence 155, App
740	3	12.5	6	5	US-10-699-113-278	Sequence 278, App	813	3	12.5	6	5	US-10-650-467-164	Sequence 164, App
741	3	12.5	6	5	US-10-699-113-279	Sequence 279, App	814	3	12.5	6	5	US-10-807-807-564	Sequence 564, App
742	3	12.5	6	5	US-10-699-113-438	Sequence 438, App	815	3	12.5	6	5	US-10-807-807-1041	Sequence 1041, Ap
743	3	12.5	6	5	US-10-699-113-561	Sequence 561, App	816	3	12.5	6	5	US-10-807-807-2165	Sequence 2165, Ap
744	3	12.5	6	5	US-10-699-113-613	Sequence 613, App	817	3	12.5	6	5	US-10-952-557-256	Sequence 256, App
745	3	12.5	6	5	US-10-486-582-7	Sequence 7, Appl	818	3	12.5	6	5	US-10-820-057A-286	Sequence 286, App
746	3	12.5	6	5	US-10-759-379-241	Sequence 241, App	819	3	12.5	6	6	US-11-066-697-1180	Sequence 1180, Ap
747	3	12.5	6	5	US-10-759-379-256	Sequence 256, App	820	3	12.5	6	6	US-11-066-697-1186	Sequence 1186, Ap
748	3	12.5	6	5	US-10-759-507-241	Sequence 241, App	821	3	12.5	6	6	US-11-037-396-1	Sequence 1, Appl
749	3	12.5	6	5	US-10-759-507-241	Sequence 241, App	822	3	12.5	6	6	US-11-004-107-855	Sequence 855, App
750	3	12.5	6	5	US-10-759-507-256	Sequence 256, App	823	3	12.5	6	6	US-11-004-107-870	Sequence 870, App
751	3	12.5	6	5	US-10-691-157-13	Sequence 13, Appl	824	3	12.5	6	6	US-11-131-054-36	Sequence 36, Appl
752	3	12.5	6	5	US-10-894-834-3	Sequence 3, Appl	825	3	12.5	6	6	US-11-003-150-243	Sequence 243, App
753	3	12.5	6	5	US-10-808-187-564	Sequence 564, App	826	3	12.5	6	6		
754	3	12.5	6	5	US-10-808-187-1041	Sequence 1041, Ap	827	3	12.5	6	6		
755	3	12.5	6	5	US-10-808-187-2165	Sequence 2165, Ap	828	3	12.5	6	6		
756	3	12.5	6	5	US-10-637-317-30	Sequence 30, Appl	829	3	12.5	6	6		
757	3	12.5	6	5	US-10-637-317-31	Sequence 31, Appl	830	3	12.5	6	6		

831	3	12.5	6	US-11-003-150-258	Sequence 258, App	904	3	12.5	7	3	US-09-989-994-941	Sequence 941, App
832	3	12.5	6	US-11-131-042-36	Sequence 36, App	905	3	12.5	7	3	US-09-990-586-5	Sequence 5, Appl
833	3	12.5	7	US-08-765-837-7	Sequence 7, Appl	906	3	12.5	7	3	US-09-968-744A-15	Sequence 15, Appl
834	3	12.5	7	US-09-785-474-16	Sequence 16, Appl	907	3	12.5	7	3	US-09-968-744A-39	Sequence 39, Appl
835	3	12.5	7	US-09-865-483-10	Sequence 10, Appl	908	3	12.5	7	3	US-09-968-744A-57	Sequence 57, Appl
836	3	12.5	7	US-09-845-667-9	Sequence 9, Appl	909	3	12.5	7	3	US-09-968-744A-60	Sequence 60, Appl
837	3	12.5	7	US-09-845-667-14	Sequence 14, Appl	910	3	12.5	7	3	US-09-968-744A-75	Sequence 75, Appl
838	3	12.5	7	US-09-845-667-40	Sequence 40, Appl	911	3	12.5	7	3	US-09-968-744A-135	Sequence 135, App
839	3	12.5	7	US-09-845-667-41	Sequence 41, Appl	912	3	12.5	7	3	US-09-968-744A-171	Sequence 171, App
840	3	12.5	7	US-09-845-667-48	Sequence 48, Appl	913	3	12.5	7	3	US-09-968-744A-189	Sequence 189, App
841	3	12.5	7	US-09-845-667-49	Sequence 49, Appl	914	3	12.5	7	3	US-09-968-744A-261	Sequence 261, App
842	3	12.5	7	US-09-845-667-50	Sequence 50, Appl	915	3	12.5	7	3	US-09-968-744A-273	Sequence 273, App
843	3	12.5	7	US-09-192-854-11	Sequence 11, Appl	916	3	12.5	7	3	US-09-968-744A-303	Sequence 303, App
844	3	12.5	7	US-09-192-854-27	Sequence 27, Appl	917	3	12.5	7	3	US-09-962-756-2014	Sequence 2014, App
845	3	12.5	7	US-09-192-854-38	Sequence 38, Appl	918	3	12.5	7	3	US-09-261-894-68	Sequence 68, Appl
846	3	12.5	7	US-09-192-854-40	Sequence 40, Appl	919	3	12.5	7	3	US-09-968-561A-15	Sequence 15, Appl
847	3	12.5	7	US-09-192-854-50	Sequence 50, Appl	920	3	12.5	7	3	US-09-968-561A-39	Sequence 39, Appl
848	3	12.5	7	US-09-192-854-80	Sequence 80, Appl	921	3	12.5	7	3	US-09-968-561A-57	Sequence 57, Appl
849	3	12.5	7	US-09-192-854-97	Sequence 97, Appl	922	3	12.5	7	3	US-09-968-561A-60	Sequence 60, Appl
850	3	12.5	7	US-09-192-854-109	Sequence 109, App	923	3	12.5	7	3	US-09-968-561A-75	Sequence 75, Appl
851	3	12.5	7	US-09-192-854-148	Sequence 148, App	924	3	12.5	7	3	US-09-968-561A-135	Sequence 135, App
852	3	12.5	7	US-09-192-854-155	Sequence 155, App	925	3	12.5	7	3	US-09-968-561A-171	Sequence 171, App
853	3	12.5	7	US-09-192-854-172	Sequence 172, App	926	3	12.5	7	3	US-09-968-561A-189	Sequence 189, App
854	3	12.5	7	US-09-853-080-7	Sequence 7, Appl	927	3	12.5	7	3	US-09-968-561A-261	Sequence 261, App
855	3	12.5	7	US-09-822-270-4	Sequence 4, Appl	928	3	12.5	7	3	US-09-968-561A-273	Sequence 273, App
856	3	12.5	7	US-09-234-395-243	Sequence 243, App	929	3	12.5	7	3	US-09-968-561A-303	Sequence 303, App
857	3	12.5	7	US-09-234-395-258	Sequence 258, App	930	3	12.5	7	3	US-09-973-278-521	Sequence 521, App
858	3	12.5	7	US-09-848-585-22	Sequence 22, Appl	931	3	12.5	7	4	US-10-104-019-47	Sequence 47, Appl
859	3	12.5	7	US-09-305-928-243	Sequence 243, App	932	3	12.5	7	4	US-10-104-019-48	Sequence 48, Appl
860	3	12.5	7	US-09-305-928-258	Sequence 258, App	933	3	12.5	7	4	US-10-104-019-49	Sequence 49, Appl
861	3	12.5	7	US-09-823-829-80	Sequence 80, Appl	934	3	12.5	7	4	US-10-104-019-50	Sequence 50, Appl
862	3	12.5	7	US-09-956-086-18	Sequence 18, Appl	935	3	12.5	7	4	US-10-032-482-16	Sequence 16, Appl
863	3	12.5	7	US-09-956-087-18	Sequence 18, Appl	936	3	12.5	7	4	US-10-127-691-8	Sequence 8, Appl
864	3	12.5	7	US-09-968-561A-15	Sequence 15, Appl	937	3	12.5	7	4	US-10-024-123-2	Sequence 2, Appl
865	3	12.5	7	US-09-968-561A-39	Sequence 39, Appl	938	3	12.5	7	4	US-10-113-417-7	Sequence 7, Appl
866	3	12.5	7	US-09-968-561A-57	Sequence 57, Appl	939	3	12.5	7	4	US-10-015-979-98	Sequence 98, Appl
867	3	12.5	7	US-09-968-561A-60	Sequence 60, Appl	940	3	12.5	7	4	US-10-062-710-232	Sequence 232, App
868	3	12.5	7	US-09-968-561A-75	Sequence 75, Appl	941	3	12.5	7	4	US-10-014-340-424	Sequence 424, App
869	3	12.5	7	US-09-968-561A-135	Sequence 135, App	942	3	12.5	7	4	US-10-014-340-648	Sequence 648, App
870	3	12.5	7	US-09-968-561A-171	Sequence 171, App	943	3	12.5	7	4	US-10-273-541-39	Sequence 39, Appl
871	3	12.5	7	US-09-968-561A-189	Sequence 189, App	944	3	12.5	7	4	US-10-273-541-43	Sequence 43, Appl
872	3	12.5	7	US-09-968-561A-261	Sequence 261, App	945	3	12.5	7	4	US-10-273-541-44	Sequence 44, Appl
873	3	12.5	7	US-09-968-561A-273	Sequence 273, App	946	3	12.5	7	4	US-10-273-541-46	Sequence 46, Appl
874	3	12.5	7	US-09-968-561A-303	Sequence 303, App	947	3	12.5	7	4	US-10-273-541-50	Sequence 50, Appl
875	3	12.5	7	US-09-486-734A-25	Sequence 25, Appl	948	3	12.5	7	4	US-10-273-541-64	Sequence 64, Appl
876	3	12.5	7	US-09-293-854-5	Sequence 5, Appl	949	3	12.5	7	4	US-10-006-869-857	Sequence 857, App
877	3	12.5	7	US-09-264-516A-267	Sequence 267, App	950	3	12.5	7	4	US-10-006-869-872	Sequence 872, App
878	3	12.5	7	US-09-264-516A-282	Sequence 282, App	951	3	12.5	7	4	US-10-006-869-1833	Sequence 1833, App
879	3	12.5	7	US-09-884-767A-85	Sequence 85, Appl	952	3	12.5	7	4	US-10-006-869-1863	Sequence 1863, App
880	3	12.5	7	US-09-861-687-8	Sequence 8, Appl	953	3	12.5	7	4	US-10-006-869-2121	Sequence 2121, App
881	3	12.5	7	US-09-983-803-366	Sequence 366, App	954	3	12.5	7	4	US-10-006-869-2141	Sequence 2141, App
882	3	12.5	7	US-09-995-973-20	Sequence 20, Appl	955	3	12.5	7	4	US-10-006-869-2189	Sequence 2189, App
883	3	12.5	7	US-09-995-973-24	Sequence 24, Appl	956	3	12.5	7	4	US-10-006-869-2219	Sequence 2219, App
884	3	12.5	7	US-09-995-973-27	Sequence 27, Appl	957	3	12.5	7	4	US-10-006-869-2863	Sequence 2863, App
885	3	12.5	7	US-09-229-751A-78	Sequence 78, Appl	958	3	12.5	7	4	US-10-006-869-2926	Sequence 2926, App
886	3	12.5	7	US-09-281-495-5	Sequence 5, Appl	959	3	12.5	7	4	US-10-006-869-3805	Sequence 3805, App
887	3	12.5	7	US-09-997-961-29	Sequence 29, Appl	960	3	12.5	7	4	US-10-293-417-5	Sequence 5, Appl
888	3	12.5	7	US-09-984-490-366	Sequence 366, App	961	3	12.5	7	4	US-10-155-922-128	Sequence 128, App
889	3	12.5	7	US-09-990-186-733	Sequence 733, App	962	3	12.5	7	4	US-10-155-922-129	Sequence 129, App
890	3	12.5	7	US-09-990-186-836	Sequence 836, App	963	3	12.5	7	4	US-10-155-922-130	Sequence 130, App
891	3	12.5	7	US-09-990-186-941	Sequence 941, App	964	3	12.5	7	4	US-10-141-357-267	Sequence 267, App
892	3	12.5	7	US-09-940-727B-32	Sequence 32, Appl	965	3	12.5	7	4	US-10-141-357-282	Sequence 282, App
893	3	12.5	7	US-09-940-727B-35	Sequence 35, Appl	966	3	12.5	7	4	US-10-272-411-49	Sequence 49, Appl
894	3	12.5	7	US-09-563-222-53	Sequence 53, Appl	967	3	12.5	7	4	US-10-062-623A-19	Sequence 19, Appl
895	3	12.5	7	US-09-996-484-20	Sequence 20, Appl	968	3	12.5	7	4	US-10-062-623A-20	Sequence 20, Appl
896	3	12.5	7	US-09-996-484-24	Sequence 24, Appl	969	3	12.5	7	4	US-10-091-300-11	Sequence 11, Appl
897	3	12.5	7	US-09-996-484-27	Sequence 27, Appl	970	3	12.5	7	4	US-10-272-328A-49	Sequence 49, Appl
898	3	12.5	7	US-09-954-385-214	Sequence 214, App	971	3	12.5	7	4	US-10-209-323-30	Sequence 30, Appl
899	3	12.5	7	US-09-954-385-229	Sequence 229, App	972	3	12.5	7	4	US-10-052-578-156	Sequence 156, App
900	3	12.5	7	US-09-954-385-238	Sequence 238, App	973	3	12.5	7	4	US-10-052-578-158	Sequence 158, App
901	3	12.5	7	US-09-954-385-260	Sequence 260, App	974	3	12.5	7	4	US-10-052-578-171	Sequence 171, App
902	3	12.5	7	US-09-989-994-733	Sequence 733, App	975	3	12.5	7	4	US-10-052-578-263	Sequence 263, App
903	3	12.5	7	US-09-989-994-836	Sequence 836, App	976	3	12.5	7	4	US-10-052-578-269	Sequence 269, App

977 3 12.5 7 4 US-10-052-578-302 Sequence 302, App
978 3 12.5 7 4 US-10-104-019-47 Sequence 47, Appl
979 3 12.5 7 4 US-10-104-019-48 Sequence 48, Appl
980 3 12.5 7 4 US-10-104-019-49 Sequence 49, Appl
981 3 12.5 7 4 US-10-104-019-50 Sequence 50, Appl
982 3 12.5 7 4 US-10-190-082-23 Sequence 23, Appl
983 3 12.5 7 4 US-10-190-082-34 Sequence 34, Appl
984 3 12.5 7 4 US-10-190-082-85 Sequence 85, Appl
985 3 12.5 7 4 US-10-190-082-232 Sequence 232, App
986 3 12.5 7 4 US-10-190-082-297 Sequence 297, App
987 3 12.5 7 4 US-10-169-351-21 Sequence 21, Appl
988 3 12.5 7 4 US-10-203-754A-14 Sequence 14, Appl
989 3 12.5 7 4 US-10-253-904-7 Sequence 7, Appl
990 3 12.5 7 4 US-10-271-708-12 Sequence 12, Appl
991 3 12.5 7 4 US-10-271-708-28 Sequence 28, Appl
992 3 12.5 7 4 US-10-283-423-42 Sequence 42, Appl
993 3 12.5 7 4 US-10-283-423-99 Sequence 99, Appl
994 3 12.5 7 4 US-10-283-423-136 Sequence 136, App
995 3 12.5 7 4 US-10-283-423-137 Sequence 137, App
996 3 12.5 7 4 US-10-283-423-168 Sequence 168, App
997 3 12.5 7 4 US-10-062-109A-727 Sequence 727, App
998 3 12.5 7 4 US-10-053-520-156 Sequence 156, App
999 3 12.5 7 4 US-10-053-520-158 Sequence 158, App
1000 3 12.5 7 5 US-10-471-934-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-978-343-4
; Sequence 4, Application US/09978343
; Publication No. US20030082680A1
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; GALE, CHERYL A.
; BENDEL, CATHERINE M.
; TAO, NIAN-JUN
; KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE
; PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH, GERHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/978,343
; FILING DATE: 15-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00280101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-978-343-4
Query Match 25.0%; Score 6; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TNNNNS 20
Db 5 TNNNNS 10
RESULT 2
US-09-935-384-41
; Sequence 41, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-41
Query Match 20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
Db 4 DSQTK 8
RESULT 3
US-09-935-384-131
; Sequence 131, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-131

Query Match 20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8
Db 3 DSQTK 7

RESULT 4
US-09-935-384-229
; Sequence 229, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 229
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-229

Query Match 20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8
Db 5 DSQTK 9

RESULT 5
US-09-935-384-310
; Sequence 310, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384

; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 310
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-310

Query Match 20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8
Db 5 DSQTK 9

RESULT 6
US-09-935-384-419
; Sequence 419, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 419
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-419

Query Match 20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DSQTK 8
Db 1 DSQTK 5

RESULT 7
US-09-935-384-529
; Sequence 529, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

```
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-529

Query Match      20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTK 8
Db      1 DSQTK 5

RESULT 8
US-09-935-384-616
; Sequence 616, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARI, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PLH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 616
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-616

Query Match      20.8%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DSQTK 8
Db      1 DSQTK 5

RESULT 9
US-10-808-187-1154
; Sequence 1154, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: FOON, LIT YAN
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: CHAN, YI
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
```

```
; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1154

Query Match      20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNNS 20
Db      5 NNNNS 9

RESULT 10
US-10-705-459-307
; Sequence 307, Application US/10705459
; Publication No. US20050053918A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; APPLICANT: Dasseau, Lior
; APPLICANT: Buchsbaum, Samuel
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 26884
; CURRENT APPLICATION NUMBER: US/10/705,459
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 307
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-705-459-307

Query Match      20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KSIPE 12
Db      4 KSIPE 8
```

RESULT 11
US-10-807-807-1154
; Sequence 1154, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: Patent in ver. 3.2
; SEQ ID NO 1154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1154
Query Match 20.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 NNNNS 20
Db 5 NNNNS 9
RESULT 12
US-09-935-384-368
; Sequence 368, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 661
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-661
Query Match 20.8%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
Db 6 DSQTK 10
RESULT 13
US-09-935-384-661
; Sequence 661, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 661
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-661
Query Match 20.8%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
Db 6 DSQTK 10
RESULT 14
US-09-982-172-186
; Sequence 186, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Ismael Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERA
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 186
; LENGTH: 12
; TYPE: PRT

; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 368
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-368
Query Match 20.8%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
Db 6 DSQTK 10

RESULT 13
US-09-935-384-661
; Sequence 661, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 661
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-661

Query Match 20.8%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DSQTK 8
Db 5 DSQTK 9

RESULT 14
US-09-982-172-186
; Sequence 186, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Ismael Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERA
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 186
; LENGTH: 12
; TYPE: PRT

```
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-186

Query Match      20.8%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 NSSFY 23
Db      7 NSSFY 11

RESULT 15
US-09-982-172-245
; Sequence 245, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-245

Query Match      20.8%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 NSSFY 23
Db      7 NSSFY 11

Search completed: January 20, 2006, 17:57:56
Job time : 67 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:54:55 ; Search time 8 Seconds
(without alignments)
30.402 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24

Sequence: 1 LRFDSTQKSIPEQETNNNSFYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 10133881 residues

Word size : 0

Total number of hits satisfying chosen parameters: 36235

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : Published Applications AA.New.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US03_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.8	9	7 US-11-045-024-616	Sequence 616, App
2	5	20.8	10	7 US-11-045-024-770	Sequence 770, App
3	5	20.8	23	6 US-10-467-657-8871	Sequence 8871, Ap
4	4	16.7	6	6 US-10-615-668-23	Sequence 23, Appl
5	4	16.7	7	7 US-11-096-706-96	Sequence 96, Appl
6	4	16.7	10	7 US-11-041-893-31	Sequence 31, Appl
7	4	16.7	11	6 US-10-914-842A-12	Sequence 12, Appl
8	4	16.7	12	7 US-11-069-834-14	Sequence 14, Appl
9	4	16.7	12	7 US-11-069-834-16	Sequence 16, Appl
10	4	16.7	12	7 US-11-069-834-18	Sequence 18, Appl
11	4	16.7	12	7 US-11-069-834-34	Sequence 34, Appl
12	4	16.7	15	6 US-10-467-657-8838	Sequence 8838, Ap
13	4	16.7	15	7 US-11-045-024-13116	Sequence 13116, A
14	4	16.7	18	7 US-11-033-039-1242	Sequence 1242, Ap
15	4	16.7	18	7 US-11-033-039-1308	Sequence 1308, Ap
16	4	16.7	19	6 US-10-503-575-312	Sequence 312, App
17	4	16.7	20	6 US-10-509-917-4	Sequence 4, Appli
18	4	16.7	20	7 US-11-022-562-134	Sequence 134, App
19	4	16.7	20	7 US-11-022-562-135	Sequence 135, App
20	4	16.7	25	7 US-11-006-119-8	Sequence 8, Appli
21	3	12.5	5	6 US-10-956-755A-53	Sequence 53, Appl
22	3	12.5	5	6 US-10-956-755A-55	Sequence 54, Appl
23	3	12.5	5	6 US-10-956-755A-55	Sequence 55, Appl
24	3	12.5	6	7 US-11-127-677-94	Sequence 94, Appl
25	3	12.5	6	7 US-11-127-677-106	Sequence 106, App

Sequence 101, App	7	US-11-038-980-101	12.5	26
Sequence 19, Appl	7	US-10-997-066-19	12.5	27
Sequence 10, Appl	7	US-10-726-554-10	12.5	28
Sequence 249, App	7	US-10-485-788A-249	12.5	29
Sequence 319, App	7	US-10-485-788A-319	12.5	30
Sequence 727, App	7	US-10-853-643-727	12.5	31
Sequence 17, Appl	7	US-11-035-682-17	12.5	32
Sequence 86, Appl	7	US-11-096-706-86	12.5	33
Sequence 204, App	7	US-11-097-864-727	12.5	34
Sequence 727, App	7	US-11-097-912-727	12.5	35
Sequence 727, App	7	US-11-062-186-38	12.5	36
Sequence 38, Appl	7	US-11-087-528-5	12.5	37
Sequence 5, Appli	7	US-10-494-781-9	12.5	38
Sequence 12, Appl	8	US-10-989-226-12	12.5	39
Sequence 135, App	8	US-10-928-446A-135	12.5	40
Sequence 250, App	8	US-10-485-788A-250	12.5	41
Sequence 320, App	8	US-10-485-788A-320	12.5	42
Sequence 465, App	8	US-10-485-788A-465	12.5	43
Sequence 77, Appl	8	US-11-033-365-77	12.5	44
Sequence 311, Ap	8	US-11-054-515-311	12.5	45
Sequence 95, Appl	8	US-11-073-347-95	12.5	46
Sequence 15, Appl	8	US-11-045-024-15	12.5	47
Sequence 232, App	8	US-11-045-024-232	12.5	48
Sequence 235, App	8	US-11-045-024-235	12.5	49
Sequence 477, App	8	US-11-045-024-477	12.5	50
Sequence 478, App	8	US-11-045-024-478	12.5	51
Sequence 480, App	8	US-11-045-024-480	12.5	52
Sequence 1081, Ap	8	US-11-045-024-1081	12.5	53
Sequence 1723, Ap	8	US-11-045-024-1723	12.5	54
Sequence 1724, Ap	8	US-11-045-024-1724	12.5	55
Sequence 1754, Ap	8	US-11-045-024-1754	12.5	56
Sequence 1755, Ap	8	US-11-045-024-1755	12.5	57
Sequence 1756, Ap	8	US-11-045-024-1756	12.5	58
Sequence 2756, Ap	8	US-11-045-024-2756	12.5	59
Sequence 3186, Ap	8	US-11-045-024-3186	12.5	60
Sequence 3622, Ap	8	US-11-045-024-3622	12.5	61
Sequence 3657, Ap	8	US-11-045-024-3657	12.5	62
Sequence 4024, Ap	8	US-11-045-024-4024	12.5	63
Sequence 4385, Ap	8	US-11-045-024-4385	12.5	64
Sequence 4387, Ap	8	US-11-045-024-4387	12.5	65
Sequence 4399, Ap	8	US-11-045-024-4399	12.5	66
Sequence 5486, Ap	8	US-11-045-024-5486	12.5	67
Sequence 6098, Ap	8	US-11-045-024-6098	12.5	68
Sequence 6521, Ap	8	US-11-045-024-6521	12.5	69
Sequence 6803, Ap	8	US-11-045-024-6803	12.5	70
Sequence 6805, Ap	8	US-11-045-024-6805	12.5	71
Sequence 6981, Ap	8	US-11-045-024-6981	12.5	72
Sequence 7300, Ap	8	US-11-045-024-7300	12.5	73
Sequence 7765, Ap	8	US-11-045-024-7765	12.5	74
Sequence 7973, Ap	8	US-11-045-024-7973	12.5	75
Sequence 8265, Ap	8	US-11-045-024-8265	12.5	76
Sequence 8286, Ap	8	US-11-045-024-8286	12.5	77
Sequence 8348, Ap	8	US-11-045-024-8348	12.5	78
Sequence 9658, Ap	8	US-11-045-024-9658	12.5	79
Sequence 1008, A	8	US-11-045-024-1008	12.5	80
Sequence 10241, A	8	US-11-045-024-10241	12.5	81
Sequence 10284, A	8	US-11-045-024-10284	12.5	82
Sequence 10321, A	8	US-11-045-024-10321	12.5	83
Sequence 10332, A	8	US-11-045-024-10332	12.5	84
Sequence 10765, A	8	US-11-045-024-10765	12.5	85
Sequence 10777, A	8	US-11-045-024-10777	12.5	86
Sequence 10820, A	8	US-11-045-024-10820	12.5	87
Sequence 10839, A	8	US-11-045-024-10839	12.5	88
Sequence 10950, A	8	US-11-045-024-10950	12.5	89
Sequence 11442, A	8	US-11-045-024-11442	12.5	90
Sequence 11668, A	8	US-11-045-024-11668	12.5	91
Sequence 11915, A	8	US-11-045-024-11915	12.5	92
Sequence 12128, A	8	US-11-045-024-12128	12.5	93

99	3	12.5	8	7	US-11-045-024-12160	Sequence 12160, A	172	3	12.5	9	7	US-11-045-024-6337	Sequence 6337, Ap
100	3	12.5	8	7	US-11-045-024-12625	Sequence 12625, A	173	3	12.5	9	7	US-11-045-024-6386	Sequence 6386, Ap
101	3	12.5	8	7	US-11-021-305-53	Sequence 53, Appl	174	3	12.5	9	7	US-11-045-024-6539	Sequence 6539, Ap
102	3	12.5	8	7	US-11-021-358-10	Sequence 10, Appl	175	3	12.5	9	7	US-11-045-024-6572	Sequence 6572, Ap
103	3	12.5	9	6	US-10-986-501-241	Sequence 241, App	176	3	12.5	9	7	US-11-045-024-6717	Sequence 6717, Ap
104	3	12.5	9	6	US-10-491-096-12	Sequence 12, Appl	177	3	12.5	9	7	US-11-045-024-6750	Sequence 6750, Ap
105	3	12.5	9	6	US-10-982-145-93	Sequence 93, Appl	178	3	12.5	9	7	US-11-045-024-6791	Sequence 6791, Ap
106	3	12.5	9	6	US-10-982-145-97	Sequence 97, Appl	179	3	12.5	9	7	US-11-045-024-6807	Sequence 6807, Ap
107	3	12.5	9	6	US-10-982-145-109	Sequence 109, App	180	3	12.5	9	7	US-11-045-024-8216	Sequence 8216, Ap
108	3	12.5	9	6	US-10-982-145-111	Sequence 111, App	181	3	12.5	9	7	US-11-045-024-8293	Sequence 8293, Ap
109	3	12.5	9	6	US-10-982-145-113	Sequence 113, App	182	3	12.5	9	7	US-11-045-024-8295	Sequence 8295, Ap
110	3	12.5	9	6	US-10-517-784-44	Sequence 44, Appl	183	3	12.5	9	7	US-11-045-024-8668	Sequence 8668, Ap
111	3	12.5	9	6	US-10-859-643-48	Sequence 48, Appl	184	3	12.5	9	7	US-11-045-024-8982	Sequence 8982, Ap
112	3	12.5	9	6	US-10-859-643-285	Sequence 265, App	185	3	12.5	9	7	US-11-045-024-9349	Sequence 9349, Ap
113	3	12.5	9	6	US-10-859-643-481	Sequence 481, App	186	3	12.5	9	7	US-11-045-024-9398	Sequence 9398, Ap
114	3	12.5	9	6	US-10-859-643-488	Sequence 488, App	187	3	12.5	9	7	US-11-045-024-9664	Sequence 9664, Ap
115	3	12.5	9	6	US-10-859-643-552	Sequence 552, App	188	3	12.5	9	7	US-11-045-024-9996	Sequence 9996, Ap
116	3	12.5	9	6	US-10-859-643-576	Sequence 576, App	189	3	12.5	9	7	US-11-045-024-10117	Sequence 10117, A
117	3	12.5	9	6	US-10-859-643-579	Sequence 579, App	190	3	12.5	9	7	US-11-045-024-10247	Sequence 10247, A
118	3	12.5	9	6	US-10-859-643-684	Sequence 684, App	191	3	12.5	9	7	US-11-045-024-10269	Sequence 10269, A
119	3	12.5	9	6	US-11-019-894A-2	Sequence 2, Appli	192	3	12.5	9	7	US-11-045-024-10325	Sequence 10325, A
120	3	12.5	9	7	US-11-044-899-18	Sequence 18, Appl	193	3	12.5	9	7	US-11-045-024-10999	Sequence 10999, A
121	3	12.5	9	7	US-11-073-347-98	Sequence 98, Appl	194	3	12.5	9	7	US-11-045-024-11211	Sequence 11211, A
122	3	12.5	9	7	US-11-073-347-100	Sequence 100, App	195	3	12.5	9	7	US-11-045-024-11443	Sequence 11443, A
123	3	12.5	9	7	US-11-073-347-109	Sequence 109, App	196	3	12.5	9	7	US-11-045-024-11480	Sequence 11480, A
124	3	12.5	9	7	US-11-009-939-10	Sequence 10, Appl	197	3	12.5	9	7	US-11-045-024-11570	Sequence 11570, A
125	3	12.5	9	7	US-11-097-864-48	Sequence 48, Appl	198	3	12.5	9	7	US-11-045-024-11672	Sequence 11672, A
126	3	12.5	9	7	US-11-097-864-265	Sequence 265, App	199	3	12.5	9	7	US-11-045-024-11905	Sequence 11905, A
127	3	12.5	9	7	US-11-097-864-481	Sequence 481, App	200	3	12.5	9	7	US-11-045-024-12006	Sequence 12006, A
128	3	12.5	9	7	US-11-097-864-488	Sequence 488, App	201	3	12.5	9	7	US-11-045-024-12165	Sequence 12165, A
129	3	12.5	9	7	US-11-097-864-552	Sequence 552, App	202	3	12.5	9	7	US-11-045-024-12623	Sequence 12623, A
130	3	12.5	9	7	US-11-097-864-576	Sequence 576, App	203	3	12.5	9	7	US-11-045-024-13564	Sequence 13564, A
131	3	12.5	9	7	US-11-097-864-579	Sequence 579, App	204	3	12.5	9	7	US-11-045-024-13572	Sequence 13572, A
132	3	12.5	9	7	US-11-097-864-684	Sequence 684, App	205	3	12.5	9	7	US-11-045-024-13584	Sequence 13584, A
133	3	12.5	9	7	US-11-097-912-48	Sequence 48, Appl	206	3	12.5	9	7	US-11-045-024-13628	Sequence 13628, A
134	3	12.5	9	7	US-11-097-912-265	Sequence 265, App	207	3	12.5	9	7	US-11-045-024-13703	Sequence 13703, A
135	3	12.5	9	7	US-11-097-912-481	Sequence 481, App	208	3	12.5	9	7	US-11-045-024-13704	Sequence 13704, A
136	3	12.5	9	7	US-11-097-912-488	Sequence 488, App	209	3	12.5	9	7	US-11-045-024-13772	Sequence 13772, A
137	3	12.5	9	7	US-11-097-912-552	Sequence 552, App	210	3	12.5	9	7	US-11-045-024-13827	Sequence 13827, A
138	3	12.5	9	7	US-11-097-912-576	Sequence 576, App	211	3	12.5	9	7	US-11-045-024-13841	Sequence 13841, A
139	3	12.5	9	7	US-11-097-912-579	Sequence 579, App	212	3	12.5	9	7	US-11-045-024-13917	Sequence 13917, A
140	3	12.5	9	7	US-11-097-912-684	Sequence 684, App	213	3	12.5	9	7	US-11-045-024-13920	Sequence 13920, A
141	3	12.5	9	7	US-11-102-743-5	Sequence 5, Appli	214	3	12.5	9	7	US-11-045-024-14046	Sequence 14046, A
142	3	12.5	9	7	US-11-045-024-133	Sequence 133, App	215	3	12.5	9	7	US-11-045-024-14068	Sequence 14068, A
143	3	12.5	9	7	US-11-045-024-271	Sequence 271, App	216	3	12.5	9	7	US-11-045-024-14069	Sequence 14069, A
144	3	12.5	9	7	US-11-045-024-634	Sequence 634, App	217	3	12.5	9	7	US-11-045-024-14086	Sequence 14086, A
145	3	12.5	9	7	US-11-045-024-636	Sequence 636, App	218	3	12.5	9	7	US-11-045-024-14102	Sequence 14102, A
146	3	12.5	9	7	US-11-045-024-645	Sequence 645, App	219	3	12.5	9	7	US-11-045-024-14145	Sequence 14145, A
147	3	12.5	9	7	US-11-045-024-684	Sequence 684, App	220	3	12.5	9	7	US-11-045-024-14188	Sequence 14188, A
148	3	12.5	9	7	US-11-045-024-1198	Sequence 1198, App	221	3	12.5	9	7	US-11-045-024-14234	Sequence 14234, A
149	3	12.5	9	7	US-11-045-024-1222	Sequence 1222, App	222	3	12.5	9	7	US-11-045-024-14287	Sequence 14287, A
150	3	12.5	9	7	US-11-045-024-1251	Sequence 1251, App	223	3	12.5	9	7	US-11-045-024-14364	Sequence 14364, A
151	3	12.5	9	7	US-11-045-024-1281	Sequence 1281, App	224	3	12.5	9	7	US-11-193-512-48	Sequence 48, Appl
152	3	12.5	9	7	US-11-045-024-1788	Sequence 1788, App	225	3	12.5	9	7	US-11-033-039-12	Sequence 12, Appl
153	3	12.5	9	7	US-11-045-024-1838	Sequence 1838, App	226	3	12.5	9	7	US-11-033-039-291	Sequence 291, App
154	3	12.5	9	7	US-11-045-024-1840	Sequence 1840, App	227	3	12.5	9	7	US-11-033-039-474	Sequence 474, App
155	3	12.5	9	7	US-11-045-024-1921	Sequence 1921, App	228	3	12.5	9	7	US-11-033-039-608	Sequence 608, App
156	3	12.5	9	7	US-11-045-024-1922	Sequence 1922, App	229	3	12.5	9	7	US-11-033-039-614	Sequence 614, App
157	3	12.5	9	7	US-11-045-024-1949	Sequence 1949, App	230	3	12.5	9	7	US-11-033-039-692	Sequence 692, App
158	3	12.5	9	7	US-11-045-024-1950	Sequence 1950, App	231	3	12.5	9	7	US-11-033-039-693	Sequence 693, App
159	3	12.5	9	7	US-11-045-024-1951	Sequence 1951, App	232	3	12.5	9	7	US-11-033-039-788	Sequence 788, App
160	3	12.5	9	7	US-11-045-024-1983	Sequence 1983, App	233	3	12.5	9	7	US-11-033-039-803	Sequence 803, App
161	3	12.5	9	7	US-11-045-024-1984	Sequence 1984, App	234	3	12.5	9	7	US-11-033-039-806	Sequence 806, App
162	3	12.5	9	7	US-11-045-024-2801	Sequence 2801, App	235	3	12.5	9	7	US-11-033-039-1076	Sequence 1076, Ap
163	3	12.5	9	7	US-11-045-024-3260	Sequence 3260, App	236	3	12.5	9	7	US-11-041-893-30	Sequence 30, Appl
164	3	12.5	9	7	US-11-045-024-3361	Sequence 3361, App	237	3	12.5	9	7	US-11-041-893-162	Sequence 162, App
165	3	12.5	9	7	US-11-045-024-4094	Sequence 4094, App	238	3	12.5	9	7	US-11-107-096-30	Sequence 30, Appl
166	3	12.5	9	7	US-11-045-024-4455	Sequence 4455, App	239	3	12.5	10	6	US-10-966-371-4	Sequence 4, Appli
167	3	12.5	9	7	US-11-045-024-4517	Sequence 4517, App	240	3	12.5	10	6	US-10-473-037-5	Sequence 5, Appli
168	3	12.5	9	7	US-11-045-024-4532	Sequence 4532, App	241	3	12.5	10	6	US-10-491-096-89	Sequence 89, Appl
169	3	12.5	9	7	US-11-045-024-4551	Sequence 4551, App	242	3	12.5	10	6	US-10-491-096-120	Sequence 120, App
170	3	12.5	9	7	US-11-045-024-4552	Sequence 4552, App	243	3	12.5	10	6	US-10-491-096-185	Sequence 185, App
171	3	12.5	9	7	US-11-045-024-6309	Sequence 6309, App	244	3	12.5	10	6	US-10-929-988-436	Sequence 436, App

245	3	12.5	10	6	US-10-859-643-63	Sequence 63, Appl	318	10	7	US-11-045-024-6114	Sequence 6114, Ap
246	3	12.5	10	6	US-10-859-643-79	Sequence 79, Appl	319	10	7	US-11-045-024-6278	Sequence 6278, Ap
247	3	12.5	10	6	US-10-859-643-180	Sequence 180, App	320	10	7	US-11-045-024-6312	Sequence 6312, Ap
248	3	12.5	10	6	US-10-859-643-420	Sequence 420, App	321	10	7	US-11-045-024-6522	Sequence 6522, Ap
249	3	12.5	10	6	US-10-859-643-535	Sequence 535, App	322	10	7	US-11-045-024-6531	Sequence 6531, Ap
250	3	12.5	10	6	US-10-859-643-617	Sequence 617, App	323	10	7	US-11-045-024-6544	Sequence 6544, Ap
251	3	12.5	10	6	US-10-859-643-639	Sequence 639, App	324	10	7	US-11-045-024-6577	Sequence 6577, Ap
252	3	12.5	10	6	US-10-859-643-646	Sequence 646, App	325	10	7	US-11-045-024-6666	Sequence 6666, Ap
253	3	12.5	10	6	US-10-973-977-6	Sequence 6, Appl	326	10	7	US-11-045-024-6705	Sequence 6705, Ap
254	3	12.5	10	7	US-11-173-071-7	Sequence 7, Appl	327	10	7	US-11-045-024-6719	Sequence 6719, Ap
255	3	12.5	10	7	US-11-057-708-21	Sequence 21, Appl	328	10	7	US-11-045-024-6797	Sequence 6797, Ap
256	3	12.5	10	7	US-11-152-747-30	Sequence 30, Appl	329	10	7	US-11-045-024-6798	Sequence 6798, Ap
257	3	12.5	10	7	US-11-152-747-42	Sequence 42, Appl	330	10	7	US-11-045-024-6995	Sequence 6995, Ap
258	3	12.5	10	7	US-11-053-076-243	Sequence 243, App	331	10	7	US-11-045-024-7049	Sequence 7049, Ap
259	3	12.5	10	7	US-11-054-515-3205	Sequence 3205, Ap	332	10	7	US-11-045-024-7197	Sequence 7197, Ap
260	3	12.5	10	7	US-11-053-546-5	Sequence 5, Appl	333	10	7	US-11-045-024-7301	Sequence 7301, Ap
261	3	12.5	10	7	US-11-073-347-99	Sequence 99, Appl	334	10	7	US-11-045-024-7839	Sequence 7839, Ap
262	3	12.5	10	7	US-11-097-864-63	Sequence 63, Appl	335	10	7	US-11-045-024-7946	Sequence 7946, Ap
263	3	12.5	10	7	US-11-097-864-79	Sequence 79, Appl	336	10	7	US-11-045-024-8182	Sequence 8182, Ap
264	3	12.5	10	7	US-11-097-864-180	Sequence 180, App	337	10	7	US-11-045-024-8205	Sequence 8205, Ap
265	3	12.5	10	7	US-11-097-864-420	Sequence 420, App	338	10	7	US-11-045-024-8211	Sequence 8211, Ap
266	3	12.5	10	7	US-11-097-864-535	Sequence 535, App	339	10	7	US-11-045-024-8263	Sequence 8263, Ap
267	3	12.5	10	7	US-11-097-864-617	Sequence 617, App	340	10	7	US-11-045-024-8299	Sequence 8299, Ap
268	3	12.5	10	7	US-11-097-864-639	Sequence 639, App	341	10	7	US-11-045-024-8301	Sequence 8301, Ap
269	3	12.5	10	7	US-11-097-864-646	Sequence 646, App	342	10	7	US-11-045-024-8330	Sequence 8330, Ap
270	3	12.5	10	7	US-11-097-912-63	Sequence 63, Appl	343	10	7	US-11-045-024-8628	Sequence 8628, Ap
271	3	12.5	10	7	US-11-097-912-79	Sequence 79, Appl	344	10	7	US-11-045-024-8629	Sequence 8629, Ap
272	3	12.5	10	7	US-11-097-912-180	Sequence 180, App	345	10	7	US-11-045-024-9551	Sequence 9551, Ap
273	3	12.5	10	7	US-11-097-912-420	Sequence 420, App	346	10	7	US-11-045-024-9557	Sequence 9557, Ap
274	3	12.5	10	7	US-11-097-912-535	Sequence 535, App	347	10	7	US-11-045-024-9674	Sequence 9674, Ap
275	3	12.5	10	7	US-11-097-912-617	Sequence 617, App	348	10	7	US-11-045-024-9989	Sequence 9989, Ap
276	3	12.5	10	7	US-11-097-912-639	Sequence 639, App	349	10	7	US-11-045-024-9999	Sequence 9999, Ap
277	3	12.5	10	7	US-11-097-912-646	Sequence 646, App	350	10	7	US-11-045-024-10274	Sequence 10274, A
278	3	12.5	10	7	US-11-166-288-10	Sequence 10, Appl	351	10	7	US-11-045-024-10291	Sequence 10291, A
279	3	12.5	10	7	US-11-045-024-70	Sequence 70, Appl	352	10	7	US-11-045-024-10773	Sequence 10773, A
280	3	12.5	10	7	US-11-045-024-75	Sequence 75, Appl	353	10	7	US-11-045-024-10800	Sequence 10800, A
281	3	12.5	10	7	US-11-045-024-304	Sequence 304, App	354	10	7	US-11-045-024-10973	Sequence 10973, A
282	3	12.5	10	7	US-11-045-024-767	Sequence 767, App	355	10	7	US-11-045-024-10974	Sequence 10974, A
283	3	12.5	10	7	US-11-045-024-789	Sequence 789, App	356	10	7	US-11-045-024-11168	Sequence 11168, A
284	3	12.5	10	7	US-11-045-024-853	Sequence 853, App	357	10	7	US-11-045-024-11571	Sequence 11571, A
285	3	12.5	10	7	US-11-045-024-855	Sequence 855, App	358	10	7	US-11-045-024-11587	Sequence 11587, A
286	3	12.5	10	7	US-11-045-024-1271	Sequence 1271, Ap	359	10	7	US-11-045-024-11593	Sequence 11593, A
287	3	12.5	10	7	US-11-045-024-1319	Sequence 1319, Ap	360	10	7	US-11-045-024-11678	Sequence 11678, A
288	3	12.5	10	7	US-11-045-024-1339	Sequence 1339, Ap	361	10	7	US-11-045-024-11900	Sequence 11900, A
289	3	12.5	10	7	US-11-045-024-2007	Sequence 2007, App	362	10	7	US-11-045-024-11908	Sequence 11908, A
290	3	12.5	10	7	US-11-045-024-2079	Sequence 2079, App	363	10	7	US-11-045-024-12122	Sequence 12122, A
291	3	12.5	10	7	US-11-045-024-2153	Sequence 2153, Ap	364	10	7	US-11-045-024-12132	Sequence 12132, A
292	3	12.5	10	7	US-11-045-024-2154	Sequence 2154, Ap	365	10	7	US-11-045-024-14295	Sequence 14295, A
293	3	12.5	10	7	US-11-045-024-2186	Sequence 2186, Ap	366	10	7	US-11-045-024-14334	Sequence 14334, A
294	3	12.5	10	7	US-11-045-024-2187	Sequence 2187, Ap	367	10	7	US-11-045-024-14457	Sequence 14457, A
295	3	12.5	10	7	US-11-045-024-2188	Sequence 2188, Ap	368	10	7	US-11-129-104-81	Sequence 81, Appl
296	3	12.5	10	7	US-11-045-024-2217	Sequence 2217, Ap	369	10	7	US-11-129-104-82	Sequence 82, Appl
297	3	12.5	10	7	US-11-045-024-2218	Sequence 2218, Ap	370	10	7	US-11-107-096-35	Sequence 35, Appl
298	3	12.5	10	7	US-11-045-024-2219	Sequence 2219, Ap	371	10	6	US-10-665-658-16	Sequence 16, Appl
299	3	12.5	10	7	US-11-045-024-2220	Sequence 2220, Ap	372	10	6	US-10-841-956A-22	Sequence 22, Appl
300	3	12.5	10	7	US-11-045-024-2221	Sequence 2221, Ap	373	10	6	US-10-834-397-275	Sequence 275, App
301	3	12.5	10	7	US-11-045-024-2221	Sequence 2221, Ap	374	10	6	US-10-877-961B-143	Sequence 143, App
302	3	12.5	10	7	US-11-045-024-2847	Sequence 2847, Ap	375	10	6	US-10-877-961B-165	Sequence 165, App
303	3	12.5	10	7	US-11-045-024-3299	Sequence 3299, App	376	10	6	US-10-877-961B-183	Sequence 183, App
304	3	12.5	10	7	US-11-045-024-3346	Sequence 3346, Ap	377	10	6	US-10-877-961B-209	Sequence 209, App
305	3	12.5	10	7	US-11-045-024-3347	Sequence 3347, Ap	378	10	6	US-10-877-961B-210	Sequence 210, App
306	3	12.5	10	7	US-11-045-024-3846	Sequence 3846, Ap	379	10	6	US-10-877-961B-211	Sequence 211, App
307	3	12.5	10	7	US-11-045-024-3874	Sequence 3874, Ap	380	10	6	US-10-877-961B-212	Sequence 212, App
308	3	12.5	10	7	US-11-045-024-4666	Sequence 4666, Ap	381	10	6	US-10-877-961B-213	Sequence 213, App
309	3	12.5	10	7	US-11-045-024-4667	Sequence 4667, Ap	382	10	6	US-10-877-961B-214	Sequence 214, App
310	3	12.5	10	7	US-11-045-024-4688	Sequence 4688, Ap	383	10	6	US-10-877-961B-215	Sequence 215, App
311	3	12.5	10	7	US-11-045-024-4685	Sequence 4685, Ap	384	10	6	US-10-877-961B-216	Sequence 216, App
312	3	12.5	10	7	US-11-045-024-4686	Sequence 4686, Ap	385	10	6	US-10-877-961B-217	Sequence 217, App
313	3	12.5	10	7	US-11-045-024-4702	Sequence 4702, Ap	386	10	6	US-10-877-961B-218	Sequence 218, App
314	3	12.5	10	7	US-11-045-024-5139	Sequence 5139, Ap	387	10	6	US-10-877-961B-219	Sequence 219, App
315	3	12.5	10	7	US-11-045-024-5375	Sequence 5375, Ap	388	10	6	US-10-877-961B-220	Sequence 220, App
316	3	12.5	10	7	US-11-045-024-5367	Sequence 5367, Ap	389	10	6	US-10-877-961B-227	Sequence 227, App
317	3	12.5	10	7	US-11-045-024-6087	Sequence 6087, Ap	390	10	6	US-10-877-961B-239	Sequence 239, App
					Sequence 6095, Ap						

391	3	12.5	11	7	US-11-025-712-8	Sequence 8, Appli	464	11	7	US-11-045-024-9532	Sequence 9532, Ap
392	3	12.5	11	7	US-11-054-515-3164	Sequence 3164, Ap	465	11	7	US-11-045-024-9561	Sequence 9561, Ap
393	3	12.5	11	7	US-11-029-003-26	Sequence 26, Appl	466	11	7	US-11-045-024-9562	Sequence 9562, Ap
394	3	12.5	11	7	US-11-058-735-33	Sequence 33, Appl	467	11	7	US-11-045-024-9570	Sequence 9570, Ap
395	3	12.5	11	7	US-11-045-024-87	Sequence 87, Appl	468	11	7	US-11-045-024-9571	Sequence 9571, Ap
396	3	12.5	11	7	US-11-045-024-98	Sequence 98, Appl	469	11	7	US-11-045-024-9572	Sequence 9572, Ap
397	3	12.5	11	7	US-11-045-024-323	Sequence 323, App	470	11	7	US-11-045-024-9841	Sequence 9841, Ap
398	3	12.5	11	7	US-11-045-024-337	Sequence 337, App	471	11	7	US-11-045-024-9991	Sequence 9991, Ap
399	3	12.5	11	7	US-11-045-024-929	Sequence 929, App	472	11	7	US-11-045-024-9968	Sequence 9968, Ap
400	3	12.5	11	7	US-11-045-024-980	Sequence 980, App	473	11	7	US-11-045-024-9979	Sequence 9979, Ap
401	3	12.5	11	7	US-11-045-024-983	Sequence 983, App	474	11	7	US-11-045-024-10001	Sequence 10001, Ap
402	3	12.5	11	7	US-11-045-024-1416	Sequence 1416, Ap	475	11	7	US-11-045-024-10239	Sequence 10239, A
403	3	12.5	11	7	US-11-045-024-1449	Sequence 1449, Ap	476	11	7	US-11-045-024-10279	Sequence 10279, A
404	3	12.5	11	7	US-11-045-024-2383	Sequence 2383, Ap	477	11	7	US-11-045-024-10281	Sequence 10281, A
405	3	12.5	11	7	US-11-045-024-2384	Sequence 2384, Ap	478	11	7	US-11-045-024-10295	Sequence 10295, A
406	3	12.5	11	7	US-11-045-024-2385	Sequence 2385, Ap	479	11	7	US-11-045-024-10774	Sequence 10774, A
407	3	12.5	11	7	US-11-045-024-2422	Sequence 2422, Ap	480	11	7	US-11-045-024-10802	Sequence 10802, A
408	3	12.5	11	7	US-11-045-024-2423	Sequence 2423, Ap	481	11	7	US-11-045-024-10834	Sequence 10834, A
409	3	12.5	11	7	US-11-045-024-2424	Sequence 2424, Ap	482	11	7	US-11-045-024-10881	Sequence 10881, A
410	3	12.5	11	7	US-11-045-024-2425	Sequence 2425, Ap	483	11	7	US-11-045-024-10947	Sequence 10947, A
411	3	12.5	11	7	US-11-045-024-2426	Sequence 2426, Ap	484	11	7	US-11-045-024-10976	Sequence 10976, A
412	3	12.5	11	7	US-11-045-024-2427	Sequence 2427, Ap	485	11	7	US-11-045-024-11146	Sequence 11146, A
413	3	12.5	11	7	US-11-045-024-2451	Sequence 2451, Ap	486	11	7	US-11-045-024-11440	Sequence 11440, A
414	3	12.5	11	7	US-11-045-024-2452	Sequence 2452, Ap	487	11	7	US-11-045-024-11461	Sequence 11461, A
415	3	12.5	11	7	US-11-045-024-2453	Sequence 2453, Ap	488	11	7	US-11-045-024-11556	Sequence 11556, A
416	3	12.5	11	7	US-11-045-024-2454	Sequence 2454, Ap	489	11	7	US-11-045-024-11568	Sequence 11568, A
417	3	12.5	11	7	US-11-045-024-2455	Sequence 2455, Ap	490	11	7	US-11-045-024-11597	Sequence 11597, A
418	3	12.5	11	7	US-11-045-024-2891	Sequence 2891, Ap	491	11	7	US-11-045-024-11598	Sequence 11598, A
419	3	12.5	11	7	US-11-045-024-2910	Sequence 2910, Ap	492	11	7	US-11-045-024-11603	Sequence 11603, A
420	3	12.5	11	7	US-11-045-024-3379	Sequence 3379, Ap	493	11	7	US-11-045-024-11620	Sequence 11620, A
421	3	12.5	11	7	US-11-045-024-3437	Sequence 3437, Ap	494	11	7	US-11-045-024-11604	Sequence 11604, A
422	3	12.5	11	7	US-11-045-024-3438	Sequence 3438, Ap	495	11	7	US-11-045-024-11800	Sequence 11800, A
423	3	12.5	11	7	US-11-045-024-3439	Sequence 3439, Ap	496	11	7	US-11-045-024-11835	Sequence 11835, A
424	3	12.5	11	7	US-11-045-024-3440	Sequence 3440, Ap	497	11	7	US-11-045-024-11889	Sequence 11889, A
425	3	12.5	11	7	US-11-045-024-3933	Sequence 3933, Ap	498	11	7	US-11-045-024-11897	Sequence 11897, A
426	3	12.5	11	7	US-11-045-024-3961	Sequence 3961, Ap	499	11	7	US-11-045-024-11910	Sequence 11910, A
427	3	12.5	11	7	US-11-045-024-4195	Sequence 4195, Ap	500	11	7	US-11-127-677-80	Sequence 80, Appl
428	3	12.5	11	7	US-11-045-024-4761	Sequence 4761, Ap	501	11	7	US-11-127-677-84	Sequence 84, Appl
429	3	12.5	11	7	US-11-045-024-4819	Sequence 4819, Ap	502	11	7	US-11-127-677-88	Sequence 88, Appl
430	3	12.5	11	7	US-11-045-024-4820	Sequence 4820, Ap	503	11	7	US-11-192-219-43	Sequence 43, Appl
431	3	12.5	11	7	US-11-045-024-4840	Sequence 4840, Ap	504	11	7	US-11-157-360-32	Sequence 32, Appl
432	3	12.5	11	7	US-11-045-024-4841	Sequence 4841, Ap	505	11	7	US-11-038-980-72	Sequence 72, Appl
433	3	12.5	11	7	US-11-045-024-4860	Sequence 4860, Ap	506	11	7	US-11-038-980-100	Sequence 100, App
434	3	12.5	11	7	US-11-045-024-4861	Sequence 4861, Ap	507	11	6	US-10-997-086-44	Sequence 44, Appl
435	3	12.5	11	7	US-11-045-024-4862	Sequence 4862, Ap	508	11	6	US-10-507-662-12	Sequence 12, Appl
436	3	12.5	11	7	US-11-045-024-5390	Sequence 5390, Ap	509	11	6	US-10-467-657-9168	Sequence 8660, Ap
437	3	12.5	11	7	US-11-045-024-5407	Sequence 5407, Ap	510	11	6	US-10-467-657-9168	Sequence 172, App
438	3	12.5	11	7	US-11-045-024-5586	Sequence 5586, Ap	511	11	6	US-10-929-988-172	Sequence 268, App
439	3	12.5	11	7	US-11-045-024-6088	Sequence 6088, Ap	512	11	6	US-10-834-397-268	Sequence 3, Appl
440	3	12.5	11	7	US-11-045-024-6089	Sequence 6089, Ap	513	11	6	US-11-045-173-3	Sequence 3197, Ap
441	3	12.5	11	7	US-11-045-024-6118	Sequence 6118, Ap	514	11	6	US-11-054-515-3197	Sequence 22, Appl
442	3	12.5	11	7	US-11-045-024-6338	Sequence 6338, Ap	515	11	6	US-11-069-834-22	Sequence 30, Appl
443	3	12.5	11	7	US-11-045-024-6523	Sequence 6523, Ap	516	11	6	US-11-069-834-30	Sequence 32, Appl
444	3	12.5	11	7	US-11-045-024-6547	Sequence 6547, Ap	517	11	6	US-11-069-834-32	Sequence 32, Appl
445	3	12.5	11	7	US-11-045-024-6669	Sequence 6669, Ap	518	11	6	US-11-098-763-21	Sequence 21, Appl
446	3	12.5	11	7	US-11-045-024-6707	Sequence 6707, Ap	519	11	6	US-11-129-104-24	Sequence 24, Appl
447	3	12.5	11	7	US-11-045-024-6785	Sequence 6785, Ap	520	11	6	US-11-129-104-36	Sequence 36, Appl
448	3	12.5	11	7	US-11-045-024-6800	Sequence 6800, Ap	521	11	6	US-11-047-383-25	Sequence 25, Appl
449	3	12.5	11	7	US-11-045-024-7222	Sequence 7222, Ap	522	11	6	US-10-986-501-290	Sequence 290, App
450	3	12.5	11	7	US-11-045-024-7287	Sequence 7287, Ap	523	11	6	US-10-511-559-193	Sequence 193, App
451	3	12.5	11	7	US-11-045-024-7494	Sequence 7494, Ap	524	11	6	US-10-511-559-194	Sequence 194, App
452	3	12.5	11	7	US-11-045-024-7509	Sequence 7509, Ap	525	11	6	US-10-511-559-195	Sequence 195, App
453	3	12.5	11	7	US-11-045-024-7840	Sequence 7840, Ap	526	11	6	US-10-511-559-196	Sequence 196, App
454	3	12.5	11	7	US-11-045-024-7937	Sequence 7937, Ap	527	11	6	US-10-511-559-197	Sequence 197, App
455	3	12.5	11	7	US-11-045-024-7938	Sequence 7938, Ap	528	11	6	US-10-511-559-234	Sequence 234, App
456	3	12.5	11	7	US-11-045-024-8180	Sequence 8180, Ap	529	11	6	US-10-511-559-235	Sequence 235, App
457	3	12.5	11	7	US-11-045-024-8236	Sequence 8236, Ap	530	11	6	US-10-511-559-236	Sequence 236, App
458	3	12.5	11	7	US-11-045-024-8264	Sequence 8264, Ap	531	11	6	US-10-511-559-237	Sequence 237, App
459	3	12.5	11	7	US-11-045-024-8304	Sequence 8304, Ap	532	11	6	US-10-511-559-238	Sequence 238, App
460	3	12.5	11	7	US-11-045-024-8333	Sequence 8333, Ap	533	11	6	US-10-511-559-304	Sequence 304, App
461	3	12.5	11	7	US-11-045-024-8387	Sequence 8387, Ap	534	11	6	US-10-511-559-305	Sequence 305, App
462	3	12.5	11	7	US-11-045-024-8574	Sequence 8574, Ap	535	11	6	US-10-511-559-306	Sequence 306, App
463	3	12.5	11	7	US-11-045-024-8878	Sequence 8878, Ap	536	11	6	US-10-511-559-307	Sequence 307, App

537	3	12.5	13	6	US-10-511-559-308	Sequence 308, App	610	3	12.5	14	6	US-10-726-554-9	Sequence 9, Appl
538	3	12.5	13	6	US-10-511-559-309	Sequence 309, App	611	3	12.5	14	6	US-10-467-657-9003	Sequence 9003, Ap
539	3	12.5	13	6	US-10-511-559-310	Sequence 310, App	612	3	12.5	14	7	US-11-012-353-41	Sequence 41, Appl
540	3	12.5	13	6	US-10-511-559-311	Sequence 311, App	613	3	12.5	14	7	US-11-054-515-2360	Sequence 2360, Ap
541	3	12.5	13	6	US-10-511-559-348	Sequence 348, App	614	3	12.5	14	7	US-11-054-515-2375	Sequence 2375, Ap
542	3	12.5	13	6	US-10-511-559-349	Sequence 349, App	615	3	12.5	14	7	US-11-054-515-2393	Sequence 2393, Ap
543	3	12.5	13	6	US-10-511-559-350	Sequence 350, App	616	3	12.5	14	7	US-11-054-515-2410	Sequence 2410, Ap
544	3	12.5	13	6	US-10-511-559-351	Sequence 351, App	617	3	12.5	14	7	US-11-054-515-2418	Sequence 2418, Ap
545	3	12.5	13	6	US-10-511-559-352	Sequence 352, App	618	3	12.5	14	7	US-11-054-515-2421	Sequence 2421, Ap
546	3	12.5	13	6	US-10-511-559-353	Sequence 353, App	619	3	12.5	14	7	US-11-054-515-2422	Sequence 2422, Ap
547	3	12.5	13	6	US-10-511-559-354	Sequence 354, App	620	3	12.5	14	7	US-11-054-515-2440	Sequence 2440, Ap
548	3	12.5	13	6	US-10-511-559-433	Sequence 433, App	621	3	12.5	14	7	US-11-054-515-2451	Sequence 2451, Ap
549	3	12.5	13	6	US-10-511-559-434	Sequence 434, App	622	3	12.5	14	7	US-11-054-515-2462	Sequence 2462, Ap
550	3	12.5	13	6	US-10-511-559-435	Sequence 435, App	623	3	12.5	14	7	US-11-054-515-2469	Sequence 2469, Ap
551	3	12.5	13	6	US-10-511-559-466	Sequence 466, App	624	3	12.5	14	7	US-11-054-515-2493	Sequence 2493, Ap
552	3	12.5	13	6	US-10-511-559-467	Sequence 467, App	625	3	12.5	14	7	US-11-054-515-2495	Sequence 2495, Ap
553	3	12.5	13	6	US-10-511-559-468	Sequence 468, App	626	3	12.5	14	7	US-11-054-515-2498	Sequence 2498, Ap
554	3	12.5	13	6	US-10-511-559-469	Sequence 469, App	627	3	12.5	14	7	US-11-054-515-2522	Sequence 2522, Ap
555	3	12.5	13	6	US-10-511-559-470	Sequence 470, App	628	3	12.5	14	7	US-11-054-515-2542	Sequence 2542, Ap
556	3	12.5	13	6	US-10-511-559-501	Sequence 501, App	629	3	12.5	14	7	US-11-054-515-2549	Sequence 2549, Ap
557	3	12.5	13	6	US-10-511-559-502	Sequence 502, App	630	3	12.5	14	7	US-11-054-515-2559	Sequence 2559, Ap
558	3	12.5	13	6	US-10-511-559-503	Sequence 503, App	631	3	12.5	14	7	US-11-054-515-2593	Sequence 2593, Ap
559	3	12.5	13	6	US-10-511-559-504	Sequence 504, App	632	3	12.5	14	7	US-11-054-515-2642	Sequence 2642, Ap
560	3	12.5	13	6	US-10-511-559-630	Sequence 630, App	633	3	12.5	14	7	US-11-054-515-2645	Sequence 2645, Ap
561	3	12.5	13	6	US-10-511-559-631	Sequence 631, App	634	3	12.5	14	7	US-11-054-515-2719	Sequence 2719, Ap
562	3	12.5	13	6	US-10-511-559-632	Sequence 632, App	635	3	12.5	14	7	US-11-054-515-2722	Sequence 2722, Ap
563	3	12.5	13	6	US-10-511-559-633	Sequence 633, App	636	3	12.5	14	7	US-11-054-515-2756	Sequence 2756, Ap
564	3	12.5	13	6	US-10-511-559-634	Sequence 634, App	637	3	12.5	14	7	US-11-045-024-14250	Sequence 14250, A
565	3	12.5	13	6	US-10-511-559-676	Sequence 676, App	638	3	12.5	14	7	US-11-045-024-14252	Sequence 14252, A
566	3	12.5	13	6	US-10-511-559-677	Sequence 677, App	639	3	12.5	14	7	US-11-045-024-14264	Sequence 14264, A
567	3	12.5	13	6	US-10-511-559-678	Sequence 678, App	640	3	12.5	14	7	US-11-045-024-14514	Sequence 14514, A
568	3	12.5	13	6	US-10-511-559-679	Sequence 679, App	641	3	12.5	14	7	US-11-045-024-14515	Sequence 14515, A
569	3	12.5	13	6	US-10-511-559-680	Sequence 680, App	642	3	12.5	14	7	US-11-045-024-14525	Sequence 14525, A
570	3	12.5	13	6	US-10-511-559-681	Sequence 681, App	643	3	12.5	14	7	US-11-116-144-2233	Sequence 223, App
571	3	12.5	13	6	US-10-511-559-682	Sequence 682, App	644	3	12.5	14	7	US-11-116-144-2238	Sequence 238, App
572	3	12.5	13	6	US-10-511-559-683	Sequence 683, App	645	3	12.5	14	7	US-11-116-144-268	Sequence 268, App
573	3	12.5	13	6	US-10-511-559-689	Sequence 689, App	646	3	12.5	14	7	US-11-116-144-269	Sequence 269, App
574	3	12.5	13	6	US-10-511-559-690	Sequence 690, App	647	3	12.5	14	7	US-11-116-144-286	Sequence 286, App
575	3	12.5	13	6	US-10-511-559-691	Sequence 691, App	648	3	12.5	14	7	US-11-016-542-13	Sequence 13, Appl
576	3	12.5	13	6	US-10-511-559-692	Sequence 692, App	649	3	12.5	14	7	US-11-033-039-30	Sequence 30, Appl
577	3	12.5	13	6	US-10-511-559-693	Sequence 693, App	650	3	12.5	14	7	US-11-152-697-41	Sequence 41, Appl
578	3	12.5	13	6	US-10-511-559-694	Sequence 694, App	651	3	12.5	14	7	US-11-152-697-42	Sequence 42, Appl
579	3	12.5	13	6	US-10-511-559-695	Sequence 695, App	652	3	12.5	14	7	US-11-152-697-47	Sequence 47, Appl
580	3	12.5	13	6	US-10-511-559-867	Sequence 867, App	653	3	12.5	14	7	US-11-152-697-50	Sequence 50, Appl
581	3	12.5	13	6	US-10-511-559-868	Sequence 868, App	654	3	12.5	14	7	US-11-152-697-51	Sequence 51, Appl
582	3	12.5	13	6	US-10-511-559-869	Sequence 869, App	655	3	12.5	14	7	US-11-152-697-53	Sequence 53, Appl
583	3	12.5	13	6	US-10-511-559-870	Sequence 870, App	656	3	12.5	15	6	US-10-816-768-102	Sequence 102, App
584	3	12.5	13	6	US-10-511-559-871	Sequence 871, App	657	3	12.5	15	6	US-10-511-559-77	Sequence 77, Appl
585	3	12.5	13	6	US-10-511-559-908	Sequence 908, App	658	3	12.5	15	6	US-10-511-559-78	Sequence 78, Appl
586	3	12.5	13	6	US-10-511-559-909	Sequence 909, App	659	3	12.5	15	6	US-10-467-657-8918	Sequence 8918, Ap
587	3	12.5	13	6	US-10-511-559-910	Sequence 910, App	660	3	12.5	15	6	US-10-973-977-50	Sequence 50, Appl
588	3	12.5	13	6	US-10-511-559-911	Sequence 911, App	661	3	12.5	15	7	US-11-019-894A-1	Sequence 1, Appl
589	3	12.5	13	6	US-10-511-559-912	Sequence 912, App	662	3	12.5	15	7	US-11-038-501-20	Sequence 20, Appl
590	3	12.5	13	6	US-10-353-783-72	Sequence 72, Appl	663	3	12.5	15	7	US-11-022-562-61	Sequence 61, Appl
591	3	12.5	13	6	US-10-467-657-8844	Sequence 8844, Ap	664	3	12.5	15	7	US-11-022-562-62	Sequence 62, Appl
592	3	12.5	13	6	US-10-530-252-15	Sequence 15, Appl	665	3	12.5	15	7	US-11-022-562-63	Sequence 63, Appl
593	3	12.5	13	7	US-11-054-515-2990	Sequence 2990, Ap	666	3	12.5	15	7	US-11-054-515-2757	Sequence 2757, Ap
594	3	12.5	13	7	US-11-054-515-3033	Sequence 3033, Ap	667	3	12.5	15	7	US-11-054-515-2803	Sequence 2803, Ap
595	3	12.5	13	7	US-11-058-735-75	Sequence 75, Appl	668	3	12.5	15	7	US-11-059-633-23	Sequence 23, Appl
596	3	12.5	13	7	US-11-137-315A-57	Sequence 57, Appl	669	3	12.5	15	7	US-11-059-633-23	Sequence 23, Appl
597	3	12.5	13	7	US-11-069-834-45	Sequence 45, Appl	670	3	12.5	15	7	US-11-106-932-68	Sequence 68, Appl
598	3	12.5	13	7	US-11-116-144-82	Sequence 82, Appl	671	3	12.5	15	7	US-11-106-932-112	Sequence 112, App
599	3	12.5	13	7	US-11-016-542-11	Sequence 11, Appl	672	3	12.5	15	7	US-11-045-024-12908	Sequence 12908, A
600	3	12.5	13	7	US-11-007-282-1	Sequence 1, Appl	673	3	12.5	15	7	US-11-045-024-12916	Sequence 12916, A
601	3	12.5	13	7	US-11-033-039-792	Sequence 792, App	674	3	12.5	15	7	US-11-045-024-12918	Sequence 12918, A
602	3	12.5	13	7	US-11-033-039-1386	Sequence 1386, Ap	675	3	12.5	15	7	US-11-045-024-12938	Sequence 12938, A
603	3	12.5	13	7	US-11-033-039-1399	Sequence 1399, Ap	676	3	12.5	15	7	US-11-045-024-12939	Sequence 12939, A
604	3	12.5	13	7	US-11-033-039-1401	Sequence 1401, Ap	677	3	12.5	15	7	US-11-045-024-12941	Sequence 12941, A
605	3	12.5	13	7	US-11-033-039-1405	Sequence 1405, Ap	678	3	12.5	15	7	US-11-045-024-12972	Sequence 12972, A
606	3	12.5	13	7	US-11-152-697-28	Sequence 28, Appl	679	3	12.5	15	7	US-11-045-024-12999	Sequence 12999, A
607	3	12.5	14	6	US-10-655-855-10	Sequence 10, Appl	680	3	12.5	15	7	US-11-045-024-13047	Sequence 13047, A
608	3	12.5	14	6	US-10-655-855-12	Sequence 12, Appl	681	3	12.5	15	7	US-11-045-024-13048	Sequence 13048, A
609	3	12.5	14	6	US-10-655-855-12	Sequence 12, Appl	682	3	12.5	15	7		

683	3	12.5	15	7	US-11-045-024-13107	Sequence 13107, A	756	17	7	US-11-054-515-2878	Sequence 2878, Ap
684	3	12.5	15	7	US-11-045-024-13127	Sequence 13127, A	757	17	7	US-11-054-515-3126	Sequence 3126, Ap
685	3	12.5	15	7	US-11-045-024-13136	Sequence 13136, A	758	17	7	US-11-193-512-47	Sequence 47, Appl
686	3	12.5	15	7	US-11-045-024-13171	Sequence 13171, A	759	17	7	US-11-124-708-4	Sequence 4, Appl
687	3	12.5	15	7	US-11-045-024-13185	Sequence 13185, A	760	17	6	US-11-033-039-1427	Sequence 1427, Ap
688	3	12.5	15	7	US-11-045-024-13197	Sequence 13197, A	761	17	6	US-10-467-657-9113	Sequence 9113, Ap
689	3	12.5	15	7	US-11-045-024-13198	Sequence 13198, A	762	18	6	US-10-467-657-9127	Sequence 9127, Ap
690	3	12.5	15	7	US-11-045-024-13213	Sequence 13213, A	763	18	6	US-10-532-480-38	Sequence 38, Appl
691	3	12.5	15	7	US-11-045-024-13261	Sequence 13261, A	764	18	6	US-10-532-480-39	Sequence 39, Appl
692	3	12.5	15	7	US-11-045-024-13264	Sequence 13264, A	765	18	6	US-10-532-480-40	Sequence 40, Appl
693	3	12.5	15	7	US-11-045-024-13274	Sequence 13274, A	766	18	6	US-10-532-480-41	Sequence 41, Appl
694	3	12.5	15	7	US-11-045-024-13275	Sequence 13275, A	767	18	6	US-10-871-260A-1	Sequence 1, Appl
695	3	12.5	15	7	US-11-045-024-13276	Sequence 13276, A	768	18	6	US-10-509-787A-91	Sequence 91, Appl
696	3	12.5	15	7	US-11-045-024-13277	Sequence 13277, A	769	18	6	US-10-509-787A-92	Sequence 92, Appl
697	3	12.5	15	7	US-11-045-024-13281	Sequence 13281, A	770	18	6	US-10-729-121-43	Sequence 43, Appl
698	3	12.5	15	7	US-11-045-024-13290	Sequence 13290, A	771	18	7	US-11-092-496-18	Sequence 18, Appl
699	3	12.5	15	7	US-11-045-024-13412	Sequence 13412, A	772	18	7	US-11-109-161-13	Sequence 13, Appl
700	3	12.5	15	7	US-11-045-024-13413	Sequence 13413, A	773	18	7	US-11-054-515-2168	Sequence 2168, Ap
701	3	12.5	15	7	US-11-045-024-13430	Sequence 13430, A	774	18	7	US-11-054-515-2748	Sequence 2748, Ap
702	3	12.5	15	7	US-11-045-024-13446	Sequence 13446, A	775	18	7	US-11-033-039-1175	Sequence 1175, Ap
703	3	12.5	15	7	US-11-045-024-13489	Sequence 13489, A	776	18	7	US-11-033-039-1201	Sequence 1201, Ap
704	3	12.5	15	7	US-11-045-024-14485	Sequence 14485, A	777	18	7	US-11-033-039-1226	Sequence 1226, Ap
705	3	12.5	15	7	US-11-107-364-32	Sequence 32, Appl	778	18	7	US-11-033-039-1227	Sequence 1227, Ap
706	3	12.5	15	7	US-11-187-558-1	Sequence 1, Appl	779	18	7	US-11-033-039-1235	Sequence 1235, Ap
707	3	12.5	15	7	US-11-157-360-33	Sequence 33, Appl	780	18	7	US-11-033-039-1255	Sequence 1255, Ap
708	3	12.5	15	7	US-11-145-035-11	Sequence 11, Appl	781	18	7	US-11-033-039-1299	Sequence 1299, Ap
709	3	12.5	16	7	US-11-033-039-635	Sequence 635, App	782	18	7	US-11-033-039-1300	Sequence 1300, Ap
710	3	12.5	16	6	US-10-984-376-17	Sequence 17, Appl	783	18	7	US-11-033-039-1336	Sequence 1336, Ap
711	3	12.5	16	6	US-10-939-890-10	Sequence 10, Appl	784	18	7	US-11-033-039-1426	Sequence 1426, Ap
712	3	12.5	16	6	US-10-939-890-204	Sequence 204, App	785	18	7	US-11-041-893-25	Sequence 25, Appl
713	3	12.5	16	6	US-10-467-657-8903	Sequence 8903, Ap	786	18	7	US-11-156-163-13	Sequence 13, Appl
714	3	12.5	16	6	US-10-467-657-8935	Sequence 8935, Ap	787	18	7	US-11-079-139-5	Sequence 5, Appl
715	3	12.5	16	6	US-10-985-023-1	Sequence 1, Appl	788	19	5	US-09-993-295-2	Sequence 2, Appl
716	3	12.5	16	6	US-10-834-397-197	Sequence 197, App	789	19	6	US-10-503-575-117	Sequence 117, App
717	3	12.5	16	7	US-11-011-666-11	Sequence 11, Appl	790	19	6	US-10-503-575-140	Sequence 140, App
718	3	12.5	16	7	US-11-012-353-10	Sequence 10, Appl	791	19	6	US-10-503-575-142	Sequence 142, App
719	3	12.5	16	7	US-11-180-997-16	Sequence 16, Appl	792	19	6	US-10-503-575-190	Sequence 190, App
720	3	12.5	16	7	US-11-054-515-2246	Sequence 2246, Ap	793	19	6	US-10-503-575-231	Sequence 231, App
721	3	12.5	16	7	US-11-054-669-106	Sequence 106, App	794	19	6	US-10-503-575-256	Sequence 256, App
722	3	12.5	16	7	US-11-060-005-34	Sequence 34, Appl	795	19	6	US-10-503-575-257	Sequence 257, App
723	3	12.5	16	7	US-11-061-848-30	Sequence 30, Appl	796	19	6	US-10-503-575-287	Sequence 287, App
724	3	12.5	16	7	US-11-033-039-1428	Sequence 1428, Ap	797	19	6	US-10-467-657-6706	Sequence 6706, Ap
725	3	12.5	16	7	US-11-004-590-108	Sequence 108, App	798	19	6	US-10-467-657-9094	Sequence 9094, Ap
726	3	12.5	16	7	US-11-226-325-9	Sequence 9, Appl	799	19	6	US-10-623-155-481	Sequence 481, App
727	3	12.5	17	6	US-10-655-855-21	Sequence 21, Appl	800	19	6	US-10-763-712A-126	Sequence 126, App
728	3	12.5	17	6	US-10-655-855-22	Sequence 22, Appl	801	19	6	US-10-929-988-405	Sequence 405, App
729	3	12.5	17	6	US-10-939-890-92	Sequence 92, Appl	802	19	6	US-10-485-788A-591	Sequence 591, App
730	3	12.5	17	6	US-10-945-853-4	Sequence 4, Appl	803	19	6	US-10-956-755A-11	Sequence 11, Appl
731	3	12.5	17	6	US-10-989-226-2	Sequence 2, Appl	804	19	6	US-10-997-074-51	Sequence 51, Appl
732	3	12.5	17	6	US-10-467-657-6632	Sequence 6632, Ap	805	19	7	US-11-054-515-3036	Sequence 3036, Ap
733	3	12.5	17	6	US-10-925-368A-89	Sequence 89, Appl	806	19	7	US-11-058-384-13	Sequence 13, Appl
734	3	12.5	17	6	US-10-665-658-44	Sequence 44, Appl	807	19	7	US-11-127-601-38	Sequence 38, Appl
735	3	12.5	17	6	US-10-509-292-53	Sequence 53, Appl	808	19	7	US-11-040-488-25	Sequence 25, Appl
736	3	12.5	17	6	US-10-509-292-59	Sequence 59, Appl	809	19	7	US-11-111-900-23	Sequence 23, Appl
737	3	12.5	17	6	US-10-509-787A-15	Sequence 15, Appl	810	19	7	US-11-111-900-24	Sequence 24, Appl
738	3	12.5	17	6	US-10-509-787A-16	Sequence 16, Appl	811	19	7	US-11-033-039-479	Sequence 479, App
739	3	12.5	17	6	US-10-509-787A-137	Sequence 137, App	812	19	7	US-11-033-039-794	Sequence 794, App
740	3	12.5	17	6	US-10-489-866-12	Sequence 12, Appl	813	19	7	US-11-033-039-1097	Sequence 1097, Ap
741	3	12.5	17	6	US-10-834-397-203	Sequence 203, App	814	19	7	US-11-033-039-1101	Sequence 1101, Ap
742	3	12.5	17	6	US-10-834-397-204	Sequence 204, App	815	19	7	US-11-033-039-1116	Sequence 1116, Ap
743	3	12.5	17	6	US-10-834-397-205	Sequence 205, App	816	19	7	US-11-033-039-1425	Sequence 1425, Ap
744	3	12.5	17	6	US-10-834-397-206	Sequence 206, App	817	20	6	US-10-939-890-150	Sequence 150, App
745	3	12.5	17	6	US-10-834-397-212	Sequence 212, App	818	20	6	US-10-623-155-250	Sequence 250, App
746	3	12.5	17	6	US-10-834-397-213	Sequence 213, App	819	20	6	US-10-623-155-397	Sequence 397, App
747	3	12.5	17	6	US-10-834-397-214	Sequence 214, App	820	20	6	US-10-623-155-398	Sequence 398, App
748	3	12.5	17	6	US-10-834-397-217	Sequence 217, App	821	20	6	US-10-623-155-416	Sequence 416, App
749	3	12.5	17	6	US-10-834-397-218	Sequence 218, App	822	20	6	US-10-623-155-417	Sequence 417, App
750	3	12.5	17	6	US-10-834-397-221	Sequence 221, App	823	20	6	US-10-623-155-460	Sequence 460, App
751	3	12.5	17	6	US-10-834-397-246	Sequence 246, App	824	20	6	US-10-623-155-505	Sequence 505, App
752	3	12.5	17	6	US-10-834-397-254	Sequence 254, App	825	20	6	US-10-623-155-506	Sequence 506, App
753	3	12.5	17	6	US-10-834-397-258	Sequence 258, App	826	20	6	US-10-623-155-537	Sequence 527, App
754	3	12.5	17	6	US-10-834-397-259	Sequence 259, App	827	20	6	US-10-623-155-528	Sequence 528, App
755	3	12.5	17	7	US-11-033-365-169	Sequence 169, App	828	20	6		

829	3	12.5	20	6	US-10-623-155-529	Sequence 529, App	902	3	12.5	23	7	US-11-127-622-5	Sequence 5, Appli
830	3	12.5	20	6	US-10-623-155-544	Sequence 544, App	903	3	12.5	23	7	US-11-127-877-562	Sequence 562, App
831	3	12.5	20	6	US-10-485-788A-552	Sequence 552, App	904	3	12.5	23	7	US-11-007-282-4	Sequence 4, Appli
832	3	12.5	20	6	US-10-485-788A-573	Sequence 573, App	905	3	12.5	24	6	US-10-986-501-237	Sequence 237, App
833	3	12.5	20	6	US-10-485-788A-579	Sequence 579, App	906	3	12.5	24	6	US-10-467-657-8757	Sequence 8757, Ap
834	3	12.5	20	6	US-10-485-788A-588	Sequence 588, App	907	3	12.5	24	6	US-10-928-446A-148	Sequence 148, App
835	3	12.5	20	6	US-10-485-788A-601	Sequence 601, App	908	3	12.5	24	6	US-11-119-404-4	Sequence 4, Appli
836	3	12.5	20	6	US-11-022-562-138	Sequence 138, App	909	3	12.5	25	6	US-10-632-150-83	Sequence 83, Appl
837	3	12.5	20	7	US-11-022-562-139	Sequence 139, App	910	3	12.5	25	6	US-10-723-207-75	Sequence 75, Appl
838	3	12.5	20	7	US-11-022-562-159	Sequence 159, App	911	3	12.5	25	6	US-10-928-446A-139	Sequence 139, App
839	3	12.5	20	7	US-11-022-562-198	Sequence 198, App	912	3	12.5	25	7	US-11-073-457-83	Sequence 83, Appl
840	3	12.5	20	7	US-11-022-562-302	Sequence 302, App	913	3	12.5	25	7	US-11-083-624-34	Sequence 34, Appl
841	3	12.5	20	7	US-11-022-562-303	Sequence 303, App	914	3	12.5	25	7	US-11-073-460-83	Sequence 83, Appl
842	3	12.5	20	7	US-11-022-562-304	Sequence 304, App	915	2	8.3	3	6	US-10-431-638-11	Sequence 11, Appl
843	3	12.5	20	7	US-11-022-562-305	Sequence 305, App	916	2	8.3	3	6	US-10-506-223-9	Sequence 9, Appli
844	3	12.5	20	7	US-11-187-989-4	Sequence 4, Appli	917	2	8.3	3	6	US-10-506-223-10	Sequence 10, Appl
845	3	12.5	20	7	US-11-058-735-45	Sequence 45, Appl	918	2	8.3	3	6	US-10-506-223-13	Sequence 13, Appl
846	3	12.5	20	7	US-11-094-142-26	Sequence 26, Appl	919	2	8.3	3	6	US-11-053-168A-4	Sequence 4, Appli
847	3	12.5	20	7	US-11-094-142-27	Sequence 27, Appl	920	2	8.3	3	6	US-10-503-575-62	Sequence 62, Appl
848	3	12.5	20	7	US-11-094-142-32	Sequence 32, Appl	921	2	8.3	4	6	US-10-467-657-1356	Sequence 1356, Ap
849	3	12.5	20	7	US-11-094-142-35	Sequence 35, Appl	922	2	8.3	4	6	US-10-467-657-7388	Sequence 7388, Ap
850	3	12.5	20	7	US-11-127-601-32	Sequence 32, Appl	923	2	8.3	4	6	US-10-467-657-7512	Sequence 7512, Ap
851	3	12.5	20	7	US-11-127-601-35	Sequence 35, Appl	924	2	8.3	4	6	US-10-467-657-8723	Sequence 8723, Ap
852	3	12.5	20	7	US-11-127-601-36	Sequence 36, Appl	925	2	8.3	4	6	US-10-467-657-8894	Sequence 8894, Ap
853	3	12.5	20	7	US-11-127-601-39	Sequence 39, Appl	926	2	8.3	4	6	US-10-467-657-9125	Sequence 9125, Ap
854	3	12.5	20	7	US-11-127-601-40	Sequence 40, Appl	927	2	8.3	4	6	US-10-467-657-9134	Sequence 9134, Ap
855	3	12.5	20	7	US-11-127-601-42	Sequence 42, Appl	928	2	8.3	4	6	US-10-492-170C-48	Sequence 48, Appl
856	3	12.5	20	7	US-11-127-601-43	Sequence 43, Appl	929	2	8.3	4	6	US-10-492-170C-49	Sequence 49, Appl
857	3	12.5	20	7	US-11-127-601-44	Sequence 44, Appl	930	2	8.3	4	6	US-10-492-170C-50	Sequence 50, Appl
858	3	12.5	20	7	US-11-127-601-45	Sequence 45, Appl	931	2	8.3	4	6	US-10-661-478-16	Sequence 16, Appl
859	3	12.5	20	7	US-11-127-601-48	Sequence 48, Appl	932	2	8.3	4	6	US-10-533-355-16	Sequence 16, Appl
860	3	12.5	20	7	US-11-127-601-50	Sequence 50, Appl	933	2	8.3	4	6	US-10-485-788A-36	Sequence 36, Appl
861	3	12.5	20	7	US-11-127-601-51	Sequence 51, Appl	934	2	8.3	4	6	US-10-485-788A-41	Sequence 41, Appl
862	3	12.5	20	7	US-11-127-601-52	Sequence 52, Appl	935	2	8.3	4	6	US-10-485-788A-66	Sequence 66, Appl
863	3	12.5	20	7	US-11-104-741-5	Sequence 5, Appli	936	2	8.3	4	6	US-10-485-788A-91	Sequence 91, Appl
864	3	12.5	20	7	US-11-107-023-12	Sequence 12, Appl	937	2	8.3	4	6	US-10-485-788A-106	Sequence 106, App
865	3	12.5	20	7	US-11-106-415-104	Sequence 104, App	938	2	8.3	4	6	US-10-485-788A-116	Sequence 116, App
866	3	12.5	20	7	US-11-033-039-815	Sequence 815, App	939	2	8.3	4	6	US-10-485-788A-121	Sequence 121, App
867	3	12.5	20	7	US-11-033-039-1424	Sequence 1424, Ap	940	2	8.3	4	6	US-10-485-788A-146	Sequence 146, App
868	3	12.5	20	7	US-11-041-893-49	Sequence 49, Appl	941	2	8.3	4	6	US-10-485-788A-151	Sequence 151, App
869	3	12.5	20	7	US-11-041-893-51	Sequence 51, Appl	942	2	8.3	4	6	US-10-485-788A-161	Sequence 161, App
870	3	12.5	20	7	US-11-041-893-61	Sequence 61, Appl	943	2	8.3	4	6	US-10-485-788A-181	Sequence 181, App
871	3	12.5	20	7	US-11-144-630-36	Sequence 36, Appl	944	2	8.3	4	6	US-10-485-788A-186	Sequence 186, App
872	3	12.5	21	6	US-10-939-890-524	Sequence 524, App	945	2	8.3	4	6	US-10-485-788A-191	Sequence 191, App
873	3	12.5	21	6	US-10-939-890-568	Sequence 568, App	946	2	8.3	4	6	US-10-485-788A-196	Sequence 196, App
874	3	12.5	21	6	US-10-939-890-573	Sequence 573, App	947	2	8.3	4	6	US-10-485-788A-201	Sequence 201, App
875	3	12.5	21	6	US-10-939-890-574	Sequence 574, App	948	2	8.3	4	6	US-10-485-788A-216	Sequence 216, App
876	3	12.5	21	6	US-10-939-890-595	Sequence 595, App	949	2	8.3	4	6	US-10-485-788A-301	Sequence 301, App
877	3	12.5	21	6	US-10-939-890-599	Sequence 599, App	950	2	8.3	4	6	US-10-485-788A-306	Sequence 306, App
878	3	12.5	21	6	US-10-467-657-5326	Sequence 5326, Ap	951	2	8.3	4	6	US-10-485-788A-326	Sequence 326, App
879	3	12.5	21	6	US-10-467-657-8648	Sequence 8648, Ap	952	2	8.3	4	6	US-10-485-788A-446	Sequence 446, App
880	3	12.5	21	6	US-10-467-657-8920	Sequence 8920, Ap	953	2	8.3	4	6	US-10-485-788A-451	Sequence 451, App
881	3	12.5	21	6	US-10-475-204-7	Sequence 7, Appli	954	2	8.3	4	6	US-10-485-788A-466	Sequence 466, App
882	3	12.5	21	7	US-11-054-515-2363	Sequence 2363, Ap	955	2	8.3	4	6	US-10-485-788A-486	Sequence 486, App
883	3	12.5	21	7	US-11-187-989-2	Sequence 2, Appli	956	2	8.3	4	6	US-10-485-788A-529	Sequence 529, App
884	3	12.5	21	7	US-11-069-642-144	Sequence 144, App	957	2	8.3	4	6	US-10-500-755A-99	Sequence 99, Appl
885	3	12.5	21	7	US-11-192-450-16	Sequence 16, Appl	958	2	8.3	4	6	US-10-793-388-6	Sequence 6, Appli
886	3	12.5	21	7	US-11-033-039-1212	Sequence 1212, Ap	959	2	8.3	4	6	US-10-859-643-702	Sequence 702, App
887	3	12.5	21	7	US-11-033-039-1423	Sequence 1423, Ap	960	2	8.3	4	6	US-10-859-643-706	Sequence 706, App
888	3	12.5	21	7	US-11-041-893-205	Sequence 205, App	961	2	8.3	4	6	US-10-859-643-710	Sequence 710, App
889	3	12.5	21	7	US-11-147-111-15	Sequence 15, Appl	962	2	8.3	4	6	US-10-859-643-716	Sequence 716, App
890	3	12.5	22	6	US-10-353-783-75	Sequence 75, Appl	963	2	8.3	4	6	US-10-859-643-717	Sequence 717, App
891	3	12.5	22	6	US-10-353-783-76	Sequence 76, Appl	964	2	8.3	4	6	US-10-859-643-721	Sequence 721, App
892	3	12.5	22	6	US-10-509-787A-149	Sequence 149, App	965	2	8.3	4	6	US-10-859-643-723	Sequence 723, App
893	3	12.5	22	6	US-10-997-074-50	Sequence 50, Appl	966	2	8.3	4	6	US-10-859-643-724	Sequence 724, App
894	3	12.5	22	7	US-11-108-185-45	Sequence 45, Appl	967	2	8.3	4	6	US-10-506-223-1	Sequence 1, Appli
895	3	12.5	22	7	US-11-148-149-9	Sequence 9, Appli	968	2	8.3	4	6	US-10-506-223-2	Sequence 2, Appli
896	3	12.5	22	7	US-11-016-542-12	Sequence 12, Appl	969	2	8.3	4	6		
897	3	12.5	23	6	US-10-623-155-543	Sequence 543, App	970	2	8.3	4	6		
898	3	12.5	23	7	US-11-060-005-15	Sequence 15, Appl	971	2	8.3	4	6		
899	3	12.5	23	7	US-11-118-031-1	Sequence 1, Appli	972	2	8.3	4	6		
900	3	12.5	23	7	US-11-016-542-15	Sequence 15, App	973	2	8.3	4	6		
901	3	12.5	23	7	US-11-016-542-19	Sequence 19, App	974	2	8.3	4	6		

```
975      2      8.3      4      6 US-10-506-223-5
976      2      8.3      4      7 US-11-188-281-7
977      2      8.3      4      7 US-11-188-281-8
978      2      8.3      4      7 US-11-032-794-58
979      2      8.3      4      7 US-11-075-185-31
980      2      8.3      4      7 US-11-097-864-702
981      2      8.3      4      7 US-11-097-864-706
982      2      8.3      4      7 US-11-097-864-710
983      2      8.3      4      7 US-11-097-864-716
984      2      8.3      4      7 US-11-097-864-717
985      2      8.3      4      7 US-11-097-864-721
986      2      8.3      4      7 US-11-097-864-723
987      2      8.3      4      7 US-11-097-864-724
988      2      8.3      4      7 US-11-097-912-702
989      2      8.3      4      7 US-11-097-912-706
990      2      8.3      4      7 US-11-097-912-710
991      2      8.3      4      7 US-11-097-912-716
992      2      8.3      4      7 US-11-097-912-717
993      2      8.3      4      7 US-11-097-912-721
994      2      8.3      4      7 US-11-097-912-723
995      2      8.3      4      7 US-11-097-912-724
996      2      8.3      4      7 US-11-119-098-62
997      2      8.3      4      7 US-11-127-629-23
998      2      8.3      4      7 US-11-166-099-19
999      2      8.3      4      7 US-11-191-574-4
1000     2      8.3      4      7 US-11-019-027-11
```

ALIGNMENTS

```
RESULT 1
US-11-045-024-616
; Sequence 616, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

Sequence 5, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 58, Appl
Sequence 31, Appl
Sequence 702, App
Sequence 706, App
Sequence 710, App
Sequence 716, App
Sequence 717, App
Sequence 721, App
Sequence 723, App
Sequence 724, App
Sequence 702, App
Sequence 706, App
Sequence 710, App
Sequence 716, App
Sequence 717, App
Sequence 721, App
Sequence 723, App
Sequence 724, App
Sequence 702, App
Sequence 706, App
Sequence 710, App
Sequence 716, App
Sequence 717, App
Sequence 721, App
Sequence 723, App
Sequence 724, App
Sequence 62, Appl
Sequence 23, Appl
Sequence 19, Appl
Sequence 4, Appli
Sequence 11, Appli
```

```
US-11-045-024-616
Query Match      20.8%; Score 5; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 NNNNS 20
Db      3 NNNNS 7

RESULT 2
US-11-045-024-770
; Sequence 770, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-770
Query Match      20.8%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 NNNNS 20
Db      4 NNNNS 8

RESULT 3
US-10-467-657-8871
; Sequence 8871, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8871
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8871

Query Match 20.8%; Score 5; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TKSIF 11
|||
Db 18 TKSIF 22

RESULT 4
US-10-615-668-23
; Sequence 23, Application US/10615668
; Publication No. US20050276819A1
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; APPLICANT: Bugnoli, Massimo
; APPLICANT: Telford, John
; APPLICANT: Macchia, Giovanni
; APPLICANT: Rappuoli, Rino
; TITLE OF INVENTION: Helicobacter Pylori CAI Antigen Polynucleotides
; FILE REFERENCE: CHIR0337
; CURRENT APPLICATION NUMBER: US/10/615,668
; CURRENT FILING DATE: 2003-07-08
; PRIOR FILING DATE: 08/471,491
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/256,848
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: 09/410,835
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-615-668-23

Query Match 16.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 NNNN 19
|||
Db 1 NNNN 4

RESULT 5
US-11-096-706-96
; Sequence 96, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535

; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-96

Query Match 16.7%; Score 4; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 NNNN 20
|||
Db 1 NNNN 4

RESULT 6
US-11-041-893-31
; Sequence 31, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahairas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-31

Query Match 16.7%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 SSFY 23
|||
Db 7 SSFY 10

RESULT 7
US-10-914-842A-12
; Sequence 12, Application US/10914842A
; Publication No. US20050260730A1
; GENERAL INFORMATION:
; APPLICANT: FISCHER, PETER MARTIN
; FILE REFERENCE: CCI-032
; CURRENT APPLICATION NUMBER: US/10/914,842A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: UK 0324465.4
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-914-842A-12

Query Match 16.7%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFD 4
|||
Db 8 LRFD 11

RESULT 8
US-11-069-834-14
; Sequence 14, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS B.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Variable amino acid
US-11-069-834-14

Query Match 16.7%; Score 4; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNN 19
|||
Db 9 NNNN 12

RESULT 9
US-11-069-834-16
; Sequence 16, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS B.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834

; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-069-834-16

Query Match 16.7%; Score 4; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNN 19
|||
Db 2 NNNN 5

RESULT 10
US-11-069-834-18
; Sequence 18, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS B.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-069-834-18

Query Match 16.7%; Score 4; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNN 18
|||
Db 8 TNNN 11

RESULT 11
US-11-069-834-34
; Sequence 34, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS B.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01

```
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 34
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-069-834-34

Query Match      16.7%; Score 4; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 NNNN 19
Db      3 NNNN 6

RESULT 12
US-10-467-657-8838
; Sequence 8838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 8838
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8838

Query Match      16.7%; Score 4; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 IPEQ 13
Db      1 IPEQ 4

RESULT 13
US-11-045-024-13116
; Sequence 13116, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
```

```
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13116
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13116
```

```
Query Match      16.7%; Score 4; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 RFDS 5
Db      3 RFDS 6
```

```
RESULT 14
US-11-033-039-1242
; Sequence 1242, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1242
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1242
```

```
Query Match      16.7%; Score 4; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 20 SSFY 23
 Db 8 SSFY 11

RESULT 15
 US-11-033-039-1308
 ; Sequence 1308, Application US/11033039
 ; Publication No. US20060002947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HUMPHREYS, ROBERT
 ; APPLICANT: XU, MINZHEN
 ; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
 ; FILE REFERENCE: REH-2017US01
 ; CURRENT APPLICATION NUMBER: US/11/033,039
 ; PRIOR FILING DATE: 2005-01-11
 ; PRIOR APPLICATION NUMBER: 10/245,871
 ; PRIOR FILING DATE: 2002-09-17
 ; PRIOR APPLICATION NUMBER: 10/197,000
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: 09/396,813
 ; PRIOR FILING DATE: 1999-09-14
 ; NUMBER OF SEQ ID NOS: 1452
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1308
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: hybrid peptide
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (5)..(5)
 ; OTHER INFORMATION: Ava
 US-11-033-039-1308

Query Match 16.7%; Score 4; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFY 23
 Db 8 SSFY 11

Search completed: January 20, 2006, 17:58:10
 Job time : 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:51:34 ; Search time 16 Seconds
(without alignments)
144.325 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24
Sequence: 1 LRFDSQTKSIFRQETNNNSPYT 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4989

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.8	20	I59073	MHC class II histo
2	4	16.7	12	A44874	proboscipedia - fr
3	4	16.7	17	I76673	hypothetical COII/
4	4	16.7	18	A40256	interleukin-7 rece
5	4	16.7	19	PC1323	endopeptidase Clp
6	4	16.7	20	I79432	MHC class II histo
7	4	16.7	20	S67990	neurotoxin-associ
8	4	16.7	22	B40256	interleukin-7 rece
9	3	12.5	4	D41654	hypothetical prote
10	3	12.5	5	PT0644	T-cell receptor be
11	3	12.5	7	B39127	phosphotransferase
12	3	12.5	7	A59489	protein kinase C i
13	3	12.5	8	PH1407	Ig heavy chain v r
14	3	12.5	8	S59622	metallothionein is
15	3	12.5	8	JS0316	leucokinin VI - Ma
16	3	12.5	8	B27867	homeotic protein U
17	3	12.5	8	A59028	MHC class I histoc
18	3	12.5	8	S43972	tumor-associated a
19	3	12.5	8	S43971	tumor-associated a
20	3	12.5	9	A60427	macrophage cytotox
21	3	12.5	9	A61386	macrophage inhibit
22	3	12.5	9	PD0443	3-oxoacid CoA-tran
23	3	12.5	10	PU0037	alpha-peptide/algi
24	3	12.5	10	S70721	heat shock protein
25	3	12.5	10	PH0916	T-cell receptor be
26	3	12.5	10	PH0923	T-cell receptor be
27	3	12.5	10	A43977	FMRamide-like pro
28	3	12.5	10	A56633	neomycinopressin -
29	3	12.5	10	B61033	ranatachykinin B -

30	3	12.5	10	A32543	cardioexcitatory n
31	3	12.5	11	B60769	Ig H2 chain - Paci
32	3	12.5	11	I60434	68kDa neurofilamen
33	3	12.5	11	PH0904	T-cell receptor be
34	3	12.5	12	PH1675	Ig heavy chain v r
35	3	12.5	12	S26554	T-cell receptor be
36	3	12.5	12	S26559	T-cell receptor be
37	3	12.5	12	A40763	sucrose-6-phosphat
38	3	12.5	12	S68402	NAD(+)-glycohydrol
39	3	12.5	12	PH0771	T-cell receptor be
40	3	12.5	12	PH1467	T-cell receptor be
41	3	12.5	12	PH1462	T-cell receptor be
42	3	12.5	12	PH1469	T-cell receptor be
43	3	12.5	12	PH1457	T-cell receptor be
44	3	12.5	12	PH1468	T-cell receptor be
45	3	12.5	12	S29479	hypothetical prote
46	3	12.5	12	PA0030	protein QM300025 -
47	3	12.5	12	A56878	light yellow cell
48	3	12.5	13	A44818	extracellular lipa
49	3	12.5	13	PH1676	Ig heavy chain v r
50	3	12.5	13	S09395	hypothetical prote
51	3	12.5	13	S70441	pancreatic elastas
52	3	12.5	13	PH0138	T-cell receptor be
53	3	12.5	13	I54984	aeg-46.5 protein -
54	3	12.5	13	S60046	early nodulin 40 -
55	3	12.5	13	C61576	ribosomal protein
56	3	12.5	14	PH1677	Ig heavy chain v r
57	3	12.5	14	PH1705	Ig heavy chain v r
58	3	12.5	14	PH0077	proteochondroitin c
59	3	12.5	14	PH0753	T-cell receptor be
60	3	12.5	14	I54945	gene C protein - E
61	3	12.5	14	S14336	mastoparan B - hor
62	3	12.5	14	B56884	Pax-QNR, long form
63	3	12.5	14	PC7079	unidentified 27.2K
64	3	12.5	14	B83836	hypothetical prote
65	3	12.5	14	A42473	ermk leader peptid
66	3	12.5	15	JF0101	fibrinogen alpha c
67	3	12.5	15	PS0452	32K protein 3306 -
68	3	12.5	15	PA0052	protein QF200015 -
69	3	12.5	15	D28587	T-cell receptor be
70	3	12.5	15	PH0764	T-cell receptor be
71	3	12.5	15	PH0629	integration host f
72	3	12.5	15	PA0008	lectin B2 - Psopho
73	3	12.5	15	PA0062	fumarate hydratase
74	3	12.5	15	PA0054	protein QF200017 -
75	3	12.5	15	A32921	beaded-chain filam
76	3	12.5	15	A61522	7.5K surfactant-as
77	3	12.5	16	F44908	chitinase (EC 3.2.
78	3	12.5	16	B35491	retinol-binding pr
79	3	12.5	16	PH0749	T-cell receptor be
80	3	12.5	16	S33589	beta-crystallin A4
81	3	12.5	16	PH1476	T-cell receptor be
82	3	12.5	16	PH1474	T-cell receptor be
83	3	12.5	16	T09741	photosystem I chai
84	3	12.5	16	S22040	cob protein - comm
85	3	12.5	16	S54271	GATA-2 protein - A
86	3	12.5	16	S65430	pyrogallol hydroxy
87	3	12.5	16	S15778	insulin chain B -
88	3	12.5	17	S32587	L-ascorbate peroxi
89	3	12.5	17	C37396	pollen allergen Fe
90	3	12.5	17	PH1822	T cell receptor al
91	3	12.5	17	PH0769	T-cell receptor be
92	3	12.5	17	I78870	gene R81 protein -
93	3	12.5	17	A34704	protein-tyrosine k
94	3	12.5	17	A29834	trp leader peptide
95	3	12.5	18	C40433	Nada protein - Cya
96	3	12.5	18	A56871	retinol-binding pr
97	3	12.5	18	S09731	photosystem I prot
98	3	12.5	18	S10452	hypothetical prote
99	3	12.5	18	S33125	cysteine-rich secr
100	3	12.5	18	A32917	protein phosphatas
101	3	12.5	18	S71592	serine proteinase
102	3	12.5	18	PL0025	T-cell surface gly

103	3	12.5	18	2	S48862	murine cyclin H -	176	3	12.5	23	2	PH1695	Ig heavy chain V r
104	3	12.5	18	2	T13132	protein GP45.1 - p	177	3	12.5	23	2	PH1726	Ig heavy chain V r
105	3	12.5	18	2	S48863	cyclin C - mouse (178	3	12.5	23	2	PH1708	Ig heavy chain V r
106	3	12.5	19	1	LFSAP9	ermC leader peptid	179	3	12.5	23	2	PH1724	Ig heavy chain V r
107	3	12.5	19	2	A92058	pepsin-like protei	180	3	12.5	23	2	PH1693	Ig heavy chain V r
108	3	12.5	19	2	C32735	thyroglobulin - pi	181	3	12.5	23	2	PH1728	Ig heavy chain V r
109	3	12.5	19	2	B32735	thyroglobulin - sh	182	3	12.5	23	2	PH1723	Ig heavy chain V r
110	3	12.5	19	2	B38837	T-cell receptor be	183	3	12.5	23	2	PH1681	Ig heavy chain V r
111	3	12.5	19	2	S01203	patatin (clone LFO	184	3	12.5	23	2	PH1727	Ig heavy chain V r
112	3	12.5	19	2	B26930	ermG leader peptid	185	3	12.5	23	2	PH1722	Ig heavy chain V r
113	3	12.5	19	2	T50329	wd-repeat protein	186	3	12.5	23	2	PH1682	Ig heavy chain V r
114	3	12.5	19	2	PC1315	large granule L2 c	187	3	12.5	23	2	PH1725	Ig heavy chain V r
115	3	12.5	19	2	S57515	T cell receptor be	188	3	12.5	23	2	PH1729	Ig heavy chain V r
116	3	12.5	19	2	S57516	T cell receptor be	189	3	12.5	23	2	PH1707	Ig heavy chain V r
117	3	12.5	19	2	A60459	aminopeptidase, 30	190	3	12.5	23	2	PH1691	Ig heavy chain V r
118	3	12.5	19	2	S68393	H+-transporting tw	191	3	12.5	23	2	I56028	MHC class II prote
119	3	12.5	19	2	PQ0548	capsid protein vp2	192	3	12.5	23	2	I77910	beta 3-adrenergic
120	3	12.5	19	2	S63476	dihydrolipoamide d	193	3	12.5	23	2	I54773	neural cell adhesi
121	3	12.5	19	2	I33327	pre-T/NK cell-asso	194	3	12.5	23	2	S00921	patatin (clone LFO
122	3	12.5	20	2	FN0115	insulin-like growt	195	3	12.5	23	2	S74178	4-hydroxyphenylpyr
123	3	12.5	20	2	A54083	p190/210, fatty ac	196	3	12.5	23	2	S13298	benzaldehyde dehyd
124	3	12.5	20	2	PQ0751	self-incompatibili	197	3	12.5	23	2	A56357	tyrosine kinase au
125	3	12.5	20	2	A33160	H+-transporting tw	198	3	12.5	23	2	D64707	hypothetical prote
126	3	12.5	20	2	C49164	chromogranin-B - r	199	3	12.5	23	2	B37843	vrg 18 protein - B
127	3	12.5	20	2	E38419	collagen alpha 5(I	200	3	12.5	23	2	G69812	hypothetical prote
128	3	12.5	20	2	H49034	nuclear antigen BB	201	3	12.5	23	2	S77982	cytochrome-c oxida
129	3	12.5	20	2	D37396	pollen allergen Fe	202	3	12.5	24	2	PH1698	Ig heavy chain V r
130	3	12.5	20	2	A38600	trypsin inhibitor	203	3	12.5	24	2	PH1713	Ig heavy chain V r
131	3	12.5	20	2	PH1326	Ig heavy chain DJ	204	3	12.5	24	2	PH1684	Ig heavy chain V r
132	3	12.5	20	2	A41437	alpha-1-antitrypsi	205	3	12.5	24	2	PH1685	Ig heavy chain V r
133	3	12.5	20	2	C44920	2-halobenzoate 1,2	206	3	12.5	24	2	PH1711	Ig heavy chain V r
134	3	12.5	20	2	FL0039	outer membrane pro	207	3	12.5	24	2	PH1710	Ig heavy chain V r
135	3	12.5	20	2	T48881	leader peptide [im	208	3	12.5	24	2	PH1732	Ig heavy chain V r
136	3	12.5	20	2	S29636	jacalin beta-I cha	209	3	12.5	24	2	PH1712	Ig heavy chain V r
137	3	12.5	20	2	S50743	proteinase inhibit	210	3	12.5	24	2	PH1697	Ig heavy chain V r
138	3	12.5	20	2	S65605	dimeric protein (B	211	3	12.5	24	2	PH1683	Ig heavy chain V r
139	3	12.5	20	2	S77992	cytochrome-c oxida	212	3	12.5	24	2	E39690	neural cell adhesi
140	3	12.5	20	2	JCS589	ribonuclease RCL2	213	3	12.5	24	2	S70329	omega 1-40 secalin
141	3	12.5	20	2	S71593	serine proteinase	214	3	12.5	24	2	S65714	lectin GNL alpha c
142	3	12.5	20	2	D56046	urinary tract ston	215	3	12.5	24	2	D53288	major pollen aller
143	3	12.5	20	2	A61506	alpha-1-antitrypsi	216	3	12.5	24	2	PC2001	major allergen - B
144	3	12.5	20	2	A60897	class I histocompa	217	3	12.5	24	2	S47281	hypothetical prote
145	3	12.5	20	2	I58192	glial fibrillary a	218	3	12.5	24	2	T46628	hypothetical prote
146	3	12.5	20	2	B46174	RNA-binding protei	219	3	12.5	24	2	C47689	flagellar core pro
147	3	12.5	21	2	I40066	shikimate 5-dehydr	220	3	12.5	24	2	G46615	hypothetical prote
148	3	12.5	21	2	PC2214	fibrinogenolytic p	221	3	12.5	24	2	D81853	probable transpos
149	3	12.5	21	2	I49414	gene CTLA-1 protei	222	3	12.5	24	2	PN0653	alkaline trypsin-1
150	3	12.5	21	2	D38837	T-cell receptor be	223	3	12.5	24	2	S10618	superoxide dismuta
151	3	12.5	21	2	A38837	T-cell receptor be	224	3	12.5	24	2	I73619	endothelial growth
152	3	12.5	21	2	C38837	T-cell receptor be	225	3	12.5	24	2	C85846	unknown protein en
153	3	12.5	21	2	PH1731	Ig heavy chain V r	226	3	12.5	24	2	G85602	hypothetical prote
154	3	12.5	21	2	PH1730	Ig heavy chain V r	227	3	12.5	25	1	ZJBPQ4	gene J protein - p
155	3	12.5	21	2	PH1688	Ig heavy chain V r	228	3	12.5	25	2	I51565	protein-tyrosine k
156	3	12.5	21	2	S49040	Ig heavy chain V r	229	3	12.5	25	2	S21204	H+-transporting tw
157	3	12.5	21	2	S39455	dps-protein 19K -	230	3	12.5	25	2	D41575	bovinin-like pept
158	3	12.5	21	2	S35676	34K ribonucleoprot	231	3	12.5	25	2	PH1734	Ig heavy chain V r
159	3	12.5	21	2	B33600	glutamate-ammonia	232	3	12.5	25	2	PH1716	Ig heavy chain V r
160	3	12.5	22	2	PH1680	Ig heavy chain V r	233	3	12.5	25	2	PH1733	Ig heavy chain V r
161	3	12.5	22	2	PH1706	Ig heavy chain V r	234	3	12.5	25	2	F49533	T-cell receptor be
162	3	12.5	22	2	PH1679	Ig heavy chain V r	235	3	12.5	25	2	PH1700	Ig heavy chain V r
163	3	12.5	22	2	PH1678	Ig heavy chain V r	236	3	12.5	25	2	PH1717	Ig heavy chain V r
164	3	12.5	22	2	PH1714	Ig heavy chain V r	237	3	12.5	25	2	PH1701	Ig heavy chain V r
165	3	12.5	22	2	PH1721	Ig heavy chain V r	238	3	12.5	25	2	PH1686	Ig heavy chain V r
166	3	12.5	22	2	B41833	40K iron-repressed	239	3	12.5	25	2	PH1715	Ig heavy chain V r
167	3	12.5	22	2	A41833	40K iron-repressed	240	3	12.5	25	2	A40534	ryanodine receptor
168	3	12.5	22	2	S17303	tegumental Glycopr	241	3	12.5	25	2	A60412	xenopsin-related p
169	3	12.5	22	2	B60701	31K antigen - Camp	242	3	12.5	25	2	S28993	antifungal protein
170	3	12.5	22	2	S65370	tRNA-guanine trans	243	3	12.5	25	2	D138002	calcium channel be
171	3	12.5	22	2	H49410	t-complex polypept	244	3	12.5	25	2	D47689	flagellar core pro
172	3	12.5	22	2	I40064	shikimate 5-dehydr	245	3	12.5	25	2	B47689	flagellar core pro
173	3	12.5	22	2	G83924	hypothetical prote	246	3	12.5	25	2	S78343	hypothetical prote
174	3	12.5	23	2	PH1689	Ig heavy chain V r	247	3	12.5	25	2	S30361	1,2-alpha-D-mannos
175	3	12.5	23	2	PH1694	Ig heavy chain V r	248	3	12.5	25	2	A61457	alpha-glucosidase

395	2	8.3	8	2	S78036	ribosomal protein	468	2	8.3	9	2	D44787	calliFMRamide 13
396	2	8.3	8	2	B33099	158K exoantigen -	469	2	8.3	9	2	B41978	calliFMRamide 2 -
397	2	8.3	8	2	A42057	fibroblast growth	470	2	8.3	9	2	C41978	calliFMRamide 3 -
398	2	8.3	8	2	PN0043	phosphatidylethano	471	2	8.3	9	2	D41978	calliFMRamide 4 -
399	2	8.3	8	2	PT0595	T-cell receptor be	472	2	8.3	9	2	B41978	calliFMRamide 5 -
400	2	8.3	8	2	PT0627	T-cell receptor be	473	2	8.3	9	2	B41978	calliFMRamide 6 -
401	2	8.3	8	2	PT0530	T-cell receptor be	474	2	8.3	9	2	G41978	calliFMRamide 7 -
402	2	8.3	8	2	PT0522	T-cell receptor be	475	2	8.3	9	2	JN0027	[Phe-6]-mosact - s
403	2	8.3	8	2	PT0509	T-cell receptor be	476	2	8.3	9	2	B20569	serum amyloid P-co
404	2	8.3	8	2	PT0639	T-cell receptor be	477	2	8.3	9	2	A45199	L-hyosphorin - Ja
405	2	8.3	8	2	PT0613	T-cell receptor be	478	2	8.3	9	2	S77984	cytochrome-c oxida
406	2	8.3	8	2	PT0547	T-cell receptor be	479	2	8.3	9	2	JQ0914	MHC class I histoc
407	2	8.3	8	2	PT0716	T-cell receptor be	480	2	8.3	9	2	I46016	cyokeratin 4 - bo
408	2	8.3	8	2	A38887	T-cell receptor ga	481	2	8.3	9	2	A28924	fructose-bisphosph
409	2	8.3	8	2	PH0934	T-cell receptor be	482	2	8.3	9	2	PC7076	spectrin alpha cha
410	2	8.3	8	2	PC1002	leucine-tRNA ligas	483	2	8.3	9	2	PC7078	unidentified 48.7K
411	2	8.3	8	2	S53008	citrate synthase -	484	2	8.3	9	2	G85802	hypothetical prote
412	2	8.3	8	2	S37141	rpSA protein - Erw	485	2	8.3	9	2	S30494	cat gene leader pe
413	2	8.3	8	2	S21273	cellulase (EC 3.2.	486	2	8.3	9	2	B60246	ornitho-kinin - ch
414	2	8.3	8	2	A37521	R-phycoerythrin ga	487	2	8.3	9	2	JN0026	sperm-activating p
415	2	8.3	8	2	S11078	glucose-6-phosphat	488	2	8.3	9	2	B24362	chloramphenicol O-
416	2	8.3	8	2	C61512	variant surface gl	489	2	8.3	9	4	S15595	orf 2 rara 5'-regi
417	2	8.3	8	2	D61512	variant surface gl	490	2	8.3	9	4	I73804	hypothetical B2 pr
418	2	8.3	8	2	JS0315	leucokinin V - Mad	491	2	8.3	10	1	RHPGG	gonadoliberin - pi
419	2	8.3	8	2	JS0317	leucokinin VII - M	492	2	8.3	10	1	RHSHG	gonadoliberin - sh
420	2	8.3	8	2	JS0318	leucokinin VIII -	493	2	8.3	10	1	ECLQIM	tachykinin I - mig
421	2	8.3	8	2	A23967	leucoprotekinin - M	494	2	8.3	10	1	ECLQ3M	tachykinin III - m
422	2	8.3	8	2	H41978	calliFMRamide 8 -	495	2	8.3	10	1	GMROL2	leucoaulfakinin-II
423	2	8.3	8	2	D47393	neuropeptide calla	496	2	8.3	10	2	S28055	cytochrome b559 co
424	2	8.3	8	2	S71193	alcohol dehydrogen	497	2	8.3	10	2	S63478	dihyrolipoamide d
425	2	8.3	8	2	A44683	aspartate transami	498	2	8.3	10	2	S24190	tryptase (EC 3.4.2
426	2	8.3	8	2	A61467	penalbumin - Adeli	499	2	8.3	10	2	JC1367	thyroliberin poten
427	2	8.3	8	2	I48934	apolipoprotein A-I	500	2	8.3	10	2	A60410	beta-neoendorphin
428	2	8.3	8	2	I57018	gene Cfr protein	501	2	8.3	10	2	A31571	hypertrehalosemic/
429	2	8.3	8	2	S20162	leghemoglobin III	502	2	8.3	10	2	JN0024	neurokinin A - chi
430	2	8.3	8	2	B24749	neuropeptide B - b	503	2	8.3	10	2	A61337	caerulein - frog (
431	2	8.3	9	1	YFEG	thymic factor - pi	504	2	8.3	10	2	A47593	mercury resistance
432	2	8.3	9	2	S13889	phosphoenolpyruvat	505	2	8.3	10	2	S66458	ferredoxin - Rhizo
433	2	8.3	9	2	A60957	thymocyte growth p	506	2	8.3	10	2	S74176	gluconokinase (EC
434	2	8.3	9	2	A24244	adipokinetic hormo	507	2	8.3	10	2	C39191	hypothetical prote
435	2	8.3	9	2	S07205	litorin 2-Glu - Au	508	2	8.3	10	2	S42282	paraspasal crystal
436	2	8.3	9	2	A61357	phylocaerulein -	509	2	8.3	10	2	C39745	phosphomvelinase -
437	2	8.3	9	2	A60108	exotoxin A - Strep	510	2	8.3	10	2	S62288	polyferredoxin - M
438	2	8.3	9	2	A44873	caldesmon - rabbit	511	2	8.3	10	2	PA0050	protein QAI00052 -
439	2	8.3	9	2	E28854	fibrinopeptide B -	512	2	8.3	10	2	C38925	seed storage prote
440	2	8.3	9	2	F28854	fibrinopeptide B -	513	2	8.3	10	2	H28027	protein P11 - curl
441	2	8.3	9	2	D28854	fibrinopeptide B -	514	2	8.3	10	2	C39111	Ig heavy chain C r
442	2	8.3	9	2	D59503	translation elonga	515	2	8.3	10	2	PT0230	Ig heavy chain CDR
443	2	8.3	9	2	C35730	hutu protein - kle	516	2	8.3	10	2	PT0243	Ig heavy chain CDR
444	2	8.3	9	2	S70334	endosperm protein,	517	2	8.3	10	2	PT0251	Ig heavy chain CDR
445	2	8.3	9	2	B33098	231K exoantigen -	518	2	8.3	10	2	PT0291	Ig heavy chain CDR
446	2	8.3	9	2	PT0231	Ig heavy chain CDR	519	2	8.3	10	2	PT0309	Ig heavy chain CDR
447	2	8.3	9	2	PT0247	Ig heavy chain CDR	520	2	8.3	10	2	PT0322	Ig heavy chain CDR
448	2	8.3	9	2	PT0270	Ig heavy chain CDR	521	2	8.3	10	2	S23370	T-cell receptor al
449	2	8.3	9	2	PT0288	Ig heavy chain CDR	522	2	8.3	10	2	S23371	T-cell receptor al
450	2	8.3	9	2	PT0315	Ig heavy chain CDR	523	2	8.3	10	2	B49033	T-cell receptor ga
451	2	8.3	9	2	S65865	collagen alpha 2(V	524	2	8.3	10	2	B24736	inhibin beta-B cha
452	2	8.3	9	2	S65913	pyrimidine synthes	525	2	8.3	10	2	S10785	enamelin, 22K - bo
453	2	8.3	9	2	PT0670	T-cell receptor be	526	2	8.3	10	2	A37268	Ig heavy chain C r
454	2	8.3	9	2	PT0562	T-cell receptor be	527	2	8.3	10	2	PH0807	T-cell receptor al
455	2	8.3	9	2	G41946	T-cell receptor ga	528	2	8.3	10	2	PT0215	T-cell receptor be
456	2	8.3	9	2	PH0942	T-cell receptor be	529	2	8.3	10	2	C41946	T-cell receptor ga
457	2	8.3	9	2	PH0935	T-cell receptor be	530	2	8.3	10	2	B38887	T-cell receptor ga
458	2	8.3	9	2	PH0902	T-cell receptor be	531	2	8.3	10	2	S65385	cytochrome-c oxida
459	2	8.3	9	2	PH0917	T-cell receptor be	532	2	8.3	10	2	PH0060	lysosome-associate
460	2	8.3	9	2	PH0918	T-cell receptor be	533	2	8.3	10	2	PH0900	T-cell receptor be
461	2	8.3	9	2	PH0921	T-cell receptor be	534	2	8.3	10	2	PH0927	T-cell receptor be
462	2	8.3	9	2	JP0073	ribosomal protein	535	2	8.3	10	2	PH0944	T-cell receptor be
463	2	8.3	9	2	A39841	sucrose 3-glucosyl	536	2	8.3	10	2	PH0933	T-cell receptor be
464	2	8.3	9	2	D57444	neuropeptide Grb-A	537	2	8.3	10	2	PH0894	T-cell receptor be
465	2	8.3	9	2	A29477	diuretic neurocept	538	2	8.3	10	2	PH0946	T-cell receptor be
466	2	8.3	9	2	A41978	calliFMRamide 1 -	539	2	8.3	10	2	PH0925	T-cell receptor be
467	2	8.3	9	2	A44787	calliFMRamide 10	540	2	8.3	10	2	PH0926	T-cell receptor be

541	2	8.3	10	2	PH0895	T-cell receptor be	614	2	8.3	11	2	S21127	precorrin methyltr
542	2	8.3	10	2	PH0948	T-cell receptor be	615	2	8.3	11	2	S70720	trigger factor hom
543	2	8.3	10	2	I52645	gene B-50 protein	616	2	8.3	11	2	S33782	acetylactate synth
544	2	8.3	10	2	D37397	hypothetical prote	617	2	8.3	11	2	B43669	hypothetical prote
545	2	8.3	10	2	S09387	PVI protein - huma	618	2	8.3	11	2	D60691	phycobilisome 9K 1
546	2	8.3	10	2	A24407	amicyanin - Paraco	619	2	8.3	11	2	S14087	parasporeal crystal
547	2	8.3	10	2	S18396	probable glucose-6	620	2	8.3	11	2	E41476	probable antigen 5
548	2	8.3	10	2	S70722	65.4K GTP-binding	621	2	8.3	11	2	S19301	endo-1.4-beta-xyla
549	2	8.3	10	2	I40032	trpE protein - Bac	622	2	8.3	11	2	PA0028	protein QA300042
550	2	8.3	10	2	A39745	endo-glucosylceram	623	2	8.3	11	2	G61497	seed protein ws-23
551	2	8.3	10	2	F41839	ribosomal protein	624	2	8.3	11	2	PU0029	33K protein 3218 -
552	2	8.3	10	2	A40753	aldehyde ferredoxi	625	2	8.3	11	2	S78026	ribosomal protein
553	2	8.3	10	2	PC2044	beta-Kirilowin - M	626	2	8.3	11	2	PN0167	ribosomal protein
554	2	8.3	10	2	PT0084	protein QA600021 -	627	2	8.3	11	2	I52980	glucocerebrosidase
555	2	8.3	10	2	S38305	lectin GNL2 alpha	628	2	8.3	11	2	PT0249	lg heavy chain CRD
556	2	8.3	10	2	D28027	protein P7 - curle	629	2	8.3	11	2	PT0287	lg heavy chain CRD
557	2	8.3	10	2	PS0451	24K protein 4302 -	630	2	8.3	11	2	PT0302	lg heavy chain CRD
558	2	8.3	10	2	PH0113	alpha-amylase (EC	631	2	8.3	11	2	S57575	T-cell receptor V-
559	2	8.3	10	2	S62880	polygalacturonase	632	2	8.3	11	2	S23364	T-cell receptor al
560	2	8.3	10	2	E61512	variant surface gl	633	2	8.3	11	2	S23373	T-cell receptor al
561	2	8.3	10	2	A58365	neuropeptide PRFa	634	2	8.3	11	2	S51732	T-cell receptor al
562	2	8.3	10	2	B60556	leucosulfakinin II	635	2	8.3	11	2	S68649	spermadhesin AQN-3
563	2	8.3	10	2	A2089	transcription fact	636	2	8.3	11	2	A33571	foliistatin - bovi
564	2	8.3	10	2	C44787	caliFMRamide 12	637	2	8.3	11	2	B29806	acidic proline-ric
565	2	8.3	10	2	JN0025	mosact - sea urchi	638	2	8.3	11	2	A29806	acidic proline-ric
566	2	8.3	10	2	A24196	acetylcholinestera	639	2	8.3	11	2	PH1375	T antigen variant
567	2	8.3	10	2	S43625	cytochrome-c oxida	640	2	8.3	11	2	PT0214	T-cell receptor be
568	2	8.3	10	2	A61218	alpha-gliadin 4Ha	641	2	8.3	11	2	D41946	T-cell receptor ga
569	2	8.3	10	2	T13838	cytochrome-c oxida	642	2	8.3	11	2	B41946	T-cell receptor ga
570	2	8.3	10	2	T17075	cytochrome-c oxida	643	2	8.3	11	2	C38887	T-cell receptor ga
571	2	8.3	10	2	T17057	cytochrome-c oxida	644	2	8.3	11	2	I41946	T-cell receptor ga
572	2	8.3	10	2	T17057	cytochrome-c oxida	645	2	8.3	11	2	S53436	beta-D-galactosida
573	2	8.3	10	2	T12303	cytochrome-c oxida	646	2	8.3	11	2	S45386	low density lipopr
574	2	8.3	10	2	T17060	cytochrome-c oxida	647	2	8.3	11	2	PH0939	T-cell receptor be
575	2	8.3	10	2	T12308	cytochrome-c oxida	648	2	8.3	11	2	PH0940	T-cell receptor be
576	2	8.3	10	2	T17072	cytochrome-c oxida	649	2	8.3	11	2	PH0941	T-cell receptor be
577	2	8.3	10	2	T12316	cytochrome-c oxida	650	2	8.3	11	2	PH0929	T-cell receptor be
578	2	8.3	10	2	T12321	cytochrome-c oxida	651	2	8.3	11	2	PH0891	T-cell receptor be
579	2	8.3	10	2	PQ0784	NADH2 dehydrogenas	652	2	8.3	11	2	PH0938	T-cell receptor be
580	2	8.3	10	2	B49581	sialokinin II - ye	653	2	8.3	11	2	PH0947	T-cell receptor be
581	2	8.3	10	2	H60787	sperm-activating p	654	2	8.3	11	2	PH0903	T-cell receptor be
582	2	8.3	10	2	F60787	sperm-activating p	655	2	8.3	11	2	PH0924	T-cell receptor be
583	2	8.3	10	2	D60787	sperm-activating p	656	2	8.3	11	2	PH0914	T-cell receptor be
584	2	8.3	10	2	B60787	sperm-activating p	657	2	8.3	11	2	PH0922	T-cell receptor be
585	2	8.3	10	2	D60588	sperm-activating p	658	2	8.3	11	2	PH0906	T-cell receptor be
586	2	8.3	10	2	I60527	sperm-activating p	659	2	8.3	11	2	PC2254	cytochrome F450 3A
587	2	8.3	10	2	D60527	sperm-activating p	660	2	8.3	11	2	S60294	tubulin 2 beta-3 c
588	2	8.3	10	2	C39572	sperm-activating p	661	2	8.3	11	2	S66606	quinoline 2-oxidor
589	2	8.3	10	2	D60788	sperm-activating p	662	2	8.3	11	2	PC2330	cycloinulooligosac
590	2	8.3	10	2	C60788	sperm-activating p	663	2	8.3	11	2	C59151	protein-tyrosine k
591	2	8.3	10	2	GXHU1	gastric juice pept	664	2	8.3	11	2	S19775	wound-induced prot
592	2	8.3	10	2	S23307	neurokinin A - ral	665	2	8.3	11	2	S71304	amine oxidase (cop
593	2	8.3	10	2	S39030	lysyl-bradykinin -	666	2	8.3	11	2	A61512	variant surface gl
594	2	8.3	10	2	S23186	neurokinin A - At1	667	2	8.3	11	2	A26120	6-phosphofructokin
595	2	8.3	10	2	S07202	phylomedulin - tw	668	2	8.3	11	2	A35594	buccalin - Califor
596	2	8.3	10	2	C60589	sperm-activating p	669	2	8.3	11	2	S69349	neuropeptide PPami
597	2	8.3	10	2	I60588	sperm-activating p	670	2	8.3	11	2	A34662	Achatina cardio-ex
598	2	8.3	10	2	C61033	ranatichykinin C -	671	2	8.3	11	2	S05002	corazonin - Americ
599	2	8.3	10	2	S27178	sperm-activating p	672	2	8.3	11	2	A60656	perisulfakinin - A
600	2	8.3	10	2	B37178	neurokinin A-relat	673	2	8.3	11	2	I41978	caliFMRamide 9 -
601	2	8.3	10	2	S07202	ornithine decarbox	674	2	8.3	11	2	D42965	talin - chicken (f
602	2	8.3	10	2	A60527	sperm-activating p	675	2	8.3	11	2	S68637	acetylcholinestera
603	2	8.3	10	2	A49581	sialokinin I - yel	676	2	8.3	11	2	S78765	ribosomal protein
604	2	8.3	10	2	A60787	sperm-activating p	677	2	8.3	11	2	PU0034	dextranucrase (EC
605	2	8.3	10	2	A60788	sperm-activating p	678	2	8.3	11	2	S07203	uperolein - frog (
606	2	8.3	10	2	A24867	scylliothrinin I.- s	679	2	8.3	11	2	S07201	physalaemin - frog
607	2	8.3	10	4	S14943	UGA3 leader peptid	680	2	8.3	11	2	D61033	ranatichykinin D -
608	2	8.3	11	1	ECLQ2M	tachykinin II - ml	681	2	8.3	11	2	A61033	ranatichykinin A -
609	2	8.3	11	1	GMROL	leucosulfakinin -	682	2	8.3	11	2	S00616	parasporeal crystal
610	2	8.3	11	2	G42762	proteasome endopep	683	2	8.3	11	2	A57458	gene Gax protein -
611	2	8.3	11	2	A33917	dihydroorotase (EC	684	2	8.3	11	4	S41909	hypothetical prote
612	2	8.3	11	2	PQ0682	photosystem I 17.5	685	2	8.3	11	4	PC2124	aminotransferase c
613	2	8.3	11	2	I54193	Rheaus blood group	686	2	8.3	11	4	IS4081	retinoic acid rece

687	2	8.3	12	2	S17869	glutathione transf	760	2	8.3	12	2	PH1463	T-cell receptor be
688	2	8.3	12	2	A23169	phospholipase A2 (761	2	8.3	12	2	PH1470	T-cell receptor be
689	2	8.3	12	2	164829	gene HEXA protein	762	2	8.3	12	2	PH1481	T-cell receptor be
690	2	8.3	12	2	A28856	fructose-bisphosph	763	2	8.3	12	2	PH1464	T-cell receptor be
691	2	8.3	12	2	S25485	transcription fact	764	2	8.3	12	2	PH1466	T-cell receptor be
692	2	8.3	12	2	S26552	T-cell receptor be	765	2	8.3	12	2	PH1461	T-cell receptor be
693	2	8.3	12	2	S26548	T-cell receptor be	766	2	8.3	12	2	PH1459	T-cell receptor be
694	2	8.3	12	2	S26549	T-cell receptor be	767	2	8.3	12	2	PH1461	T-cell receptor be
695	2	8.3	12	2	S26544	T-cell receptor be	768	2	8.3	12	2	B58502	43.2K bile stone p
696	2	8.3	12	2	S26556	ig heavy chain - m	769	2	8.3	12	2	B58503	outer membrane por
697	2	8.3	12	2	S26553	T-cell receptor be	770	2	8.3	12	2	S43013	hypothetical prote
698	2	8.3	12	2	S26557	T-cell receptor be	771	2	8.3	12	2	T44420	hypothetical prote
699	2	8.3	12	2	S26556	T-cell receptor be	772	2	8.3	12	2	T46794	hypothetical prote
700	2	8.3	12	2	S26547	T-cell receptor be	773	2	8.3	12	2	PA0047	protein QAI00045 -
701	2	8.3	12	2	S26558	T-cell receptor be	774	2	8.3	12	2	B61497	seed protein ws-17
702	2	8.3	12	2	S26555	T-cell receptor be	775	2	8.3	12	2	JU0356	cycloleonorinin -
703	2	8.3	12	2	S26546	T-cell receptor be	776	2	8.3	12	2	S28215	glucan endo-1,3-be
704	2	8.3	12	2	S26541	T-cell receptor be	777	2	8.3	12	2	P00730	unidentified 5.4/3
705	2	8.3	12	2	A54315	entactin/nidogen -	778	2	8.3	12	2	PN0170	alcohol dehydrogen
706	2	8.3	12	2	S36902	Em protein - wheat	779	2	8.3	12	2	PA0098	ribosomal protein
707	2	8.3	12	2	S01222	translation elonga	780	2	8.3	12	2	T46656	hypothetical prote
708	2	8.3	12	2	S15815	translation elonga	781	2	8.3	12	2	B44787	calliMIRFamide 1 -
709	2	8.3	12	2	B44818	extracellular lipa	782	2	8.3	12	2	A49261	coagulation factor
710	2	8.3	12	2	S56122	type I DNA methylt	783	2	8.3	12	2	A61503	sterol carrier pro
711	2	8.3	12	2	C64030	hypothetical prote	784	2	8.3	12	2	A49637	MHC class II histo
712	2	8.3	12	2	A49547	hypothetical prote	785	2	8.3	12	2	I77529	estrogen receptor
713	2	8.3	12	2	P00083	protein QA600022 -	786	2	8.3	12	2	S43170	kinesin light chai
714	2	8.3	12	2	A38925	seed storage prote	787	2	8.3	12	2	I46922	gene Bota protein
715	2	8.3	12	2	S18722	matk protein - bee	788	2	8.3	12	2	P84132	hypothetical prote
716	2	8.3	12	2	A33099	163K exoantigen -	789	2	8.3	12	2	S07436	tachykinin - Afric
717	2	8.3	12	2	A03985	gamma-crystallin -	790	2	8.3	12	2	S07206	kassinin - Senegal
718	2	8.3	12	2	S10626	lipovitellin - Afr	791	2	8.3	12	2	S65409	histone H2B - huma
719	2	8.3	12	2	B47171	chondroitin sulfat	792	2	8.3	12	4	PC2121	amino-transferase c
720	2	8.3	12	2	P00228	ig heavy chain CDR	793	2	8.3	13	1	NTKNAS	alpha-conotoxin SI
721	2	8.3	12	2	PT0257	ig heavy chain CDR	794	2	8.3	13	2	P00491	self-incompatibili
722	2	8.3	12	2	PT0274	ig heavy chain CDR	795	2	8.3	13	2	A53608	neurotensin - guin
723	2	8.3	12	2	PH1324	ig heavy chain CDR	796	2	8.3	13	2	A35245	histone H1a - mous
724	2	8.3	12	2	PH1308	ig heavy chain bu	797	2	8.3	13	2	B35245	histone H1.c - mou
725	2	8.3	12	2	S43957	ig mu chain V regi	798	2	8.3	13	2	S78519	ribosomal protein
726	2	8.3	12	2	S57570	T cell receptor V-	799	2	8.3	13	2	S48210	collagen alpha 1(V
727	2	8.3	12	2	S47360	T-cell antigen rec	800	2	8.3	13	2	S39413	tubulin beta chain
728	2	8.3	12	2	S47363	T-cell antigen rec	801	2	8.3	13	2	A33208	calreticulin, hepa
729	2	8.3	12	2	S47391	T-cell antigen rec	802	2	8.3	13	2	PU0038	alpha-peptide/algi
730	2	8.3	12	2	S47393	T-cell antigen rec	803	2	8.3	13	2	PC2371	probable endopepti
731	2	8.3	12	2	S47394	T-cell antigen rec	804	2	8.3	13	2	S36887	ribosomal protein
732	2	8.3	12	2	S47395	T-cell antigen rec	805	2	8.3	13	2	S38736	lipid transfer pro
733	2	8.3	12	2	PH1187	T-cell receptor al	806	2	8.3	13	2	HA0023	protein QA300052 -
734	2	8.3	12	2	S51737	T-cell receptor be	807	2	8.3	13	2	P44957	protein P18 - comm
735	2	8.3	12	2	B49033	T-cell receptor de	808	2	8.3	13	2	E60396	antigen JH8/2 - ma
736	2	8.3	12	2	S74144	aggreccan - bovine	809	2	8.3	13	2	PC1149	equinotoxin IA - s
737	2	8.3	12	2	PN0663	dyatrophin-associ	810	2	8.3	13	2	PS0443	potassium channel
738	2	8.3	12	2	A20907	ig kappa chain J1	811	2	8.3	13	2	S29488	GRP-binding protei
739	2	8.3	12	2	C20907	ig kappa-1 chain J	812	2	8.3	13	2	A33660	osteoclast functio
740	2	8.3	12	2	F20907	ig kappa-2 chain J	813	2	8.3	13	2	A54326	glandular kallikre
741	2	8.3	12	2	B60228	FC mu (IgM) recept	814	2	8.3	13	2	S23356	hypothetical prote
742	2	8.3	12	2	PH1606	ig H chain V-D-J r	815	2	8.3	13	2	PT0331	ig heavy chain CDR
743	2	8.3	12	2	PH1581	ig H chain V-D-J r	816	2	8.3	13	2	PH1309	ig heavy chain CDR
744	2	8.3	12	2	S68271	major urinary prot	817	2	8.3	13	2	S23640	ig kappa chain J s
745	2	8.3	12	2	PH0802	T-cell receptor al	818	2	8.3	13	2	B61458	ig kappa chain V-I
746	2	8.3	12	2	PH0790	T-cell receptor al	819	2	8.3	13	2	S57567	T cell receptor V-
747	2	8.3	12	2	PH0746	T-cell receptor be	820	2	8.3	13	2	S47356	T-cell antigen rec
748	2	8.3	12	2	PT0216	T-cell receptor be	821	2	8.3	13	2	S47357	T-cell antigen rec
749	2	8.3	12	2	H41946	T-cell receptor ga	822	2	8.3	13	2	S47358	T-cell antigen rec
750	2	8.3	12	2	A42324	cytochrome P450c27	823	2	8.3	13	2	S47359	T-cell antigen rec
751	2	8.3	12	2	PH0931	T-cell receptor be	824	2	8.3	13	2	S47361	T-cell antigen rec
752	2	8.3	12	2	PH0936	T-cell receptor be	825	2	8.3	13	2	S47362	T-cell antigen rec
753	2	8.3	12	2	PH0920	T-cell receptor be	826	2	8.3	13	2	S47365	T-cell antigen rec
754	2	8.3	12	2	I57678	gene rPLP-A protei	827	2	8.3	13	2	S47368	T-cell antigen rec
755	2	8.3	12	2	B56049	urinary tract ston	828	2	8.3	13	2	S47371	T-cell antigen rec
756	2	8.3	12	2	A61332	Na+/K+-exchanging	829	2	8.3	13	2	S47372	T-cell antigen rec
757	2	8.3	12	2	I41235	glutamine-tRNA lig	830	2	8.3	13	2	S47373	T-cell antigen rec
758	2	8.3	12	2	PH1454	T-cell receptor al	831	2	8.3	13	2	S47376	T-cell antigen rec
759	2	8.3	12	2	PH1458	T-cell receptor be	832	2	8.3	13	2	S47377	T-cell antigen rec

833	2	8.3	13	2	S47378	T-cell antigen rec	906	2	8.3	14	1	LFECW	trp operon leader
834	2	8.3	13	2	S47380	T-cell antigen rec	907	2	8.3	14	1	LFECFS	pheST operon leade
835	2	8.3	13	2	S47381	T-cell antigen rec	908	2	8.3	14	2	A47421	leukotriene B4-12
836	2	8.3	13	2	S47382	T-cell antigen rec	909	2	8.3	14	2	PC2373	probable IMP deny
837	2	8.3	13	2	S47383	T-cell antigen rec	910	2	8.3	14	2	C40944	S-allele-associate
838	2	8.3	13	2	S47384	T-cell antigen rec	911	2	8.3	14	2	S39932	H+-transporting tw
839	2	8.3	13	2	S47385	T-cell antigen rec	912	2	8.3	14	2	S21247	alpha-1-antichymot
840	2	8.3	13	2	S47388	T-cell antigen rec	913	2	8.3	14	2	S62374	alpha-1-antichymot
841	2	8.3	13	2	S47389	T-cell antigen rec	914	2	8.3	14	2	A60622	somatostatin - spo
842	2	8.3	13	2	S47390	T-cell antigen rec	915	2	8.3	14	2	B61309	ubiquitin - potato
843	2	8.3	13	2	S47392	T-cell antigen rec	916	2	8.3	14	2	S19803	myosin heavy chain
844	2	8.3	13	2	S47400	T-cell antigen rec	917	2	8.3	14	2	A49018	translation initia
845	2	8.3	13	2	S47374	T-cell antigen rec	918	2	8.3	14	2	B29743	avenin alpha-2 - o
846	2	8.3	13	2	S23372	T-cell receptor al	919	2	8.3	14	2	S29209	acyl carrier prote
847	2	8.3	13	2	B61233	conceptus protein	920	2	8.3	14	2	T46634	porin por 1B - Ara
848	2	8.3	13	2	S10562	zona pellucida-bin	921	2	8.3	14	2	PA0109	chlorophyll a/b-bi
849	2	8.3	13	2	B56864	dipeptidyl-peptida	922	2	8.3	14	2	S50900	trp operon leader
850	2	8.3	13	2	C53275	Ig kappa-1 chain J	923	2	8.3	14	2	E90858	trp operon leader
851	2	8.3	13	2	B53275	Ig kappa-1 chain J	924	2	8.3	14	2	B85761	pheST operon leade
852	2	8.3	13	2	B25448	Ig kappa-1 chain,	925	2	8.3	14	2	F90931	pheST operon leade
853	2	8.3	13	2	PH1593	Ig H chain V-D-J r	926	2	8.3	14	2	B85780	pheST operon leade
854	2	8.3	13	2	PH1593	Ig heavy chain C r	927	2	8.3	14	2	S60353	amylopolysaccharid
855	2	8.3	13	2	D37267	Ig heavy chain C r	928	2	8.3	14	2	B85780	36K kidney stone p
856	2	8.3	13	2	B26406	Ig kappa chain J r	929	2	8.3	14	2	BS8502	carbon-monoxide de
857	2	8.3	13	2	PH0788	T-cell receptor al	930	2	8.3	14	2	B38222	excinnuclease ABC c
858	2	8.3	13	2	PH0796	T-cell receptor al	931	2	8.3	14	2	PA0015	seed storage prote
859	2	8.3	13	2	PH0787	T-cell receptor al	932	2	8.3	14	2	SI1766	beta-glucosidase (
860	2	8.3	13	2	PH0799	T-cell receptor al	933	2	8.3	14	2	F61497	beta protein ws-21
861	2	8.3	13	2	PH0786	T-cell receptor al	934	2	8.3	14	2	A61002	photosystem II oxy
862	2	8.3	13	2	PH0928	unidentified QM02	935	2	8.3	14	2	A60737	pollen allergen Lo
863	2	8.3	13	2	PH0928	T-cell receptor be	936	2	8.3	14	2	PS0278	ribulose-bisphosph
864	2	8.3	13	2	A47630	Ig kappa chain J r	937	2	8.3	14	2	PA0101	protein QP20020 -
865	2	8.3	13	2	C47630	Ig kappa chain J r	938	2	8.3	14	2	PA0096	pyruvate decarboxy
866	2	8.3	13	2	B47630	Ig kappa chain J r	939	2	8.3	14	2	A35105	hypothetical prote
867	2	8.3	13	2	D47630	Ig kappa chain J r	940	2	8.3	14	2	B34135	DNA-binding protei
868	2	8.3	13	2	E03063	Ig lambda chain J r	941	2	8.3	14	2	C33098	223K exoantigen -
869	2	8.3	13	2	S20762	Ig lambda chain J r	942	2	8.3	14	2	PL0152	metal-binding prot
870	2	8.3	13	2	PH1479	proteasome endopep	943	2	8.3	14	2	S38307	DEB-A protein - fr
871	2	8.3	13	2	PH1479	T-cell receptor be	944	2	8.3	14	2	S29486	GTP-binding protei
872	2	8.3	13	2	S08575	botulinum neurotox	945	2	8.3	14	2	I54284	Cl-inhibitor - hum
873	2	8.3	13	2	A01825	botulinum toxins -	946	2	8.3	14	2	A60770	cell surface alloa
874	2	8.3	13	2	G22565	R-phycocerythrin ga	947	2	8.3	14	2	PT0223	Ig heavy chain CDR
875	2	8.3	13	2	S20578	ribosomal protein	948	2	8.3	14	2	PT0232	Ig heavy chain CDR
876	2	8.3	13	2	S14316	photosystem I 9K c	949	2	8.3	14	2	PT0252	Ig heavy chain CDR
877	2	8.3	13	2	D56661	S-locus specific g	950	2	8.3	14	2	PT0254	Ig heavy chain CDR
878	2	8.3	13	2	S04013	lignin peroxidase	951	2	8.3	14	2	PH1321	Ig heavy chain DJ
879	2	8.3	13	2	S04014	lignin peroxidase	952	2	8.3	14	2	PH1305	Ig heavy chain DJ
880	2	8.3	13	2	S32471	lymnaDFamide 1 - g	953	2	8.3	14	2	PH1306	Ig kappa chain J s
881	2	8.3	13	2	S32472	lymnaDFamide 2 - g	954	2	8.3	14	2	S23639	interferon alpha r
882	2	8.3	13	2	S32474	lymnaDFamide 4 - g	955	2	8.3	14	2	S41601	MUC1 enhancer bind
883	2	8.3	13	2	S32475	lymnaDFamide 5 - g	956	2	8.3	14	2	A59018	T cell receptor al
884	2	8.3	13	2	B58533	CD61 homolog - cha	957	2	8.3	14	2	PH1763	T cell receptor al
885	2	8.3	13	2	B28955	polysialoglycoprot	958	2	8.3	14	2	PH1757	T cell receptor al
886	2	8.3	13	2	S09018	hemolytic protein	959	2	8.3	14	2	PH1758	T cell receptor al
887	2	8.3	13	2	A57789	gallbladder stone	960	2	8.3	14	2	PH1759	T cell receptor al
888	2	8.3	13	2	S23638	Ig kappa chain J s	961	2	8.3	14	2	PH1765	T cell receptor al
889	2	8.3	13	2	H56046	urinary tract ston	962	2	8.3	14	2	PH1767	T cell receptor al
890	2	8.3	13	2	G56046	urinary tract ston	963	2	8.3	14	2	PH1768	T cell receptor al
891	2	8.3	13	2	S78766	ribosomal protein	964	2	8.3	14	2	PH1769	T cell receptor al
892	2	8.3	13	2	I49637	deoxynucleotidyltr	965	2	8.3	14	2	PH1806	T cell receptor al
893	2	8.3	13	2	H33932	Ig kappa chain J r	966	2	8.3	14	2	S57569	T cell receptor V-
894	2	8.3	13	2	A33933	Ig kappa chain J r	967	2	8.3	14	2	S57574	T cell receptor V-
895	2	8.3	13	2	PC4391	cysteine proteinas	968	2	8.3	14	2	S57638	T cell receptor V-
896	2	8.3	13	2	G83988	hypothetical prote	969	2	8.3	14	2	S47366	T-cell antigen rec
897	2	8.3	13	2	S66558	serine proteinase	970	2	8.3	14	2	S23369	T-cell receptor al
898	2	8.3	13	2	S01904	H+-transporting tw	971	2	8.3	14	2	A28018	very late antigen-
899	2	8.3	13	2	JZVHP1	crabrolin - Europe	972	2	8.3	14	2	S58426	spermadhesin AWN h
900	2	8.3	13	2	S21152	tryptophyllin-rela	973	2	8.3	14	2	S66234	sperm motility inh
901	2	8.3	13	2	A05174	tryptophyllin-13 -	974	2	8.3	14	2	PA0666	dysmorphin-associ
902	2	8.3	13	2	A23695	myosin heavy chain	975	2	8.3	14	2	A43847	Ig mu chain V regi
903	2	8.3	13	2	A60336	outer membrane pro	976	2	8.3	14	2	C44823	synaptosomal-assoc
904	2	8.3	13	2	I70075	glycophorin B (mis	977	2	8.3	14	2	PH1625	Ig H chain V-D-J r
905	2	8.3	14	1	NYRQ14	hypothalamic tetra	978	2	8.3	14	2	PH1627	Ig H chain V-D-J r

979 2 8.3 14 2 PH1601
980 2 8.3 14 2 PH1608
981 2 8.3 14 2 PH0792
982 2 8.3 14 2 PH0800
983 2 8.3 14 2 PH0801
984 2 8.3 14 2 PH0804
985 2 8.3 14 2 PH0776
986 2 8.3 14 2 PH0210
987 2 8.3 14 2 PH0765
988 2 8.3 14 2 PH0747
989 2 8.3 14 2 PH0755
990 2 8.3 14 2 PH0774
991 2 8.3 14 2 S65392
992 2 8.3 14 2 PH0945
993 2 8.3 14 2 PH0915
994 2 8.3 14 2 PD0020
995 2 8.3 14 2 C39170
996 2 8.3 14 2 PA0044
997 2 8.3 14 2 S72217
998 2 8.3 14 2 AG0705
999 2 8.3 14 2 PH1471
1000 2 8.3 14 2 I39753

ALIGNMENTS

RESULT 1
I59073
MHC class II histocompatibility antigen HLA-DRw6a-beta-6111 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I59073
R:Angelini, G.; de Preval, C.; Gorski, J.; Mach, B.
Proc. Natl. Acad. Sci. U.S.A. 83, 4489-4493, 1986
A:Title: High-resolution analysis of the human HLA-DR polymorphism by hybridization with
A:Reference number: I59073; MUID:86233452; PMID:3012569
A:Accession: I59073
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-20 <ANG>
A:Cross-references: UNIPROT:Q30135; UNIPARC:UPI00000894DE; GB:M13561; NID:gl88310; PIDN:
C:Genetics:
A:Gene: HLA-DRB3
A:Map position: 6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 20.8%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDS 5
Db 13 LRFDS 17

RESULT 2
A44874
proboscipedia - fruit fly (Drosophila pseudoobscura) (fragment)
C:Species: Drosophila pseudoobscura
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A44874
R:Randazzo, F.M.; Cribbs, D.L.; Kaufman, T.C.
Development 113, 257-271, 1991
A:Title: Rescue and regulation of proboscipedia: a homeotic gene of the Antennapedia Com
A:Reference number: A44874; MUID:92111389; PMID:1684932
A:Accession: A44874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <RAN>
A:Cross-references: UNIPROT:Q26429; UNIPARC:UPI0000080847; GB:S77929; NID:g242124; PIDN:
A:Note: sequence extracted from NCBI backbone (NCBIN:77929, NCBIIP:77931)

C:Genetics:
A:Gene: FlyBase:Dpse/pb
A:Cross-references: FlyBase:FBgn0012734
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 16.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NNNN 19
Db 8 NNNN 11

RESULT 3
I76673
hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)
N:Alternate names: COII/ND5 protein
C:Species: mitochondrion Mus musculus (house mouse)
C>Date: 12-Aug-1996 #sequence_revision 16-Jul-1998 #text_change 20-Apr-2000
C:Accession: I76673; I76674
R:Nelson, I.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.
Mamm. Genome 4, 680-683, 1993
A:Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic mice
A:Reference number: I57011; MUID:94108239; PMID:8281018
A:Accession: I76673
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-17 <NELI>
A:Cross-references: UNIPARC:UPI0000017CED5; GB:S68119; NID:g544777
A:Accession: I76674
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 8-17 <NEL2>
A:Cross-references: UNIPARC:UPI0000017CED6; GB:S68119; NID:g544777
C:Comment: This is the hypothetical translation of a sequence believed to result from a
C:Genetics:
A:Gene: COII/ND5
A:Genome: mitochondrion
A:Genetic code: SGC1
C:Keywords: fusion protein; mitochondrion
F:1-7/Region: cytochrome-c oxidase chain II
F:8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match 16.7%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TNNN 18
Db 10 TNNN 13

RESULT 4
A40256
interleukin-7 receptor, membrane form - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 29-Aug-1997
C:Accession: A40256
R:Pléman, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.
Mol. Cell. Biol. 11, 3052-3059, 1991
A:Title: Organization of the murine and human interleukin-7 receptor genes: two mRNAs ge
A:Reference number: A40256; MUID:91246172; PMID:2038316
A:Accession: A40256
A:Molecule type: DNA
A:Residues: 1-18 <PLN>
A:Cross-references: UNIPARC:UPI0000017C285
C:Genetics:
A:Gene: GDB:IL7R
A:Cross-references: GDB:127886; OMIM:146661
A:Map position: 5p13-5p13
C:Keywords: cytokine receptor; transmembrane protein

Query Match 16.7%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NNSS 21
|||
Db 2 NNSS 5

RESULT 5
PC1323
endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chloroplast
C;Species: Chloroplast Nicotiana glauca chloroplast (curled-leaved tobacco)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: PC1323
R;Pejters, E.; Engler, D.; Maliga, P.
Theor. Appl. Genet. 79, 28-32, 1990
A;Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana somati
A;Reference number: PC1321
A;Accession: PC1323
A;Molecule type: DNA
A;Residues: 1-19 <FEJ>
A;Cross-references: UNIPROT:Q7M2F6; UNIPARC:UPI0000175C9D
C;Genetics:
A;Genome: chloroplast
C;Function:
A;Description: ATP-driven cleavage of proteins to small peptides
A;Note: magnesium required
C;Superfamily: endopeptidase Clp chain P
C;Keywords: ATP; chloroplast; hydrolase; serine proteinase
F;3/Active site: His #status predicted

Query Match 16.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFY 23
|||
Db 7 SSFY 10

RESULT 6
I79432
MHC class II histocompatibility antigen HLA-DRw6b-beta-6III - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: I79432
R;Angelini, G.; de Preval, C.; Gorski, J.; Mach, B.
Proc. Natl. Acad. Sci. U.S.A. 83, 4489-4493, 1986
A;Title: High-resolution analysis of the human HLA-DR polymorphism by hybridization with
A;Reference number: I59073; MUID:86233452; PMID:3012569
A;Accession: I79432
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <ANG>
A;Cross-references: UNIPROT:O19726; UNIPARC:UPI000008AB92; GB:M13562; NID:gi88312; PIDN
C;Genetics:
A;Gene: HLA-DRB3
A;Map position: 6p21.3
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein

Query Match 16.7%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
|||
Db 14 RFDS 17

RESULT 7
S67990

neurotoxin-associated protein type A Hn+ 17K chain - Clostridium botulinum (fragment)
N;Alternate names: HA-15 protein
C;Species: Clostridium botulinum
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S67990; C44644
R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin component
A;Reference number: S67988; MUID:96096783; PMID:8521962
A;Accession: S67990
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <FUJ>
A;Cross-references: UNIPROT:Q9RSN8; UNIPARC:UPI0000017ACES
R;Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h
A;Reference number: A44644; MUID:92143938; PMID:1781887
A;Contents: type A
A;Accession: C44644
A;Molecule type: protein
A;Status: preliminary
A;Residues: 1-19 <SOM>
A;Cross-references: UNIPARC:UPI00000A8A14
A;Note: sequence extracted from NCBI backbone (NCBI:83795)
C;Keywords: hemagglutinin

Query Match 16.7%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSIF 11
|||
Db 15 KSIF 18

RESULT 8
B40256
interleukin-7 receptor, soluble form - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 23-May-1997
C;Accession: B40256
R;Pleiman, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.
Mol. Cell. Biol. 11, 3052-3059, 1991
A;Title: Organization of the murine and human interleukin-7 receptor genes: two mRNAs g
A;Reference number: A40256; MUID:91246172; PMID:2038316
A;Accession: B40256
A;Molecule type: DNA
A;Residues: 1-22 <PLE>
A;Cross-references: UNIPARC:UPI0000176755
A;Note: the authors translated the codon GAA for residue 20 as Gln
C;Superfamily: interleukin-7 receptor; fibronectin type III repeat homology
C;Keywords: cytokine receptor

Query Match 16.7%; Score 4; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NNSS 21
|||
Db 2 NNSS 5

RESULT 9
D41654
hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
C;Species: Haemophilus parainfluenzae
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
C;Accession: D41654
R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.
J. Bacteriol. 173, 7449-7457, 1991
A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus par
A;Reference number: A41654; MUID:92041655; PMID:1938942

A:Accession: D41654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <KRO>
A:Cross-references: UNIPARC:UPI000017AB26

Query Match 12.5%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFD 4
|||
Db 2 RFD 4

RESULT 10
PT0644
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PT0644
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0644
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Cross-references: UNIPROT:Q5Z2T6; UNIPARC:UPI000017C7D2
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 12.5%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSF 22
|||
Db 2 SSF 4

RESULT 11
B39127
phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C:Accession: B39127
R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc
rin.
A:Reference number: A39127; MUID:91100329; PMID:1846143
A:Accession: B39127
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-7 <HAR>
A:Cross-references: UNIPARC:UPI0000170D6E; GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:
C:Keywords: phosphotransferase

Query Match 12.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FEQ 13
|||
Db 3 FEQ 5

RESULT 12
A59489
protein kinase C inhibitor - rat (fragment)
C:Species: Rattus norvegicus

C:Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C:Accession: A59489
R:Negoro, M.
A:Description: Purification of PKCI from rat liver.
submitted to the Protein Sequence Database, June 2003
A:Reference number: A59489
A:Accession: A59489
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NEG>
A:Experimental source: strain Wistar, liver
A:Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match 12.5%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFE 12
|||
Db 2 IFE 4

RESULT 13
PH1407
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PH1407
R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1407
A:Molecule type: DNA
A:Residues: 1-8 <SHI>
A:Cross-references: UNIPARC:UPI0000176A1C
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 12.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRF 3
|||
Db 5 LRF 7

RESULT 14
S59622
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fra
C:Species: Ariantha arbustorum
C:Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S59622
R:Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Biochem. J. 311, 951-957, 1995
A:Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion
A:Reference number: S59621; MUID:96067616; PMID:7487956
A:Accession: S59622
A:Molecule type: protein
A:Residues: 1-8 <BER>
A:Cross-references: UNIPROT:P55946; UNIPARC:UPI0000177CA4
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 12.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 NSS 21
|||
Db 2 NSS 4

RESULT 15

JS0316
leucokinin VI - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0316
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
A;Accession: JS0316
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19988; UNIPARC:UPI000012E29E
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 12.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSF 22
|||
Db 2 SSF 4

Search completed: January 20, 2006, 17:56:07
Job time : 20 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 17:51:04 ; Search time 65 seconds
(without alignments)
260.503 Million cell updates/sec

Title: US-10-619-323-1_COPY_35_58

Perfect score: 24

Sequence: 1 LRFDSQTKSIPQETNNNSFYT 24

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 21620

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 1000 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.8	20	2	Q30135 HUMAN
2	5	20.8	23	2	Q4YXD8 PLABE
3	5	20.8	25	2	Q7REJ5 PLAYO
4	4	16.7	12	2	Q26429 DROPS
5	4	16.7	16	2	Q36731 HUMAN
6	4	16.7	17	2	Q4YCW9 PLABE
7	4	16.7	19	2	Q7M2F6 NICPL
8	4	16.7	19	2	Q9R5N8 CLOBO
9	4	16.7	20	2	Q19726 HUMAN
10	4	16.7	20	2	Q4X1L0 PLACH
11	4	16.7	21	2	Q8N337 HUMAN
12	4	16.7	21	2	Q4YK89 PLABE
13	4	16.7	21	2	Q4Z0T6 PLABE
14	4	16.7	22	2	Q7S122 NEUCR
15	4	16.7	22	2	Q8WSY1 ANOGA
16	4	16.7	22	2	Q4XN91 PLACH
17	4	16.7	22	2	Q4XS57 PLACH
18	4	16.7	22	2	Q4YH58 PLABE
19	4	16.7	22	2	Q4Z2L9 PLABE
20	4	16.7	23	2	Q9UCL8 HUMAN
21	4	16.7	23	2	Q19621 HUMAN
22	4	16.7	23	2	Q4YQV7 PLABE
23	4	16.7	24	2	Q6S8N7 HUMAN
24	4	16.7	24	2	Q7RAM4 PLAYO
25	4	16.7	24	2	Q4XGQ5 PLACH
26	4	16.7	24	2	Q4XSL3 PLACH
27	4	16.7	24	2	Q4LSM0 STRAJ
28	4	16.7	24	2	Q68W11 RICTY
29	4	16.7	25	1	SODC PAROL
30	4	16.7	25	2	Q7RLH1 PLABE
31	4	16.7	25	2	Q9BM38 CAENORHABDI

32	4	16.7	25	2	Q9BM39 CAEL
33	4	16.7	25	2	Q4XAN1 PLACH
34	4	16.7	25	2	Q570P0 ARATH
35	3	12.5	4	1	FAR3 HIRME
36	3	12.5	4	1	FLRF HELTI
37	3	12.5	4	1	FLRF HIRME
38	3	12.5	4	1	FARP CHICK
39	3	12.5	7	1	FAP2 ASCSU
40	3	12.5	7	1	FAP2 PANRE
41	3	12.5	7	1	FAR1 HELTI
42	3	12.5	7	1	FAR1 MACRS
43	3	12.5	7	1	FAR1 PROCL
44	3	12.5	7	1	FAR2 PROCL
45	3	12.5	8	1	FAR1 PANRE
46	3	12.5	8	1	FAR1 PENMO
47	3	12.5	8	1	FAR2 MACRS
48	3	12.5	8	1	FAR3 HOMAM
49	3	12.5	8	1	FAR4 HOMAM
50	3	12.5	8	1	FAR4 MACRS
51	3	12.5	8	1	LCK6 LEUMA
52	3	12.5	8	2	Q6LD47 HUMAN
53	3	12.5	8	2	Q8MC18 OUTIN
54	3	12.5	8	2	Q8MC20 SMIRT
55	3	12.5	8	2	O87471 HAIN
56	3	12.5	8	2	Q6LDH5 GLACT
57	3	12.5	8	2	Q7M066 MOUSE
58	3	12.5	8	2	Q99NX9 HYDHY
59	3	12.5	8	2	Q6LD23 MOUSE
60	3	12.5	8	2	Q91U21 9INFA
61	3	12.5	8	2	Q91U21 9INFA
62	3	12.5	9	1	FAR2 PANRE
63	3	12.5	9	1	FAR3 MACRS
64	3	12.5	9	1	FAR3 PENMO
65	3	12.5	9	1	FAR4 PENMO
66	3	12.5	9	1	FAR5 PENMO
67	3	12.5	9	1	FAR6 MACRS
68	3	12.5	9	1	FAR8 MACRS
69	3	12.5	9	1	FAR9 ASCSU
70	3	12.5	9	1	FARP CALSI
71	3	12.5	9	2	Q7M4R5 HUMAN
72	3	12.5	9	2	Q7M4R3 HUMAN
73	3	12.5	9	2	Q5G6J7 CRATH
74	3	12.5	9	2	Q5G6J8 9CHIR
75	3	12.5	9	2	Q5G6J9 NATST
76	3	12.5	9	2	Q5G6K5 9CHIR
77	3	12.5	9	2	Q5G6L3 RHIPA
78	3	12.5	9	2	Q65711 BEV
79	3	12.5	9	2	Q70140 9HIV1
80	3	12.5	10	1	FAR2 PENMO
81	3	12.5	10	1	FAR5 MACRS
82	3	12.5	10	1	FAR7 MACRS
83	3	12.5	10	1	FARP LOEMI
84	3	12.5	10	1	FARP MANSE
85	3	12.5	10	1	FARP SCHGR
86	3	12.5	10	1	LCMS LEUMA
87	3	12.5	10	1	NEMS SARBU
88	3	12.5	10	1	TKNB RANCA
89	3	12.5	10	1	UH05 RAT
90	3	12.5	10	2	Q6B958 FUSOX
91	3	12.5	10	2	Q7SC70 NEUCR
92	3	12.5	10	2	Q6EEZ7 HUMAN
93	3	12.5	10	2	Q96QT9 HUMAN
94	3	12.5	10	2	Q52RG3 HUMAN
95	3	12.5	10	2	Q82217 BOMMO
96	3	12.5	10	2	Q9TWU1 FUSFE
97	3	12.5	10	2	Q4X386 PLACH
98	3	12.5	10	2	Q4Z638 PLABE
99	3	12.5	10	2	Q5G6L0 9CHIR
100	3	12.5	10	2	Q58U15 PSAST
101	3	12.5	10	2	Q58U20 CRIDE
102	3	12.5	10	2	Q58U37 9POAL
103	3	12.5	10	2	Q58U47 9POAL
104	3	12.5	10	2	Q58U47 9POAL

Q9bm39	caenorhabdi
Q4xan1	plasmodium
Q570p0	arabidopsis
P42562	hirudo medi
P69138	helisoma tr
P69137	hirudo medi
P67308	gallus gall
P67879	ascaris suu
P67880	panagrellus
P41871	helisoma tr
P83274	macrobrachi
P38499	procambarus
P38498	procambarus
P41872	panagrellus
P83316	penaeus mon
P83275	macrobrachi
P41866	homo sapien
P41867	homo sapien
P19388	leucophaea
Q61d47	homo sapien
Q8mc18	quisqualis
Q8mc20	combretum w
O87471	haemophilus
Q6ldh5	lactococcus
Q7m066	mus musculu
Q7m067	mus musculu
Q99nx9	hydrochoeru
Q6ld23	mus musculu
Q91u21	influenza a
Q91u21	influenza a
P41873	panagrellus
P83276	macrobrachi
P83318	penaeus mon
P83319	penaeus mon
P83320	penaeus mon
P83279	macrobrachi
P83281	macrobrachi
P43172	ascaris suu
P38495	callinectes
Q7mar5	homo sapien
Q7mar3	homo sapien
Q5g6j7	craseonycte
Q5g6j8	eumops auri
Q5g6j9	natalus str
Q5g6k5	rhogeessa t
Q5g6l3	rhinopoma h
Q70140	berne virus
Q70140	human immun
P83317	penaeus mon
P83278	macrobrachi
P83280	macrobrachi
P84306	locusta mig
P18523	manduca sex
P84307	schistocerc
P21144	leucophaea
P61850	sarcophaga
P22889	rana catesb
P56573	rattus norv
Q6b958	fusarium ox
Q7sc70	neurospora
Q6eez7	homo sapien
Q96qt9	homo sapien
Q52rg3	homo sapien
P82217	bombyx mori
Q9twu1	fusinus fer
Q4x386	plasmodium
Q4z638	plasmodium
Q5g6l0	rhynchonyc
Q58u15	peathyrosta
Q58u20	crithopesta
Q58u37	eremopyrum
Q58u47	australopyr

105	3	12.5	10	2	Q58U54_BROST	Q58U54	bromus ster	178	3	12.5	12	2	Q9BFT8_LEMCA	Q9BFT8	lemur catia
106	3	12.5	10	2	Q9L5W6_LIBAC	Q9L5W6	liberibacte	179	3	12.5	12	2	Q9BFT9_TUPMI	Q9BFT9	tupaia mino
107	3	12.5	10	2	Q71V02_PSEAE	Q71V02	pseudomonas	180	3	12.5	12	2	Q9BFU0_CYNVA	Q9BFU0	cynocephalu
108	3	12.5	10	2	Q47651_ECOLI	Q47651	escherichia	181	3	12.5	12	2	Q9BFU1_OCHHY	Q9BFU1	ochotona hy
109	3	12.5	10	2	Q53VQ7_MOUSE	Q53VQ7	mus musculus	182	3	12.5	12	2	Q9BFU2_SYLFL	Q9BFU2	syllilagus
110	3	12.5	10	2	Q84140_9INFA	Q84140	influenza a	183	3	12.5	12	2	Q9BFU3_ORYAF	Q9BFU3	orycteropus
111	3	12.5	10	2	Q85563_MLYMO	Q85563	moloney mur	184	3	12.5	12	2	Q9BFU4_ELERU	Q9BFU4	elephantulu
112	3	12.5	10	2	Q85598_MLYMO	Q85598	moloney mur	185	3	12.5	12	2	Q9BFU5_MACPR	Q9BFU5	macroscelid
113	3	12.5	10	2	Q85619_MLYMO	Q85619	moloney mur	186	3	12.5	12	2	Q9BFU6_LOXAF	Q9BFU6	loxodonta a
114	3	12.5	11	1	FAR6_PENMO	Q6LEP5	penaeus mon	187	3	12.5	12	2	Q9BFU7_PROCA	Q9BFU7	procavia ca
115	3	12.5	11	2	Q6LEP5_HUMAN	Q6LEP5	homo sapien	188	3	12.5	12	2	Q9BFU8_TRIMA	Q9BFU8	trichechus
116	3	12.5	11	2	Q4YLN6_PLABE	Q4YLN6	plasmodium	189	3	12.5	12	2	Q9BFU9_ECHTE	Q9BFU9	echinops te
117	3	12.5	11	2	Q5G6K1_9CHIR	Q5G6K1	thyroptera	190	3	12.5	12	2	Q9BFV0_SORAR	Q9BFV0	sorex arane
118	3	12.5	11	2	Q5G6K2_PTEPA	Q5G6K2	pterototus	191	3	12.5	12	2	Q9BFV1_CONCR	Q9BFV1	condylura c
119	3	12.5	11	2	Q5G6K3_MYZAU	Q5G6K3	myzopoda au	192	3	12.5	12	2	Q9BFV2_TALAL	Q9BFV2	talpa alta
120	3	12.5	11	2	Q5G6K7_ANOGE	Q5G6K7	anoura geof	193	3	12.5	12	2	Q9BFV3_ERICO	Q9BFV3	erinaceus c
121	3	12.5	11	2	Q5G6K8_DESRO	Q5G6K8	desmodus ro	194	3	12.5	12	2	Q9BFV4_MYRTR	Q9BFV4	myrmecophag
122	3	12.5	11	2	Q5G6L1_9CHIR	Q5G6L1	taphozous n	195	3	12.5	12	2	Q9BFV5_TAMTE	Q9BFV5	tamandua te
123	3	12.5	11	2	Q9TRW5_BOVIN	Q9TRW5	bos taurus	196	3	12.5	12	2	Q9BFV6_CHAVI	Q9BFV6	chaetophrac
124	3	12.5	11	2	Q06626_SOLTM	Q06626	solanum tub	197	3	12.5	12	2	Q9BFV7_EUPSX	Q9BFV7	euphractus
125	3	12.5	11	2	Q58U09_TAECM	Q58U09	taeniatheru	198	3	12.5	12	2	Q9BFV8_CHODI	Q9BFV8	choloepus d
126	3	12.5	11	2	Q58U22_9POAL	Q58U22	peridictyon	199	3	12.5	12	2	Q9BFV9_CHOHO	Q9BFV9	choloepus h
127	3	12.5	11	2	Q58U24_AEGTA	Q58U24	aegilops ta	200	3	12.5	12	2	Q9BFW0_MACEU	Q9BFW0	macropus eu
128	3	12.5	11	2	Q58U26_LOPEL	Q58U26	lophopyrum	201	3	12.5	12	2	Q9TRU0_BOVIN	Q9TRU0	bos taurus
129	3	12.5	11	2	Q58U43_TRIMO	Q58U43	tritium mo	202	3	12.5	12	2	Q85U39_EREDI	Q85U39	eremopyrum
130	3	12.5	11	2	Q58U51_9POAL	Q58U51	amblyopyrum	203	3	12.5	12	2	Q5FBL6_9ROSI	Q5FBL6	hibiscus ma
131	3	12.5	11	2	Q7X9Y3_CUCSA	Q7X9Y3	cucumis eat	204	3	12.5	12	2	Q5FBL8_9ROSI	Q5FBL8	hibiscus ha
132	3	12.5	11	2	Q95E14_DENAA	Q95E14	dendrochili	205	3	12.5	12	2	Q5FBP4_9ROSI	Q5FBP4	hibiscus ti
133	3	12.5	11	2	Q6LBJ0_MOUSE	Q6LBJ0	mus musculus	206	3	12.5	12	2	Q5FBR0_9ROSI	Q5FBR0	hibiscus gl
134	3	12.5	12	1	FAR7_PENMO	P83322	penaeus mon	207	3	12.5	12	2	P83196_ORYSA	P83196	oryza sativ
135	3	12.5	12	1	NO40_LOTJA	O22426	lotus japon	208	3	12.5	12	2	Q7M1W6_ARATH	Q7M1W6	arabidopsis
136	3	12.5	12	1	NO40_SESRO	O2X369	sesbania ro	209	3	12.5	12	2	Q8LLC3_TRIRP	Q8LLC3	trifolium r
137	3	12.5	12	1	Q9BYI9_HUMAN	Q9BYI9	homo sapten	210	3	12.5	12	2	Q93WB7_LUPLU	Q93WB7	lupinus lut
138	3	12.5	12	2	Q9TWV4_LYMST	Q9TWV4	lymaea sta	211	3	12.5	12	2	Q93WF2_LUPLU	Q93WF2	lupinus lut
139	3	12.5	12	2	Q4X448_PLACH	Q4X448	plasmodium	212	3	12.5	12	2	Q95E12_9ASPA	Q95E12	dendrochili
140	3	12.5	12	2	Q4YGK1_PLABE	Q4YGK1	plasmodium	213	3	12.5	12	2	Q95E16_DENGL	Q95E16	dendrochili
141	3	12.5	12	2	Q5G6K0_MYSTU	Q5G6K0	mystacina t	214	3	12.5	12	2	Q95E18_9ASPA	Q95E18	dendrochili
142	3	12.5	12	2	Q5G6K3_MYODA	Q5G6K3	myotis daub	215	3	12.5	12	2	Q95EJ1_9ASPA	Q95EJ1	dendrochili
143	3	12.5	12	2	Q5G6K6_ANTPA	Q5G6K6	antrozous p	216	3	12.5	12	2	Q95EJ3_9ASPA	Q95EJ3	dendrochili
144	3	12.5	12	2	Q5G6K9_9CHIR	Q5G6K9	tonatia ep	217	3	12.5	12	2	Q95EJ5_9ASPA	Q95EJ5	dendrochili
145	3	12.5	12	2	Q5G6L2_EMBAT	Q5G6L2	emballonura	218	3	12.5	12	2	Q95EJ8_9ASPA	Q95EJ8	dendrochili
146	3	12.5	12	2	Q5G6L4_HPCPO	Q5G6L4	hipposidero	219	3	12.5	12	2	Q95EK0_9ASPA	Q95EK0	dendrochili
147	3	12.5	12	2	Q5G6L5_9CHIR	Q5G6L5	rhinolophus	220	3	12.5	12	2	Q95EK2_9ASPA	Q95EK2	dendrochili
148	3	12.5	12	2	Q5G6L6_NYCAL	Q5G6L6	nyctimene a	221	3	12.5	12	2	Q95EK4_9ASPA	Q95EK4	dendrochili
149	3	12.5	12	2	Q5G6L7_CYNBR	Q5G6L7	cynopterus	222	3	12.5	12	2	Q95EK6_9ASPA	Q95EK6	dendrochili
150	3	12.5	12	2	Q6JC79_9EUTH	Q6JC79	solenodon p	223	3	12.5	12	2	Q95EK8_9ASPA	Q95EK8	dendrochili
151	3	12.5	12	2	Q71BP8_TARSY	Q71BP8	tarsius syr	224	3	12.5	12	2	Q95EL0_9ASPA	Q95EL0	dendrochili
152	3	12.5	12	2	Q71BQ0_CYNVO	Q71BQ0	cynocephalu	225	3	12.5	12	2	Q95EL2_9ASPA	Q95EL2	dendrochili
153	3	12.5	12	2	Q71BQ1_9EUTH	Q71BQ1	urogale eve	226	3	12.5	12	2	Q95EL4_9ASPA	Q95EL4	dendrochili
154	3	12.5	12	2	Q9BFR4_9EUTH	Q9BFR4	manis penta	227	3	12.5	12	2	Q95EL6_9ASPA	Q95EL6	dendrochili
155	3	12.5	12	2	Q9BFR5_URSAR	Q9BFR5	ureus arcto	228	3	12.5	12	2	Q95EL8_9ASPA	Q95EL8	dendrochili
156	3	12.5	12	2	Q9BFR6_CANFA	Q9BFR6	canis famil	229	3	12.5	12	2	Q95EM0_9ASPA	Q95EM0	dendrochili
157	3	12.5	12	2	Q9BFR7_PANON	Q9BFR7	panthera on	230	3	12.5	12	2	Q95EM2_9ASPA	Q95EM2	dendrochili
158	3	12.5	12	2	Q9BFR8_LEOPA	Q9BFR8	leopardus p	231	3	12.5	12	2	Q546R2_LOTJA	Q546R2	lotus japon
159	3	12.5	12	2	Q9BER9_FELCA	Q9BER9	felis silve	232	3	12.5	12	2	Q58U56_BROAV	Q58U56	bromus arve
160	3	12.5	12	2	Q9BFS0_TAPIN	Q9BFS0	tapirus ind	233	3	12.5	12	2	Q8SEB7_9FIOR	Q8SEB7	grateloupia
161	3	12.5	12	2	Q9BFS1_CERSI	Q9BFS1	ceratotheri	234	3	12.5	12	2	Q4KUK6_9FLOI	Q4KUK6	grateloupia
162	3	12.5	12	2	Q9BFS2_HORSE	Q9BFS2	equus cabal	235	3	12.5	12	2	Q47251_ECOLI	Q47251	escherichia
163	3	12.5	12	2	Q9BFS3_ORAJO	Q9BFS3	okapia john	236	3	12.5	12	2	Q02128_DPSVU	Q02128	desulfovibr
164	3	12.5	12	2	Q9BFS4_PIG	Q9BFS4	sus scrofa	237	3	12.5	12	2	Q99NX7_AGOTA	Q99NX7	agouti tacz
165	3	12.5	12	2	Q9BFS5_TRAEU	Q9BFS5	tragelaphus	238	3	12.5	12	2	Q99NX8_9HYST	Q99NX8	dinomya bra
166	3	12.5	12	2	Q9BFS6_LAMGL	Q9BFS6	lama glama	239	3	12.5	12	2	Q99NY0_9HYST	Q99NY0	cavia tschu
167	3	12.5	12	2	Q9BFS7_HIPAM	Q9BFS7	hippopotamu	240	3	12.5	12	2	Q99NY1_HETGA	Q99NY1	hippocropha
168	3	12.5	12	2	Q9BFS8_TURTR	Q9BFS8	tursiops tr	241	3	12.5	12	2	Q99NY2_DIPHE	Q99NY2	dipodomys h
169	3	12.5	12	2	Q9BFS9_MEGNO	Q9BFS9	megaptera n	242	3	12.5	12	2	Q99NY3_EREDO	Q99NY3	erethizon d
170	3	12.5	12	2	Q9BFT0_NYCTH	Q9BFT0	nycteris th	243	3	12.5	12	2	Q99NY4_HYSBR	Q99NY4	hystrix bra
171	3	12.5	12	2	Q9BFT1_ROULA	Q9BFT1	rousettus l	244	3	12.5	12	2	Q99NY5_CRIGR	Q99NY5	cricetulus
172	3	12.5	12	2	Q9BFT2_PTEGI	Q9BFT2	pteropus gi	245	3	12.5	12	2	Q99NY6_RAT	Q99NY6	rattus norv
173	3	12.5	12	2	Q9BFT3_ARTJA	Q9BFT3	artibeus ja	246	3	12.5	12	2	Q99NY7_MOUSE	Q99NY7	mus musculus
174	3	12.5	12	2	Q9BFT4_CALGO	Q9BFT4	callimico g	247	3	12.5	12	2	Q99NY8_PUDCA	Q99NY8	pedetes cap
175	3	12.5	12	2	Q9BFT5_MACMU	Q9BFT5	macaca mula	248	3	12.5	12	2	Q99NY9_MUSAV	Q99NY9	muscardinus
176	3	12.5	12	2	Q9BFT6_ATEFU	Q9BFT6	ateles fusc	249	3	12.5	12	2	Q99NZ0_CASCN	Q99NZ0	caenor cana
177	3	12.5	12	2	Q9BFT7_TARBA	Q9BFT7	tarsius ban	250	3	12.5	12	2	Q99NZ1_TAMST	Q99NZ1	tamias stri

251	3	12.5	12	2	Q8AEW7_9HIV1	Q8AEW7 human immun	324	3	12.5	15	2	Q85XF8_9ROSI	Q85xf8 clusia gran
252	3	12.5	13	1	P43173 ASCSU	P43173 ascaris suu	325	3	12.5	15	2	Q85XG0_9ROSI	Q85xg0 clusia flum
253	3	12.5	13	1	P55959 PIUM	P55959 pium sativ	326	3	12.5	15	2	Q85XG2_9ROSI	Q85xg2 clusia flav
254	3	12.5	13	1	N040_VICSA	N040 vicia sativ	327	3	12.5	15	2	Q85XG4_9ROSI	Q85xg4 clusia croa
255	3	12.5	13	1	Q78CD5_NEUCR	Q78cd5 neurospora	328	3	12.5	15	2	Q85XG6_9ROSI	Q85xg6 clusia arip
256	3	12.5	13	2	Q29823_HUMAN	Q29823 homo sapien	329	3	12.5	15	2	Q988D3_CYNCA	Q988d3 cynara card
257	3	12.5	13	2	Q6SL59_HUMAN	Q6sl59 homo sapien	330	3	12.5	15	2	Q98AP4_SOUTU	Q98ap4 solanum tub
258	3	12.5	13	2	Q75MV9_HUMAN	Q75mv9 homo sapien	331	3	12.5	15	2	Q984T0_RHOSH	Q984t0 rhodobacter
259	3	12.5	13	2	Q53S92_HUMAN	Q53s92 homo sapien	332	3	12.5	15	2	Q9R4U8_ACICA	Q9r4u8 acinetobact
260	3	12.5	13	2	Q65YZ5_HORSE	Q65yz5 equus cabal	333	3	12.5	15	2	Q9R533_PSEAE	Q9r533 pseudomonas
261	3	12.5	13	2	Q7YRD1_BISBO	Q7yrd1 bison bonas	334	3	12.5	15	2	Q88175_MOUSE	Q88175 mus musculu
262	3	12.5	13	2	Q7YRI4_BOVIN	Q7yri4 bos taurus	335	3	12.5	15	2	Q6FXP1_RAT	Q6fxp1 rattus norv
263	3	12.5	13	2	Q8WNS4_BOVIN	Q8wns4 bos taurus	336	3	12.5	15	2	Q7LZ20_CHICK	Q7lhz20 gallus gall
264	3	12.5	13	2	Q9BDQ8_PIG	Q9bdq8 sus scrofa	337	3	12.5	15	2	Q8UP12_9HIV1	Q8up12 human immun
265	3	12.5	13	2	Q42373_SOLTU	Q42373 solanum tub	338	3	12.5	16	2	Q5EEK4_HUMAN	Q5eek4 homo sapien
266	3	12.5	13	2	Q71N39_TRIRP	Q71n39 trifolium r	339	3	12.5	16	2	Q9UC44_HUMAN	Q9uc44 homo sapien
267	3	12.5	13	2	Q7X955_CABPU	Q7x955 caprella bu	340	3	12.5	16	2	Q9UCJ7_HUMAN	Q9ucj7 homo sapien
268	3	12.5	13	2	Q53300_ECOLI	Q53300 escherichia	341	3	12.5	16	2	Q75MY2_HUMAN	Q75my2 homo sapien
269	3	12.5	13	2	Q6XFQ8_BACCS	Q6xfq8 bacillus cl	342	3	12.5	16	2	Q7R661_PLAYO	Q7r661 plasmodium
270	3	12.5	13	2	Q7MOJ0_9ACTO	Q7moj0 actinomadr	343	3	12.5	16	2	Q7RPP5_PLAYO	Q7rpp5 plasmodium
271	3	12.5	13	2	Q6RSM3_COXBU	Q6rsm3 coxiella bu	344	3	12.5	16	2	Q4XD98_PLACH	Q4xd98 plasmodium
272	3	12.5	13	2	Q71R59_MOUSE	Q71r59 mus musculu	345	3	12.5	16	2	Q5G554_BALMU	Q5g554 balaeopter
273	3	12.5	13	2	Q80WZ0_RAT	Q80wz0 rattus norv	346	3	12.5	16	2	Q19971_GOSHI	Q19971 gossypium h
274	3	12.5	13	2	Q9CU06_MOUSE	Q9cu06 mus musculu	347	3	12.5	16	2	Q19973_GOSBA	Q19973 gossypium b
275	3	12.5	13	1	BNCE_BENHI	BNCE61 benincasa h	348	3	12.5	16	2	Q19975_GOSTO	Q19975 gossypium t
276	3	12.5	14	1	GLGS_SPIOL	P55235 spinacia ol	349	3	12.5	16	2	Q19977_GOSMU	Q19977 gossypium m
277	3	12.5	14	1	LPER_BACAN	P62187 bacillus an	350	3	12.5	16	2	Q34699_HELAN	Q34699 helianthus
278	3	12.5	14	1	LPER_BACLI	P62188 bacillus li	351	3	12.5	16	2	Q5G6V0_9ARAE	Q5g6v0 philodendro
279	3	12.5	14	1	MAST_VESBA	P21554 vespa basal	352	3	12.5	16	2	Q988Y6_LUPAR	Q988y6 lupinus arb
280	3	12.5	14	1	UN46_CLOPA	P81362 clostridium	353	3	12.5	16	2	Q6R8J3_COXBU	Q6r8j3 coxiella bu
281	3	12.5	14	2	Q6E144_BIOGL	Q6e144 biophalari	354	3	12.5	16	2	Q9KJ10_STAHA	Q9kj10 staphylococ
282	3	12.5	14	2	Q6Q9S8_9CARA	Q6q9s8 zabrus colf	355	3	12.5	16	2	Q9L923_SHIBO	Q9l923 shigella bo
283	3	12.5	14	2	Q4XLP6_PLACH	Q4xlp6 plasmodium	356	3	12.5	16	2	Q9L925_SHIFL	Q9l925 shigella fl
284	3	12.5	14	2	Q4XS12_PLACH	Q4xsi2 plasmodium	357	3	12.5	16	2	Q9L937_SHISO	Q9l937 shigella so
285	3	12.5	14	2	P83333_PEA	P82333 pisum sativ	358	3	12.5	16	2	Q9R4H3_PORGI	Q9r4h3 porphyromon
286	3	12.5	14	2	Q7X9Y5_CUCSA	Q7x9y5 cucumis sat	359	3	12.5	16	2	Q9R5K7_STROI	Q9r5k7 streptomyce
287	3	12.5	14	2	Q9ZR83_ARATH	Q9zr83 arabidopsis	360	3	12.5	16	2	Q9R4H3_PORGI	Q9r4h3 porphyromon
288	3	12.5	14	2	Q47599_ECOLI	Q47599 escherichia	361	3	12.5	16	2	Q8TSR1_9SPHN	Q8tsr1 erythrobact
289	3	12.5	14	2	Q9R224_CAMJE	Q9r224 campylobact	362	3	12.5	16	2	Q810X4_CRGR	Q810x4 cricetulus
290	3	12.5	14	2	Q9KCS9_BACHD	Q9kcs9 bacillus ha	363	3	12.5	16	2	Q9CTB2_MOUSE	Q9ctb2 mus musculu
291	3	12.5	14	2	Q73591_CHICK	Q73591 gallus gall	364	3	12.5	16	2	Q04246_9PARA	Q04246 sendai viru
292	3	12.5	14	2	Q07378_COTCO	Q07378 coturnix co	365	3	12.5	16	2	Q718K5_9PARA	Q718k5 newcasttle d
293	3	12.5	15	1	Q0X5A_SCYCA	P83012 scyliorhinu	366	3	12.5	16	2	Q99154_9PARA	Q99154 sendai viru
294	3	12.5	15	1	FIBA_ANAPL	P12801 anas platyr	367	3	12.5	16	2	Q7LZS2_XENLA	Q7lzs2 xenopus lae
295	3	12.5	15	1	LECB2_PSOSC	P22585 psophocartu	368	3	12.5	16	2	Q75710_9HIV1	Q75710 human immun
296	3	12.5	15	1	LG29_VIGUS	P83955 vigna ungui	369	3	12.5	17	1	BIOP1_EHYAT	BIOP1 phyllomedus
297	3	12.5	15	1	LG31_VIGUS	P83956 vigna ungui	370	3	12.5	17	1	CHXI_ASPFL	CHXI aspergillus
298	3	12.5	15	1	TLP_CASCH	P83957 castanopsis	371	3	12.5	17	1	LPW_CORGL	LPW corynebacte
299	3	12.5	15	2	Q7M4Y4_FUSSP	Q7m4y4 fusarium sp	372	3	12.5	17	1	RACEY_RANES	RACEY rana escul
300	3	12.5	15	2	Q7M4Z3_FUSSP	Q7m4z3 fusarium sp	373	3	12.5	17	2	Q95795_HUMAN	Q95795 homo sapien
301	3	12.5	15	2	Q7S219_NEUCR	Q7s219 neurospora	374	3	12.5	17	2	Q7KZ00_HUMAN	Q7kz00 homo sapien
302	3	12.5	15	2	Q43378_9LECA	Q4w378 neurospora	375	3	12.5	17	2	Q92727_HUMAN	Q92727 homo sapien
303	3	12.5	15	2	Q13377_HUMAN	Q13377 homo sapien	376	3	12.5	17	2	Q9UCD3_HUMAN	Q9ucd3 homo sapien
304	3	12.5	15	2	Q7M4R1_HUMAN	Q7m4r1 homo sapien	377	3	12.5	17	2	Q9UCP4_HUMAN	Q9ucp4 homo sapien
305	3	12.5	15	2	Q5CLX6_BOMJO	Q5clx6 bombyx mori	378	3	12.5	17	2	Q61238_ONCVO	Q61238 onchocerca
306	3	12.5	15	2	P82206_SCHJA	P82206 schistosoma	379	3	12.5	17	2	Q5BX20_SCHJA	Q5bx20 schistosoma
307	3	12.5	15	2	Q9TWE9_GALME	Q9twe9 galleria me	380	3	12.5	17	2	Q5K157_DROBP	Q5k157 drosophila
308	3	12.5	15	2	Q7RHM0_PLAYO	Q7rhm0 plasmodium	381	3	12.5	17	2	Q6E154_BIOGL	Q6e154 biophalari
309	3	12.5	15	2	Q4X8J7_PLACH	Q4x8j7 plasmodium	382	3	12.5	17	2	Q8HKG6_9ACAR	Q8hkg6 boophilus k
310	3	12.5	15	2	Q4XH30_PLACH	Q4xh30 plasmodium	383	3	12.5	17	2	Q7R6U3_PLAYO	Q7raj1 plasmodium
311	3	12.5	15	2	Q6JJD7_CANFA	Q6jjd7 canis famil	384	3	12.5	17	2	Q7RAJ1_PLAYO	Q7ra1 plasmodium
312	3	12.5	15	2	Q85C67_9ROSI	Q85c67 clusia mult	385	3	12.5	17	2	Q7RCI9_PLAYO	Q7rci9 plasmodium
313	3	12.5	15	2	Q85C68_9ROSI	Q85c68 clusia mino	386	3	12.5	17	2	Q7RQU2_PLAYO	Q7rqu2 plasmodium
314	3	12.5	15	2	Q85C69_9ROSI	Q85c69 clusia duc	387	3	12.5	17	2	Q4X3Y9_PLACH	Q4x3y9 plasmodium
315	3	12.5	15	2	Q85XD9_9ROSI	Q85xd9 clusia vale	388	3	12.5	17	2	Q4X480_PLACH	Q4x480 plasmodium
316	3	12.5	15	2	Q85X81_9ROSI	Q85x81 clusia-toxr	389	3	12.5	17	2	Q4X8E1_PLACH	Q4x8e1 plasmodium
317	3	12.5	15	2	Q85XE3_9ROSI	Q85xe3 clusia tocu	390	3	12.5	17	2	Q4XB01_PLACH	Q4xb01 plasmodium
318	3	12.5	15	2	Q85XE5_9ROSI	Q85xe5 clusia sten	391	3	12.5	17	2	Q4XBX8_PLACH	Q4xbx8 plasmodium
319	3	12.5	15	2	Q85XE7_9ROSI	Q85xe7 clusia rose	392	3	12.5	17	2	Q4XT04_PLACH	Q4xt04 plasmodium
320	3	12.5	15	2	Q85XE9_9ROSI	Q85xe9 clusia nemo	393	3	12.5	17	2	Q95JAI_PIG	Q95jai sus scrofa
321	3	12.5	15	2	Q85XF2_9ROSI	Q85xf2 clusia majo	394	3	12.5	17	2	Q714T4_9RHOD	Q714t4 rhodosorus
322	3	12.5	15	2	Q85XF4_9ROSI	Q85xf4 clusia lanc	395	3	12.5	17	2	Q7XY76_9ROSI	Q7xy76 kandelia ca
323	3	12.5	15	2	Q85XF6_9ROSI	Q85xf6 clusia inte	396	3	12.5	17	2	Q7YMZ1_9BRYO	Q7ymz1 porotrichum

397	3	12.5	17	2	Q7YMZ4_9BRVO	Q7ymz4	porothamniu	470	3	12.5	18	2	Q73559_9HIV1	Q73559	human	immun
398	3	12.5	17	2	Q7YN51_HOOLU	Q7yn51	hookeria lu	471	3	12.5	18	2	Q73561_9HIV1	Q73561	human	immun
399	3	12.5	17	2	Q85UP3_9BRVO	Q85up3	acrocladium	472	3	12.5	18	2	Q73563_9HIV1	Q73563	human	immun
400	3	12.5	17	2	Q8HAS3_MAIZE	Q8has3	zea mays (m	473	3	12.5	18	2	Q73565_9HIV1	Q73565	human	immun
401	3	12.5	17	2	Q8HCD7_MAIZE	Q8hcd7	zea mays (m	474	3	12.5	18	2	Q73567_9HIV1	Q73567	human	immun
402	3	12.5	17	2	Q9S7E8_ARATH	Q9s7e8	arabidopsis	475	3	12.5	18	2	Q73569_9HIV1	Q73569	human	immun
403	3	12.5	17	2	Q6UGR4_PETHY	Q6ugr4	petunia hyb	476	3	12.5	18	2	Q73571_9HIV1	Q73571	human	immun
404	3	12.5	17	2	Q7X4Q4_NODSP	Q7x4q4	nodularia s	477	3	12.5	18	2	Q73573_9HIV1	Q73573	human	immun
405	3	12.5	17	2	Q4ZGZ9_9CHRO	Q4zgz9	aphanocapea	478	3	12.5	18	2	Q73575_9HIV1	Q73575	human	immun
406	3	12.5	17	2	Q9QVC2_9MURI	Q9qvc2	rattus sp.	479	3	12.5	18	2	Q73577_9HIV1	Q73577	human	immun
407	3	12.5	17	2	Q9QVH8_9MURI	Q9qv8	mus sp. sup	480	3	12.5	18	2	Q73579_9HIV1	Q73579	human	immun
408	3	12.5	17	2	Q9QVK3_9MURI	Q9qvk3	rattus sp.	481	3	12.5	18	2	Q73581_9HIV1	Q73581	human	immun
409	3	12.5	17	2	Q8QTK3_MOUSE	Q8qt36	mus musculus	482	3	12.5	18	2	Q73583_9HIV1	Q73583	human	immun
410	3	12.5	17	2	Q6PV10_9HEPC	Q6pv10	hepatitis c	483	3	12.5	18	2	Q73585_9HIV1	Q73585	human	immun
411	3	12.5	17	2	Q6PV18_9HEPC	Q6pv18	hepatitis c	484	3	12.5	18	2	Q73587_9HIV1	Q73587	human	immun
412	3	12.5	17	2	Q6PV21_9HEPC	Q6pv21	hepatitis c	485	3	12.5	18	2	Q73589_9HIV1	Q73589	human	immun
413	3	12.5	17	2	Q9DPB5_BRARE	Q9dfb5	brachydanio	486	3	12.5	18	2	Q73591_9HIV1	Q73591	human	immun
414	3	12.5	17	2	Q73531_9HIV1	Q73531	human immun	487	3	12.5	18	2	Q73593_9HIV1	Q73593	human	immun
415	3	12.5	17	2	Q73533_9HIV1	Q73533	human immun	488	3	12.5	18	2	Q73595_9HIV1	Q73595	human	immun
416	3	12.5	17	2	Q73535_9HIV1	Q73535	human immun	489	3	12.5	18	2	Q73597_9HIV1	Q73597	human	immun
417	3	12.5	17	2	Q73537_9HIV1	Q73537	human immun	490	3	12.5	18	2	Q73599_9HIV1	Q73599	human	immun
418	3	12.5	17	2	Q73539_9HIV1	Q73539	human immun	491	3	12.5	18	2	Q73601_9HIV1	Q73601	human	immun
419	3	12.5	17	2	Q73541_9HIV1	Q73541	human immun	492	3	12.5	18	2	Q73603_9HIV1	Q73603	human	immun
420	3	12.5	17	2	Q73543_9HIV1	Q73543	human immun	493	3	12.5	18	2	Q73605_9HIV1	Q73605	human	immun
421	3	12.5	17	2	Q73545_9HIV1	Q73545	human immun	494	3	12.5	18	2	Q73607_9HIV1	Q73607	human	immun
422	3	12.5	17	2	Q73547_9HIV1	Q73547	human immun	495	3	12.5	18	2	Q73609_9HIV1	Q73609	human	immun
423	3	12.5	17	2	Q78381_9HIV1	Q78381	human immun	496	3	12.5	18	2	Q73611_9HIV1	Q73611	human	immun
424	3	12.5	18	1	AROF_STRMB	P80575	streptomyce	497	3	12.5	18	2	Q73613_9HIV1	Q73613	human	immun
425	3	12.5	18	1	SULT_1CTPU	P82609	ictalurus p	498	3	12.5	18	2	Q73615_9HIV1	Q73615	human	immun
426	3	12.5	18	1	TAMP_STRMB	P83543	streptomyce	499	3	12.5	18	2	Q73617_9HIV1	Q73617	human	immun
427	3	12.5	18	2	Q7S757_NEUCR	Q7s757	neurospora	500	3	12.5	18	2	Q73619_9HIV1	Q73619	human	immun
428	3	12.5	18	2	Q9UC87_HUMAN	Q9uc87	homo sapien	501	3	12.5	18	2	Q73621_9HIV1	Q73621	human	immun
429	3	12.5	18	2	Q6LCK5_HUMAN	Q6lck5	homo sapien	502	3	12.5	18	2	Q73623_9HIV1	Q73623	human	immun
430	3	12.5	18	2	Q5BRP6_SCHJA	Q5brp6	schistosoma	503	3	12.5	18	2	Q73625_9HIV1	Q73625	human	immun
431	3	12.5	18	2	Q5BY25_SCHJA	Q5by25	schistosoma	504	3	12.5	18	2	Q73627_9HIV1	Q73627	human	immun
432	3	12.5	18	2	Q5K168_9DIPT	Q5k168	drosophila	505	3	12.5	18	2	Q73629_9HIV1	Q73629	human	immun
433	3	12.5	18	2	Q6JCM1_9HME	Q6jcm1	prenolepis	506	3	12.5	18	2	Q73631_9HIV1	Q73631	human	immun
434	3	12.5	18	2	Q8HK12_9ACAR	Q8hk12	apnonoma co	507	3	12.5	18	2	Q73633_9HIV1	Q73633	human	immun
435	3	12.5	18	2	Q9X778_9HYME	Q9x778	gryon sp. c	508	3	12.5	18	2	Q73635_9HIV1	Q73635	human	immun
436	3	12.5	18	2	Q4X7V0_PLACH	Q4x7v0	plasmidium	509	3	12.5	18	2	Q73637_9HIV1	Q73637	human	immun
437	3	12.5	18	2	Q4XHC9_PLACH	Q4xhc9	plasmidium	510	3	12.5	18	2	Q73639_9HIV1	Q73639	human	immun
438	3	12.5	18	2	Q4XKA7_PLACH	Q4xka7	plasmidium	511	3	12.5	18	2	Q73641_9HIV1	Q73641	human	immun
439	3	12.5	18	2	Q4Y8A5_PLACH	Q4y8a5	plasmidium	512	3	12.5	18	2	Q73643_9HIV1	Q73643	human	immun
440	3	12.5	18	2	Q4YAB9_PLABE	Q4yab9	plasmidium	513	3	12.5	18	2	Q73645_9HIV1	Q73645	human	immun
441	3	12.5	18	2	Q4YIB9_PLABE	Q4yib9	plasmidium	514	3	12.5	18	2	Q73647_9HIV1	Q73647	human	immun
442	3	12.5	18	2	Q4Z4N4_PLABE	Q4z4n4	plasmidium	515	3	12.5	18	2	Q73649_9HIV1	Q73649	human	immun
443	3	12.5	18	2	Q4Z7I4_PLABE	Q4z7i4	plasmidium	516	3	12.5	18	2	Q73651_9HIV1	Q73651	human	immun
444	3	12.5	18	2	Q7M3F4_RABIT	Q7m3f4	oryctolagus	517	3	12.5	18	2	Q73653_9HIV1	Q73653	human	immun
445	3	12.5	18	2	Q9TQR0_PIG	Q9tqr0	sus scrofa	518	3	12.5	18	2	Q73920_9HIV1	Q73920	human	immun
446	3	12.5	18	2	Q9TRG2_RABIT	Q9trg2	oryctolagus	519	3	12.5	18	2	Q73921_9HIV1	Q73921	human	immun
447	3	12.5	18	2	Q9TS26_PIG	Q9ts26	sus scrofa	520	3	12.5	18	2	Q73921_9HIV1	Q73921	human	immun
448	3	12.5	18	2	O64353_BPN15	O64353	bacterioph	521	3	12.5	19	1	CUCN_CUCMA	P84158	cucurbita m	
449	3	12.5	18	2	O19969_GOSAR	O19969	gossypium a	522	3	12.5	19	1	CX6A2_SHEEP	P61901	ovis aries	
450	3	12.5	18	2	O19979_GOSDA	O19979	gossypium d	523	3	12.5	19	1	LPRM_STAATU	P03063	staphylococ	
451	3	12.5	18	2	O85UNI_9BRVO	O85un1	camptochaet	524	3	12.5	19	2	Q07603_HUMAN	Q07603	homo sapien	
452	3	12.5	18	2	Q9S7E5_ARATH	Q9s7e5	arabidopsis	525	3	12.5	19	2	Q9UDB7_HUMAN	Q9udb7	homo sapien	
453	3	12.5	18	2	Q9ZG65_CHLTR	Q9zg65	chlamydia t	526	3	12.5	19	2	Q9Y3R8_HUMAN	Q9y3r8	homo sapien	
454	3	12.5	18	2	Q9R334_PSEME	Q9r334	pseudomonas	527	3	12.5	19	2	Q7M4R0_HUMAN	Q7m4r0	homo sapien	
455	3	12.5	18	2	Q49250_MYCGE	Q49250	mycoplasma	528	3	12.5	19	2	Q9BVX6_HUMAN	Q9bv6	homo sapien	
456	3	12.5	18	2	Q61840_MOUSE	Q61840	mus musculus	529	3	12.5	19	2	Q9BVX6_HUMAN	Q9bv6	homo sapien	
457	3	12.5	18	2	Q61CE8_MOUSE	Q61ce8	mus musculus	530	3	12.5	19	2	Q4X4E2_PLACH	Q4x4e2	plasmidium	
458	3	12.5	18	2	Q99MD5_MOUSE	Q99md5	mus musculus	531	3	12.5	19	2	Q4XAW0_PLACH	Q4xaw0	plasmidium	
459	3	12.5	18	2	Q77WL5_ADE04	Q77wl5	human adeno	532	3	12.5	19	2	Q4XQC6_PLACH	Q4xqc6	plasmidium	
460	3	12.5	18	2	Q9DSS9_ADE04	Q9dss9	human adeno	533	3	12.5	19	2	Q4XUR2_PLACH	Q4xur2	plasmidium	
461	3	12.5	18	2	Q9W9C1_ADE04	Q9w9c1	human adeno	534	3	12.5	19	2	Q4Y326_PLACH	Q4y326	plasmidium	
462	3	12.5	18	2	Q94PS2_9PERC	Q94ps2	macropodus	535	3	12.5	19	2	Q4Y4A8_PLACH	Q4y4a8	plasmidium	
463	3	12.5	18	2	Q9PSD2_CHICK	Q9psd2	gallus gall	536	3	12.5	19	2	Q4YJ03_PLABE	Q4yju3	plasmidium	
464	3	12.5	18	2	Q73517_9HIV1	Q73517	human immun	537	3	12.5	19	2	Q4YSN2_PLABE	Q4ysn2	plasmidium	
465	3	12.5	18	2	Q73523_9HIV1	Q73523	human immun	538	3	12.5	19	2				
466	3	12.5	18	2	Q73549_9HIV1	Q73549	human immun	539	3	12.5	19	2				
467	3	12.5	18	2	Q73551_9HIV1	Q73551	human immun	540	3	12.5	19	2				
468	3	12.5	18	2	Q73553_9HIV1	Q73553	human immun	541	3	12.5	19	2				
469	3	12.5	18	2	Q73555_9HIV1	Q73555	human immun	542	3	12.5	19	2				

543	3	12.5	19	2	Q7M221_SHEEP	Q7m221 ovis aries	616	3	12.5	20	2	Q426T1_PLABE	Q426t1 plasmodium
544	3	12.5	19	2	Q7M222_PIG	Q7m222 sus scrofa	617	3	12.5	20	2	Q7M357_PIG	Q7m357 sus scrofa
545	3	12.5	19	2	Q82685_GERHY	Q82685 gerbera hyb	618	3	12.5	20	2	Q7M2X3_BOVIN	Q7m2x3 bos taurus
546	3	12.5	19	2	Q39381_BRAOL	Q39381 brassica ol	619	3	12.5	20	2	Q38458_BPPH1	Q38458 bacterioph
547	3	12.5	19	2	Q41466_SOLITU	Q41466 solanum tub	620	3	12.5	20	2	Q41468_SOLITU	Q41468 solanum tub
548	3	12.5	19	2	Q41471_SOLITU	Q41471 solanum tub	621	3	12.5	20	2	Q41469_SOLITU	Q41469 solanum tub
549	3	12.5	19	2	Q41474_SOLITU	Q41474 solanum tub	622	3	12.5	20	2	Q41475_SOLITU	Q41475 solanum tub
550	3	12.5	19	2	Q8LVH6_9STRA	Q8lvh6 aulacoseira	623	3	12.5	20	2	Q5J4U3_9POAL	Q5j4u3 phyllostach
551	3	12.5	19	2	Q8MCJ2_9STRA	Q8mcj2 aulacoseira	624	3	12.5	20	2	Q5J4U4_9ORYZ	Q5j4u4 chikusichlo
552	3	12.5	19	2	Q8MCJ2_9STRA	Q8mcj2 aulacoseira	625	3	12.5	20	2	Q5J4U5_9ORYZ	Q5j4u5 hygoriza a
553	3	12.5	19	2	Q9S8G6_COLES	Q9s8g6 colocasia e	626	3	12.5	20	2	Q5J4U6_9ORYZ	Q5j4u6 luziola lei
554	3	12.5	19	2	Q562K7_ARATHP	Q562k7 arabidopsis	627	3	12.5	20	2	Q5J4U7_9ORYZ	Q5j4u7 rhyrachoryza
555	3	12.5	19	2	Q05601_PSESP	Q05601 pseudomonas	628	3	12.5	20	2	Q5J4U8_9ORYZ	Q5j4u8 rotamophila
556	3	12.5	19	2	Q07479_STRTP	Q07479 streptococc	629	3	12.5	20	2	Q5J4U9_9ORYZ	Q5j4u9 prophytoch
557	3	12.5	19	2	Q57313_9STAP	Q57313 staphylococ	630	3	12.5	20	2	Q5J4V0_9ORYZ	Q5j4v0 zizaniopsi
558	3	12.5	19	2	Q5D098_9STAP	Q5d098 staphylococ	631	3	12.5	20	2	Q5J4V1_9ORYZ	Q5j4v1 zizania lat
559	3	12.5	19	2	Q799A5_STRAU	Q799a5 staphylococ	632	3	12.5	20	2	Q5J4V2_9ORYZ	Q5j4v2 leersia hex
560	3	12.5	19	2	Q799E4_STARF	Q799e4 staphylococ	633	3	12.5	20	2	Q5J4V3_9ORYZ	Q5j4v3 leersia tis
561	3	12.5	19	2	Q7AY86_9STAP	Q7ay86 staphylococ	634	3	12.5	20	2	Q5J4V4_9ORYZ	Q5j4v4 oryza granu
562	3	12.5	19	2	Q7NS42_NODSP	Q7ns42 nodularia s	635	3	12.5	20	2	Q5J4V5_9ORYZ	Q5j4v5 oryza austr
563	3	12.5	19	2	Q9EWB6_STAIN	Q9ewb6 staphylococ	636	3	12.5	20	2	Q5J4V6_9ORYZ	Q5j4v6 oryza achle
564	3	12.5	19	2	Q45558_BACSH	Q45558 bacillus sp	637	3	12.5	20	2	Q5J4V7_9ORYZ	Q5j4v7 oryza coarc
565	3	12.5	19	2	Q57012_STRAU	Q57012 staphylococ	638	3	12.5	20	2	Q5J4V8_9ORYZ	Q5j4v8 oryza brach
566	3	12.5	19	2	Q7MOQ1_PSEPU	Q7moq1 pseudomonas	639	3	12.5	20	2	Q5J4V9_9ORYZ	Q5j4v9 oryza longi
567	3	12.5	19	2	Q799W9_STAHO	Q799w9 staphylococ	640	3	12.5	20	2	Q5J4W0_9ORYZ	Q5j4w0 oryza offic
568	3	12.5	19	2	Q4JH5 STAU	Q4jhs staphylococ	641	3	12.5	20	2	Q5J4W1_ORYPU	Q5j4w1 oryza punct
569	3	12.5	19	2	Q5HNP7_STAEO	Q5hnp7 staphylococ	642	3	12.5	20	2	Q5J4W2_ORYSA	Q5j4w2 oryza sattiv
570	3	12.5	19	2	P70242_MOUSE	P70242 mus musculu	643	3	12.5	20	2	P82940_HORVU	P82940 hordeum vul
571	3	12.5	19	2	P97555_RAT	P97555 rattus norv	644	3	12.5	20	2	P83423_9ROSA	P83423 morus nigra
572	3	12.5	19	2	Q78DW0_RAT	Q78dw0 rattus norv	645	3	12.5	20	2	Q9S8B8_LUPAL	Q9s8b8 lupinus alb
573	3	12.5	19	2	Q80263_MOUSE	Q80263 mus musculu	646	3	12.5	20	2	Q9S8H1_HORVU	Q9s8h1 hordeum vul
574	3	12.5	19	2	Q8K520_MOUSE	Q8k520 mus musculu	647	3	12.5	20	2	Q9S8J5_PSPOTE	Q9s8j5 psophocarpu
575	3	12.5	19	2	Q921B7_MOUSE	Q921b7 mus musculu	648	3	12.5	20	2	Q9S8K0_SOLITU	Q9s8k0 solanum tub
576	3	12.5	19	2	Q9QVN1_9MURI	Q9qvn1 rattus sp.	649	3	12.5	20	2	Q9S8T0_ARTIN	Q9s8t0 artocarpus
577	3	12.5	19	2	Q652S2_MOUSE	Q652s2 mus musculu	650	3	12.5	20	2	Q9S930_SOYBN	Q9s930 glycine max
578	3	12.5	19	2	Q6L8G3_9ZZZZ	Q6l8g3 plaemid prj	651	3	12.5	20	2	Q9SAN5_ARATH	Q9san5 arabidopsis
579	3	12.5	19	2	Q79DT6_9ZZZZ	Q79dt6 plaemid prj	652	3	12.5	20	2	Q9TK2 PEA	Q9tk2 pieum sattiv
580	3	12.5	19	2	Q65747_9REOV	Q65747 bluetongue	653	3	12.5	20	2	Q9S8B2_PRAVU	Q9s8b2 phaseolus v
581	3	12.5	19	2	Q9YQW7_9GEMI	Q9yqw7 tomato yell	654	3	12.5	20	2	Q51950_CHLTR	Q51950 chlamydia t
582	3	12.5	19	2	Q7LZW5_HV1	Q7lwz5 human herpe	655	3	12.5	20	2	Q51952_CHLTR	Q51952 chlamydia t
583	3	12.5	19	2	Q85728_9GAMR	Q85728 spleen necr	656	3	12.5	20	2	Q7BVQ6_MYCHY	Q7bvq6 mycoplasma
584	3	12.5	20	1	CER1_CICAR	C83987 cicor ariet	657	3	12.5	20	2	Q7M0N9_NEIME	Q7m0n9 neisseria m
585	3	12.5	20	1	COXM_THUOB	P80981 thunnus obe	658	3	12.5	20	2	Q7X4Q6_NODSP	Q7x4q6 nodularia s
586	3	12.5	20	1	LEC1_ARTIN	P18571 artocarpus	659	3	12.5	20	2	Q8KT83_RICHE	Q8kt83 rickettsia
587	3	12.5	20	1	LEC3_ARTIN	P18573 artocarpus	660	3	12.5	20	2	Q9R4A6_HYDTH	Q9r4a6 hydrogenoba
588	3	12.5	20	1	PGK_BACE	P83075 bacillus ce	661	3	12.5	20	2	Q9R551_BACME	Q9r551 bacillus me
589	3	12.5	20	1	PLS_LUFLU	P83367 lupinus lut	662	3	12.5	20	2	Q9R5Q4_BURCE	Q9r5q4 burkholderi
590	3	12.5	20	1	RIPX_CUCPE	P80750 cucurbita p	663	3	12.5	20	2	Q96173_9VIBR	Q96173 vibrio sp.
591	3	12.5	20	2	P82263_ASPFU	P82263 aspergillus	664	3	12.5	20	2	Q56130_SALTY	Q56130 salmonella
592	3	12.5	20	2	Q9URC7_YEAST	Q9urc7 saccharomyc	665	3	12.5	20	2	Q64619_RAT	Q64619 rattus norv
593	3	12.5	20	2	Q33623_MAGGR	Q33623 magnaporthe	666	3	12.5	20	2	Q6V0Z2_MUSSH	Q6v0z2 mus apretus
594	3	12.5	20	2	Q7MAQ3_HUMAN	Q7maq3 homo sapien	667	3	12.5	20	2	Q7M028_9MURI	Q7m028 rattus sp.
595	3	12.5	20	2	Q9NZC6_HUMAN	Q9nzc6 homo sapien	668	3	12.5	20	2	Q80Z28_MOUSE	Q80z28 mus musculu
596	3	12.5	20	2	Q9UC20_HUMAN	Q9uc20 homo sapien	669	3	12.5	20	2	Q9ET00_MOUSE	Q9et00 mus musculu
597	3	12.5	20	2	Q9UC86_HUMAN	Q9uc86 homo sapien	670	3	12.5	20	2	Q9QVH2_9MURI	Q9qvhi2 rattus sp.
598	3	12.5	20	2	Q96B47_HUMAN	Q96b47 homo sapien	671	3	12.5	20	2	Q7M0E1_MBSAU	Q7m0e1 mesocricetu
599	3	12.5	20	2	Q9UMU3_HUMAN	Q9umu3 homo sapien	672	3	12.5	20	2	Q84860_9ENTO	Q84860 unidentified
600	3	12.5	20	2	Q37688_9HYME	Q37688 tetraponera	673	3	12.5	20	2	Q86941_9GNMA	Q86941 human herpe
601	3	12.5	20	2	Q5C711_SCHJA	Q5c711 schistosoma	674	3	12.5	20	2	Q86942_9GAMA	Q86942 human herpe
602	3	12.5	20	2	P82215_BOMMO	P82215 bombyx mori	675	3	12.5	20	2	Q912B0_9VIRU	Q912b0 human eryth
603	3	12.5	20	2	Q9GNL7_DROER	Q9gnl7 drosophila	676	3	12.5	20	2	Q912B2_PAVHB	Q912b2 human parvo
604	3	12.5	20	2	Q9TWM1_9TRYP	Q9twm1 trypanosoma	677	3	12.5	20	2	Q912B4_9VIRU	Q912b4 human eryth
605	3	12.5	20	2	Q7RLS2_PLAYO	Q7rls2 plasmodium	678	3	12.5	20	2	Q77859_9ORENI	Q77859 oreochromis
606	3	12.5	20	2	Q7BSI9_PLAYO	Q7bsi9 plasmodium	679	3	12.5	20	2	Q7LZ35_RANCA	Q7l236 rana cateeb
607	3	12.5	20	2	Q4XFU6_PLACH	Q4xfu6 plasmodium	680	3	12.5	20	2	Q918U3_FUGRU	Q918u3 fugu rubrip
608	3	12.5	20	2	Q4XKU0_PLACH	Q4xku0 plasmodium	681	3	12.5	20	2	Q9PS63_CHICK	Q9ps63 gallus gall
609	3	12.5	20	2	Q4XU12_PLACH	Q4xu12 plasmodium	682	3	12.5	20	2	Q9PSH5_CHICK	Q9psh5 gallus gall
610	3	12.5	20	2	Q4Y2H3_PLACH	Q4y2h3 plasmodium	683	3	12.5	20	2	Q73917_9HIV1	Q73917 human immun
611	3	12.5	20	2	Q4VB80_PLABE	Q4vb80 plasmodium	684	3	12.5	20	2	Q73918_9HIV1	Q73918 human immun
612	3	12.5	20	2	Q4YCL5_PLABE	Q4ycl5 plasmodium	685	3	12.5	20	2	Q78486_9HIV1	Q78486 human immun
613	3	12.5	20	2	Q4YJK5_PLABE	Q4yjk5 plasmodium	686	3	12.5	21	1	CLH2_CHEAL	P59678 chenopodium
614	3	12.5	20	2	Q42105_PLABE	Q42105 plasmodium	687	3	12.5	21	1	LEC2_ARTIN	P18672 artocarpus
615	3	12.5	20	2	Q42422_PLABE	Q42422 plasmodium	688	3	12.5	21	2	Q9UW10_9EURY	Q9uw10 thermococcu

689	3	12.5	21	2	Q96W03_FUSOX	Q96W03 fusarium ox	762	3	12.5	21	2	Q958Y4_LUPAR	Q958Y4 lupinus arb
690	3	12.5	21	2	Q16366_HUMAN	Q16366 homo sapien	763	3	12.5	21	2	Q56YE9_ARATH	Q56YE9 arabidopsis
691	3	12.5	21	2	Q6LD69_HUMAN	Q6LD69 homo sapien	764	3	12.5	21	2	Q6SKV4_9NARC	Q6SKV4 trichocola
692	3	12.5	21	2	Q9UC66_HUMAN	Q9UC66 homo sapien	765	3	12.5	21	2	Q7X6U6_CAPBU	Q7X6U6 capsella bu
693	3	12.5	21	2	Q9UCC5_HUMAN	Q9UCC5 homo sapien	766	3	12.5	21	2	Q7X6U5_9BRAS	Q7X6U5 capsella ru
694	3	12.5	21	2	Q9UCH7_HUMAN	Q9UCH7 homo sapien	767	3	12.5	21	2	Q7X6U4_9BRAS	Q7X6U4 gullenia f
695	3	12.5	21	2	Q6LAB3_HUMAN	Q6LAB3 homo sapien	768	3	12.5	21	2	Q7X6U3_9BRAS	Q7X6U3 lepidium ph
696	3	12.5	21	2	Q75MT3_HUMAN	Q75MT3 homo sapien	769	3	12.5	21	2	Q7X6U2_THLAR	Q7X6U2 thlaspi arv
697	3	12.5	21	2	Q6LEI9_STRPU	Q6LEI9 strongyloce	770	3	12.5	21	2	Q44611_9ENTR	Q44611 buchnera ap
698	3	12.5	21	2	Q7R9W2_PLAYO	Q7R9W2 plasmodium	771	3	12.5	21	2	Q51540_PSEAE	Q51540 pseudomonas
699	3	12.5	21	2	Q7RG18_PLAYO	Q7RG18 plasmodium	772	3	12.5	21	2	Q9R4C5_9RHIZ	Q9R4C5 agrobacteri
700	3	12.5	21	2	Q4X3C0_PLAYO	Q4X3C0 plasmodium	773	3	12.5	21	2	Q9R4L4_HELPY	Q9R4L4 helicobacte
701	3	12.5	21	2	Q4X3C0_PLACH	Q4X3C0 plasmodium	774	3	12.5	21	2	Q9R4P4_BREDI	Q9R4P4 brevundimon
702	3	12.5	21	2	Q4X406_PLACH	Q4X406 plasmodium	775	3	12.5	21	2	P70861_BORBU	P70861 borrelia bu
703	3	12.5	21	2	Q4X813_PLACH	Q4X813 plasmodium	776	3	12.5	21	2	Q6GC12_STAAS	Q6GC12 staphylococ
704	3	12.5	21	2	Q4X813_PLACH	Q4X813 plasmodium	777	3	12.5	21	2	Q6GJJ7_STAAS	Q6GJJ7 staphylococ
705	3	12.5	21	2	Q4XK54_PLACH	Q4XK54 plasmodium	778	3	12.5	21	2	Q8NY10_STAAN	Q8NY10 staphylococ
706	3	12.5	21	2	Q4XKF6_PLACH	Q4XKF6 plasmodium	779	3	12.5	21	2	Q9QVK2_9MURI	Q9QVK2 rattus sp.
707	3	12.5	21	2	Q4XEC3_PLACH	Q4XEC3 plasmodium	780	3	12.5	21	2	Q7M035_RAT	Q7M035 mus spretus
708	3	12.5	21	2	Q4Y4Z3_PLACH	Q4Y4Z3 plasmodium	781	3	12.5	21	2	Q62538_MUSSP	Q62538 mus spretus
709	3	12.5	21	2	Q4Y553_PLACH	Q4Y553 plasmodium	782	3	12.5	21	2	Q84200_9PARA	Q84200 sendai viru
710	3	12.5	21	2	Q4YBBS_PLABE	Q4YBBS plasmodium	783	3	12.5	21	2	Q84204_9PARA	Q84204 sendai viru
711	3	12.5	21	2	Q4YGI0_PLABE	Q4YGI0 plasmodium	784	3	12.5	21	2	Q9PRW4_CROAT	Q9PRW4 crotalus at
712	3	12.5	21	2	Q4YKU4_PLABE	Q4YKU4 plasmodium	785	3	12.5	22	1	23KD_BACST	P80166 bacillus st
713	3	12.5	21	2	Q4YLA8_PLABE	Q4YLA8 plasmodium	786	3	12.5	22	1	ONPH_PASGA	P80454 pasteurella
714	3	12.5	21	2	Q4YLX0_PLABE	Q4YLX0 plasmodium	787	3	12.5	22	1	ONPH_PASVO	P80452 pasteurella
715	3	12.5	21	2	Q4YTG9_PLABE	Q4YTG9 plasmodium	788	3	12.5	22	1	PSBQ_ORYSA	P87646 oryza sativ
716	3	12.5	21	2	Q4YVJ5_PLABE	Q4YVJ5 plasmodium	789	3	12.5	22	1	Q7SE28_NEUCR	Q7SE28 neurospora
717	3	12.5	21	2	Q4YVY7_PLABE	Q4YVY7 plasmodium	790	3	12.5	22	2	Q96TJ3_FUSOX	Q96TJ3 fusarium ox
718	3	12.5	21	2	Q4YZW5_PLABE	Q4YZW5 plasmodium	791	3	12.5	22	2	Q96W00_FUSOX	Q96W00 fusarium ox
719	3	12.5	21	2	Q4Z1R2_PLABE	Q4Z1R2 plasmodium	792	3	12.5	22	2	Q96W04_FUSOX	Q96W04 fusarium ox
720	3	12.5	21	2	Q4Z1X1_PLABE	Q4Z1X1 plasmodium	793	3	12.5	22	2	Q9Y6S3_HUMAN	Q9Y6S3 homo sapien
721	3	12.5	21	2	Q4Z7X2_PLABE	Q4Z7X2 plasmodium	794	3	12.5	22	2	Q5BVS2_SCHJA	Q5BVS2 schistosoma
722	3	12.5	21	2	Q86429_CAPHI	Q86429 capra hircu	795	3	12.5	22	2	Q5BY92_SCHJA	Q5BY92 schistosoma
723	3	12.5	21	2	Q865A0_CAPHI	Q865A0 capra hircu	796	3	12.5	22	2	Q5BYM6_SCHJA	Q5BYM6 schistosoma
724	3	12.5	21	2	Q5Q23_9CAUD	Q5Q23 gossypium a	797	3	12.5	22	2	Q5C482_SCHJA	Q5C482 schistosoma
725	3	12.5	21	2	Q63060_GOSAR	Q63060 gossypium a	798	3	12.5	22	2	Q6VYEO_9NEOP	Q6VYEO heliconius
726	3	12.5	21	2	Q63061_GOSHI	Q63061 gossypium h	799	3	12.5	22	2	Q9XN00_BOOMI	Q9XN00 boophilus m
727	3	12.5	21	2	Q63062_GOSBA	Q63062 gossypium b	800	3	12.5	22	2	Q7RMA3_PLAYO	Q7RMA3 plasmodium
728	3	12.5	21	2	Q63063_GOSTO	Q63063 gossypium t	801	3	12.5	22	2	Q7RTF5_PLAYO	Q7RTF5 plasmodium
729	3	12.5	21	2	Q63064_GOSMU	Q63064 gossypium m	802	3	12.5	22	2	Q4X508_PLACH	Q4X508 plasmodium
730	3	12.5	21	2	Q63065_GOSDA	Q63065 gossypium d	803	3	12.5	22	2	Q4XB74_PLACH	Q4XB74 plasmodium
731	3	12.5	21	2	Q41559_WHEAT	Q41559 triticum ae	804	3	12.5	22	2	Q4XC36_PLACH	Q4XC36 plasmodium
732	3	12.5	21	2	Q41564_WHEAT	Q41564 triticum ae	805	3	12.5	22	2	Q4XH35_PLACH	Q4XH35 plasmodium
733	3	12.5	21	2	Q41566_WHEAT	Q41566 triticum ae	806	3	12.5	22	2	Q4XK15_PLACH	Q4XK15 plasmodium
734	3	12.5	21	2	Q6Y312_9BRYO	Q6Y312 thamnobryum	807	3	12.5	22	2	Q4XN20_PLACH	Q4XN20 plasmodium
735	3	12.5	21	2	Q7M265_SPTOL	Q7M265 spinacia ol	808	3	12.5	22	2	Q4XP53_PLACH	Q4XP53 plasmodium
736	3	12.5	21	2	Q7X6U1_9BRAS	Q7X6U1 lepidium sq	809	3	12.5	22	2	Q4XUD0_PLACH	Q4XUD0 plasmodium
737	3	12.5	21	2	Q7X931_9BRAS	Q7X931 streptanthu	810	3	12.5	22	2	Q4Y221_PLACH	Q4Y221 plasmodium
738	3	12.5	21	2	Q7X934_9BRAS	Q7X934 erysimum ch	811	3	12.5	22	2	Q4Y4T1_PLACH	Q4Y4T1 plasmodium
739	3	12.5	21	2	Q7X935_9BRAS	Q7X935 diploxaxis	812	3	12.5	22	2	Q4YCL3_PLABE	Q4YCL3 plasmodium
740	3	12.5	21	2	Q7X936_9BRAS	Q7X936 cakile mari	813	3	12.5	22	2	Q4YEM6_PLABE	Q4YEM6 plasmodium
741	3	12.5	21	2	Q7X937_9BRAS	Q7X937 thysanocarp	814	3	12.5	22	2	Q4YEW3_PLABE	Q4YEW3 plasmodium
742	3	12.5	21	2	Q7X938_CAMSA	Q7X938 camelina ea	815	3	12.5	22	2	Q4YFH9_PLABE	Q4YFH9 plasmodium
743	3	12.5	21	2	Q7X939_9BRAS	Q7X939 conringia o	816	3	12.5	22	2	Q4YGG6_PLABE	Q4YGG6 plasmodium
744	3	12.5	21	2	Q7X940_ARALY	Q7X940 arabidopsis	817	3	12.5	22	2	Q4YJG1_PLABE	Q4YJG1 plasmodium
745	3	12.5	21	2	Q7X941_9BRAS	Q7X941 nasturtium	818	3	12.5	22	2	Q4YJ33_PLABE	Q4YJ33 plasmodium
746	3	12.5	21	2	Q7X942_9BRAS	Q7X942 erysimum ea	819	3	12.5	22	2	Q4Z6P7_PLABE	Q4Z6P7 plasmodium
747	3	12.5	21	2	Q7X943_9BRAS	Q7X943 erysimum ca	820	3	12.5	22	2	Q4Z7X1_PLABE	Q4Z7X1 plasmodium
748	3	12.5	21	2	Q7X944_9BRAS	Q7X944 draba corru	821	3	12.5	22	2	Q02830_RABIT	Q02830 oryctolagus
749	3	12.5	21	2	Q7X945_RAPSA	Q7X945 raphanus sa	822	3	12.5	22	2	Q0WBC7_9ROSI	Q0WBC7 cucurbita e
750	3	12.5	21	2	Q7X946_9BRAS	Q7X946 arabis gunn	823	3	12.5	22	2	Q7YMB2_9BRYO	Q7YMB2 dicnemon ca
751	3	12.5	21	2	Q7X947_OLIFU	Q7X947 olimarabido	824	3	12.5	22	2	Q7YMB5_9BRYO	Q7YMB5 eucaleucobr
752	3	12.5	21	2	Q7X948_9BRAS	Q7X948 lobularia m	825	3	12.5	22	2	Q7YMB7_9BRYO	Q7YMB7 eucaemtodon
753	3	12.5	21	2	Q7X949_BRAOA	Q7X949 brassica ol	826	3	12.5	22	2	Q85CR4_ARATH	Q85CR4 arabidopsis
754	3	12.5	21	2	Q7X950_9BRAS	Q7X950 eruca sativ	827	3	12.5	22	2	Q85CR5_9BRAS	Q85CR5 arabidopsis
755	3	12.5	21	2	Q7X951_9BRAS	Q7X951 lepidium af	828	3	12.5	22	2	Q85513_CHLTR	Q85513 chlamydia t
756	3	12.5	21	2	Q7X952_9BRAS	Q7X952 arabidopsis	829	3	12.5	22	2	Q85515_CHLTR	Q85515 chlamydia t
757	3	12.5	21	2	Q7X953_9BRAS	Q7X953 berteroa in	830	3	12.5	22	2	Q85518_CHLTR	Q85518 chlamydia t
758	3	12.5	21	2	Q7X954_BARVU	Q7X954 barbarea vi	831	3	12.5	22	2	Q85524_CHLTR	Q85524 chlamydia t
759	3	12.5	21	2	Q85UQ3_9BRYO	Q85UQ3 meteorium i	832	3	12.5	22	2	Q44609_9ENTR	Q44609 buchnera ap
760	3	12.5	21	2	Q8GT69_MALDO	Q8GT69 malus domes	833	3	12.5	22	2	Q53516_RHITR	Q53516 rhizobium t
761	3	12.5	21	2	Q8WBC3_CUCPE	Q8WBC3 cucurbita p	834	3	12.5	22	2	Q57226_CHLTR	Q57226 chlamydia t

835	3	12.5	22	2	2	Q616B1_ECOLI	Q616D1_escherichia	908	3	12.5	23	2	2	Q8MFJ5_9FILI	Q8mfj5_hymenophyll
836	3	12.5	22	2	2	Q616B8_ECOLI	Q616b8_escherichia	909	3	12.5	23	2	2	Q8WBC5_CUCMO	Q8wbc5_cucurbita m
837	3	12.5	22	2	2	Q79DL8_CHLTR	Q79dl8_chlamydia t	910	3	12.5	23	2	2	Q9S893_ARAHV	Q9s893_arachis hyp
838	3	12.5	22	2	2	Q84EW2_LACPE	Q84ew2_lactobacill	911	3	12.5	23	2	2	Q9SC59_PICAB	Q9sc59_picea abies
839	3	12.5	22	2	2	Q93R63_YERPE	Q93r63_yersinia pe	912	3	12.5	23	2	2	Q9SC60_PICAB	Q9sc60_picea abies
840	3	12.5	22	2	2	Q9F5L1_ECOLI	Q9f5l1_escherichia	913	3	12.5	23	2	2	Q9SC61_PICAB	Q9sc61_picea abies
841	3	12.5	22	2	2	Q9R8J6_CHLTR	Q9r8j6_chlamydia t	914	3	12.5	23	2	2	Q8SUU4_ANTFO	Q8suu4_anthoceros
842	3	12.5	22	2	2	Q9R8J8_CHLTR	Q9r8j8_chlamydia t	915	3	12.5	23	2	2	Q9T3F1_9CHLO	Q9t3f1_bryopsis sp
843	3	12.5	22	2	2	Q9R8K1_CHLTR	Q9r8k1_chlamydia t	916	3	12.5	23	2	2	Q9T3F2_9CHLO	Q9t3f2_bryopsis sp
844	3	12.5	22	2	2	Q9R8K3_CHLTR	Q9r8k3_chlamydia t	917	3	12.5	23	2	2	Q9T3F3_9CHLO	Q9t3f3_bryopsis sp
845	3	12.5	22	2	2	Q9R8K5_CHLTR	Q9r8k5_chlamydia t	918	3	12.5	23	2	2	Q9T4C9_9CHLO	Q9t4c9_bryopsis sp
846	3	12.5	22	2	2	Q9R8K8_CHLTR	Q9r8k8_chlamydia t	919	3	12.5	23	2	2	Q9T4Q8_9CHLO	Q9t4q8_bryopsis sp
847	3	12.5	22	2	2	Q9R8L3_CHLTR	Q9r8l3_chlamydia t	920	3	12.5	23	2	2	Q9T4R9_9CHLO	Q9t4r9_bryopsis sp
848	3	12.5	22	2	2	Q9R8L9_CHLTR	Q9r8l9_chlamydia t	921	3	12.5	23	2	2	Q9THS4_9CHLO	Q9ths4_bryopsis sp
849	3	12.5	22	2	2	Q9R8L9_CHLTR	Q9r8l9_chlamydia t	922	3	12.5	23	2	2	Q9THS5_9CHLO	Q9ths5_bryopsis sp
850	3	12.5	22	2	2	Q9R8M2_CHLTR	Q9r8m2_chlamydia t	923	3	12.5	23	2	2	Q9TKG7_9CHLO	Q9tkg7_lambia anta
851	3	12.5	22	2	2	Q9R8M9_CHLTR	Q9r8m9_chlamydia t	924	3	12.5	23	2	2	Q5O6W7_9ROSA	Q5o6w7_ficus colub
852	3	12.5	22	2	2	Q9R8N3_CHLTR	Q9r8n3_chlamydia t	925	3	12.5	23	2	2	Q04274_BORPE	Q04274_bordetella
853	3	12.5	22	2	2	Q9R8N7_CHLTR	Q9r8n7_chlamydia t	926	3	12.5	23	2	2	Q59A23_NODSP	Q59a23_nodularia s
854	3	12.5	22	2	2	Q9R8P3_CHLTR	Q9r8p3_chlamydia t	927	3	12.5	23	2	2	Q8GL16_BORBU	Q8gl16_borrelia bu
855	3	12.5	22	2	2	Q9R8P3_CHLTR	Q9r8p3_chlamydia t	928	3	12.5	23	2	2	Q8KHT3_MYCHO	Q8kht3_mycoplasma
856	3	12.5	22	2	2	Q9R8P7_CHLTR	Q9r8p7_chlamydia t	929	3	12.5	23	2	2	Q8AJ07_VIOBE	Q8aj07_vibrio fisc
857	3	12.5	22	2	2	Q9S551_ACTPL	Q9s551_actinobacil	930	3	12.5	23	2	2	Q9R3Y4_CLOPE	Q9r3y4_clostridium
858	3	12.5	22	2	2	Q9KAT7_BACHD	Q9kat7_bacillus ha	931	3	12.5	23	2	2	Q26030_HELPY	Q26030_helicobacte
859	3	12.5	22	2	2	Q9QVE0_9MURI	Q9qve0_mus sp. . s	932	3	12.5	23	2	2	Q6GAM3_STAAS	Q6gam3_staphylococ
860	3	12.5	22	2	2	Q9QWB6_9MURI	Q9qwb6_mus sp. . s	933	3	12.5	23	2	2	Q6GCP4_STAAR	Q6gcp4_staphylococ
861	3	12.5	22	2	2	Q4H2C4_MESAU	Q4h2c4_mesocricetu	934	3	12.5	23	2	2	Q8VDS5_MOUSE	Q8vds5_mus muscucu
862	3	12.5	22	2	2	Q765Z1_CHICK	Q765z1_gallus gall	935	3	12.5	23	2	2	Q61948_MOUSE	Q61948_mus muscucu
863	3	12.5	22	2	2	Q7T191_CHICK	Q7t191_gallus gall	936	3	12.5	23	2	2	Q9S553_MOUSE	Q9s553_mus muscucu
864	3	12.5	22	2	2	Q7T191_CHICK	Q7t191_gallus gall	937	3	12.5	23	2	2	Q8CB74_MOUSE	Q8cb74_mus muscucu
865	23	12.5	23	1	1	APF2_BRANA	P30226_brassica na	938	3	12.5	23	2	2	Q6H979_9VIRU	Q6h979_torque teno
866	3	12.5	23	1	1	PA24_BOTAS	Q9prt7_bothrops as	939	3	12.5	23	2	2	Q6H983_9VIRU	Q6h983_torque teno
867	3	12.5	23	1	1	YLIC1_ACIGB	P46365_acinetobact	940	3	12.5	23	2	2	Q91KZ6_9MONO	Q91kz6_human metap
868	3	12.5	23	1	1	YFMH_BACSU	Q43990_bacillus su	941	3	12.5	23	2	2	Q91KZ7_9MONO	Q91kz7_human metap
869	3	12.5	23	2	2	O14431_CRYPA	O14431_cryphonectr	942	3	12.5	23	2	2	Q91KZ8_9MONO	Q91kz8_human metap
870	3	12.5	23	2	2	Q96TQ0_FUSOX	Q96tq0_fusarium ox	943	3	12.5	23	2	2	Q91KZ9_9MONO	Q91kz9_human metap
871	3	12.5	23	2	2	Q16209_HUMAN	Q16209_homo sapien	944	3	12.5	23	2	2	Q91L00_9MONO	Q91l00_human metap
872	3	12.5	23	2	2	Q8N674_HUMAN	Q8n674_homo sapien	945	3	12.5	23	2	2	Q91L01_9MONO	Q91l01_human metap
873	3	12.5	23	2	2	Q96F96_HUMAN	Q96f96_homo sapien	946	3	12.5	23	2	2	Q91L02_9MONO	Q91l02_human metap
874	3	12.5	23	2	2	Q9NS07_HUMAN	Q9ns07_homo sapien	947	3	12.5	23	2	2	Q91L03_9MONO	Q91l03_human metap
875	3	12.5	23	2	2	Q5BR34_SCHJA	Q5br34_schistosoma	948	3	12.5	23	2	2	Q9PSA8_XENBO	Q9psa8_xenopus bor
876	3	12.5	23	2	2	Q6QNV8_9CNID	Q6qnv8_anthopleura	949	3	12.5	23	2	2	Q9PSHA_CHICK	Q9psah_gallus gall
877	3	12.5	23	2	2	Q6QNM5_9CNID	Q6qnm5_anthopleura	950	3	12.5	23	2	2	Q64171_MELEAG	Q64171_meleagris g
878	3	12.5	23	2	2	Q9GNL8_DROYA	Q9gnl8_drosophila	951	3	12.5	23	2	2	Q9S8S7_9HIV1	Q9s8s7_human immun
879	3	12.5	23	2	2	Q4X3F1_PLACH	Q4x3f1_plasmodium	952	3	12.5	23	2	2	Q9ENM9_9HIV1	Q9enm9_human immun
880	3	12.5	23	2	2	Q4X443_PLACH	Q4x443_plasmodium	953	3	12.5	23	2	2	Q9QEX4_9HIV1	Q9qex4_human immun
881	3	12.5	23	2	2	Q4X4D7_PLACH	Q4x4d7_plasmodium	954	3	12.5	23	2	2	Q9QEX5_9HIV1	Q9qex5_human immun
882	3	12.5	23	2	2	Q4X514_PLACH	Q4x514_plasmodium	955	3	12.5	23	2	2	Q9QEX5_9HIV1	Q9qex5_human immun
883	3	12.5	23	2	2	Q4XB77_PLACH	Q4xbt7_plasmodium	956	3	12.5	24	1	1	COXC_THUOB	P803240_pandinus obe
884	3	12.5	23	2	2	Q4XCR8_PLACH	Q4xcr8_plasmodium	957	3	12.5	24	1	1	PAN2_PANIM	P233417_rana cateeb
885	3	12.5	23	2	2	Q4XBJ3_PLACH	Q4xjb3_plasmodium	958	3	12.5	24	1	1	SODC_RANCA	P233417_rana cateeb
886	3	12.5	23	2	2	Q4XBP1_PLACH	Q4xeb1_plasmodium	959	3	12.5	24	2	2	O01228_WILSA	Q01228_williopeis
887	3	12.5	23	2	2	Q4XF40_PLACH	Q4xf40_plasmodium	960	3	12.5	24	2	2	Q5MGQ5_PODAN	Q5mgq5_podospora a
888	3	12.5	23	2	2	Q4XH19_PLACH	Q4xh19_plasmodium	961	3	12.5	24	2	2	Q9UR70_ASFPU	Q9ur70_aspergillus
889	3	12.5	23	2	2	Q4Y3T7_PLACH	Q4y3t7_plasmodium	962	3	12.5	24	2	2	Q16333_HUMAN	Q16333_homo sapien
890	3	12.5	23	2	2	Q4XKG4_PLACH	Q4xkg4_plasmodium	963	3	12.5	24	2	2	Q86WP5_HUMAN	Q86wp5_homo sapien
891	3	12.5	23	2	2	Q4XKA5_PLACH	Q4xka5_plasmodium	964	3	12.5	24	2	2	Q4VFEV5_HUMAN	Q4vfev5_homo sapien
892	3	12.5	23	2	2	Q4XMT9_PLACH	Q4xmt9_plasmodium	965	3	12.5	24	2	2	Q5BR43_SCHJA	Q5br43_schistosoma
893	3	12.5	23	2	2	Q4XP80_PLACH	Q4xp80_plasmodium	966	3	12.5	24	2	2	Q5BVT5_SCHJA	Q5bvt5_schistosoma
894	3	12.5	23	2	2	Q4Y2Q2_PLACH	Q4y2q2_plasmodium	967	3	12.5	24	2	2	Q5BYW2_SCHJA	Q5byw2_schistosoma
895	3	12.5	23	2	2	Q4Y3T7_PLACH	Q4y3t7_plasmodium	968	3	12.5	24	2	2	Q5C2C4_SCHJA	Q5c2c4_schistosoma
896	3	12.5	23	2	2	Q4Y6L9_PLACH	Q4y6l9_plasmodium	969	3	12.5	24	2	2	Q5C644_SCHJA	Q5c644_schistosoma
897	3	12.5	23	2	2	Q4Y811_PLACH	Q4y811_plasmodium	970	3	12.5	24	2	2	Q7M3Q0_LUMRU	Q7m3q0_lumbricus r
898	3	12.5	23	2	2	Q4YAV9_PLABE	Q4yav9_plasmodium	971	3	12.5	24	2	2	Q7YIK2_PULIM	Q7yik2_philonesia
899	3	12.5	23	2	2	Q4YL91_PLABE	Q4yl91_plasmodium	972	3	12.5	24	2	2	Q94XE2_9HEMI	Q94xe2_tectocoris
900	3	12.5	23	2	2	Q4YLG2_PLABE	Q4ylg2_plasmodium	973	3	12.5	24	2	2	Q9GNE5_CABEL	Q9gne5_caenorhabdi
901	3	12.5	23	2	2	Q4YMK2_PLABE	Q4ymk2_plasmodium	974	3	12.5	24	2	2	Q7R8I6_PLAYO	Q7r8i6_plasmodium
902	3	12.5	23	2	2	Q4YMS1_PLABE	Q4yms1_plasmodium	975	3	12.5	24	2	2	Q7RBO0_PLAYO	Q7rbq0_plasmodium
903	3	12.5	23	2	2	Q4YXT6_PLABE	Q4yxt6_plasmodium	976	3	12.5	24	2	2	Q7RL34_PLAYO	Q7rl34_plasmodium
904	3	12.5	23	2	2	Q4YXT8_PLABE	Q4yxt8_plasmodium	977	3	12.5	24	2	2	Q9BM16_DUGTI	Q9bm16_dugesia tig
905	3	12.5	23	2	2	Q4Z0V6_PLABE	Q4z0v6_plasmodium	978	3	12.5	24	2	2	Q4X2M4_PLACH	Q4xa00_plasmodium
906	3	12.5	23	2	2	Q9TR07_CANFA	Q9tr07_canis famil	979	3	12.5	24	2	2	Q4XA00_PLACH	Q4xa00_plasmodium
907	3	12.5	23	2	2	Q9TRK2_CANFA	Q9trk2_canis famil	980	3	12.5	24	2	2	Q4XA83_PLACH	Q4xa83_plasmodium
	3	12.5	23	2	2	Q41464_SOLTU	Q41464_solanum tub							Q4XFX5_PLACH	Q4xfx5_plasmodium

981 3 12.5 24 2 Q4XB2 PLACH
 982 3 12.5 24 2 Q4X58 PLACH
 983 3 12.5 24 2 Q4XJ9 PLACH
 984 3 12.5 24 2 Q4XK2 PLACH
 985 3 12.5 24 2 Q4XV6 PLACH
 986 3 12.5 24 2 Q4YIG9 PLACH
 987 3 12.5 24 2 Q4V67 PLACH
 988 3 12.5 24 2 Q4V75 PLACH
 989 3 12.5 24 2 Q4Y98 PLACH
 990 3 12.5 24 2 Q4YAC5 PLACH
 991 3 12.5 24 2 Q4YD83 PLACH
 992 3 12.5 24 2 Q4YF84 PLACH
 993 3 12.5 24 2 Q4YF84 PLACH
 994 3 12.5 24 2 Q4YGA5 PLACH
 995 3 12.5 24 2 Q4YGD0 PLACH
 996 3 12.5 24 2 Q4YGD6 PLACH
 997 3 12.5 24 2 Q4YGS5 PLACH
 998 3 12.5 24 2 Q4YJ45 PLACH
 999 3 12.5 24 2 Q4YLA7 PLACH
 1000 3 12.5 24 2 Q4YMI4 PLACH

ALIGNMENTS

RESULT 1
 Q30135_HUMAN
 ID Q30135_HUMAN PRELIMINARY; PRT; 20 AA.
 AC Q30135;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE HLA-DRB3 protein (Fragment).
 GN Name=HLA-DRB3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86233452; PubMed=3012569;
 RA Angelini G., de Preval C., Gorski J., Mach B.;
 RT "High-resolution analysis of the human HLA-B* polymorphism by
 RT hybridization with sequence-specific oligonucleotide probes [published
 RT erratum appears in Proc Natl Acad Sci U S A 1986 Sep;83(17):6664].";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4489-4493(1986).
 DR EMBL; M13561; AAA59796.1; -; Genomic_DNA.
 DR PIR; I59073; I59073.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M...; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta_N.
 DR Pfam; PF00969; MHC_II_beta_1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR MHC II; Transmembrane.
 KW MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 20
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2551 MW; 71B5A02E98F4EA97 CRC64;

Query Match 20.8%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRFDS 5
 |||||
 Db 13 LRFDS 17

RESULT 2

Q4YXD8 PLABE
 ID Q4YXD8_PLABE PRELIMINARY; PRT; 23 AA.
 AC Q4YXD8;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB104671.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAT01001922; CAH97317.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 23 AA; 2887 MW; 909377810867FBB0 CRC64;
 Query Match 20.8%; Score 5; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 NNNNS 20
 |||||
 Db 16 NNNNS 20
 RESULT 3
 Q7REJ5 PLAYO
 ID Q7REJ5_PLAYO PRELIMINARY; PRT; 25 AA.
 AC Q7REJ5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY05069;
 OS Plasmodium yoelii yoelii
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22355706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RA "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01001596; EAA17035.1; -; Genomic_DNA.
 KW Hypothetical protein.

```

PT  NON_TER      1      1
SQ  SEQUENCE     25 AA;  2842 MW;  61CA94D3F5398F0F CRC64;

Query Match      20.8%; Score 5; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 TNNNN 19
    |||||
Db   8 TNNNN 12

RESULT 4
ID  Q26429 DROPS PRELIMINARY; PRT; 12 AA.
AC  Q26429;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Dpse\pb protein (Fragment).
GN  Name=pb; Synonyms=Dpse\pb;
OS  Drosophila pseudoobscura (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7237;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=92111389; PubMed=1694932;
RA  Randazzo F.M., Cribbs D.L., Kaufman T.C.;
RT  "Rescue and regulation of proboscipedia: a homeotic gene of the
RT  Antennapedia Complex.";
RL  Development 113:257-271(1991).
DR  EMBL; S77929; AAB20845.1; -; Genomic_DNA.
DR  PIR; A44874; A44874.
DR  FlyBase; FBgn0012734; Dpse\pb.
FT  NON_TER      12      12
SQ  SEQUENCE     12 AA;  1377 MW;  4608DB18E355A5B3 CRC64;

Query Match      16.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  16 NNNN 19
    |||||
Db   8 NNNN 11

RESULT 5
ID  Q36731 HUMAN PRELIMINARY; PRT; 16 AA.
AC  Q36731;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Voltage-dependent anion channel (Fragment).
GN  Name=VDAC5P; Synonyms=VDAC3;
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=94292188; PubMed=7517385;
RA  Blachly-Dyson E., Baldini A., Litt M., McCabe E.R., Forte M.;
RT  "Human genes encoding the voltage-dependent anion channel (VDAC) of
RT  the outer mitochondrial membrane: mapping and identification of two
RT  new isoforms.";
RL  Genomics 20:62-67(1994).
DR  EMBL; S75494; AAD14175.1; -; Genomic_DNA.
DR  HGNC; HGNC:12676; VDAC5P.
DR  GO; GO:0005739; C:mitochondrion; NAS.

```

```

DR  GO; GO:0008308; F:voltage-gated ion-selective channel activity; NAS.
DR  GO; GO:0006820; P:anion transport; NAS.
FT  NON_TER      1
SQ  SEQUENCE     16 AA;  1607 MW;  05B3FE870C1F296B CRC64;

Query Match      16.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  18 NNSS 21
    |||||
Db   8 NNSS 11

RESULT 6
ID  Q4YCW9 PLABE PRELIMINARY; PRT; 17 AA.
AC  Q4YCW9;
DT  13-SEP-2005 (TrEMBLrel. 31, Created)
DT  13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT  13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE  Hypothetical protein (Fragment).
GN  ORFNames=P8406143.00.0;
OS  Plasmodium berghei.
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX  NCBI_TaxID=5821;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA  Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA  James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA  Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA  Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA  Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT  "A comprehensive survey of the Plasmodium life cycle by genomic,
RT  transcriptomic, and proteomic analyses.";
RL  Science 307:82-86(2005).
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; CAAL01006411; CAI04150.1; -; Genomic_DNA.
KW  Hypothetical protein.
FT  NON_TER      1
SQ  SEQUENCE     17 AA;  2069 MW;  56020C69D44FA945 CRC64;

Query Match      16.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  16 NNNN 19
    |||||
Db   7 NNNN 10

RESULT 7
ID  Q7M2F6_NICPL PRELIMINARY; PRT; 19 AA.
AC  Q7M2F6;
DT  01-MAR-2004 (TrEMBLrel. 26, Created)
DT  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Endopeptidase Clp (EC 3.4.21.92) chain P (Fragment).
OS  Nicotiana glauca (Leadwort-leaved tobacco).
OC  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC  lamids; Solanales; Solanaceae; Nicotiana.
OX  NCBI_TaxID=4092;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Fejes E., Engler D., Maliga P.;
RT  "Extensive homologous chloroplast DNA recombination in the pt14
RT  Nicotiana somatic hybrid.";

```

```

RL Theor. Appl. Genet. 79:28-32(1990).
DR PIR; PC1323; PC1323.
DR GO; GO:0008462; F:endorpeptidase Clp activity; IEA.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2155 MW; CF63C012B1EBF689 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SSFY 23
   ||||
Db 7 SSFY 10

RESULT 8
Q9RSN8_CLOBO
ID Q9RSN8_CLOBO PRELIMINARY; PRT; 19 AA.
AC Q9RSN8_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neurotoxin type A HN+ 17 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
DR PIR; S67990; S67990.
DR InterPro; IPR008903; Botulinum_HA-17.
DR Pfam; PF05588; Botulinum_HA-17; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2186 MW; B9FD6ED06D1ACA18 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSIF 11
   ||||
Db 15 KSIF 18

RESULT 9
O19726_HUMAN
ID O19726_HUMAN PRELIMINARY; PRT; 20 AA.
AC O19726_
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HLA-DRB3 protein (Fragment).
GN Name=HLA-DRB3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86233452; PubMed=3012569;
RA Angelini G., de Preval C., Gorski J., Mach B.;
RT "High-resolution analysis of the human HLA-DR polymorphism by
RT hybridization with sequence-specific oligonucleotide probes [published
RT erratum appears in Proc Natl Acad Sci U S A 1986 Sep;83(17):6664].";
RL Proc. Natl. Acad. Sci. U.S.A. 83:4489-4493(1986).

```

```

DR EMBL; M13562; AAA59797.1; -; Genomic_DNA.
DR PIR; I79432; I79432.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0045012; P:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC II beta_N.
DR Pfam; PF00969; MHC II beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2497 MW; EC677B48F424EA88 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFDS 5
   ||||
Db 14 RFDS 17

RESULT 10
Q4XYLO_PLACH
ID Q4XYLO_PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XYLO_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC104353.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01002246; CAH78000.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2169 MW; B919D5390293E578 CRC64;

Query Match
Best Local Similarity 16.7%; Score 4; DB 2; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NNNS 20
   ||||
Db 1 NNNS 4

RESULT 11
Q8N337_HUMAN
ID Q8N337_HUMAN PRELIMINARY; PRT; 21 AA.
AC Q8N337_
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 RN NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bladder;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028676; AA28676.1; -; mRNA.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 2244 MW; 4A2E9597DA7B2086 CRC64;
 Query Match 16.7%; Score 4; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 NSSF 22
 Db 14 NSSF 17
 RESULT 12
 ID Q4YK89_PLABE PRELIMINARY; PRT; 21 AA.
 AC Q4YK89;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PB401728.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAI01004270; CAI01573.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 21 AA; 2498 MW; 5284B6D85E64D037 CRC64;
 Query Match 16.7%; Score 4; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TNNN 18
 Db 2 TNNN 5
 RESULT 13
 ID Q4Z0T6_PLABE PRELIMINARY; PRT; 21 AA.
 AC Q4Z0T6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB103144.00.0;
 OS Plasmodium berghei.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAI01004270; CAI01573.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 21 AA; 2498 MW; 5284B6D85E64D037 CRC64;
 Query Match 16.7%; Score 4; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 NNNN 19
 Db 9 NNNN 12
 RESULT 14
 ID Q7S122_NEUCR PRELIMINARY; PRT; 22 AA.
 AC Q7S122;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU04971.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothre G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 RA Krzytofiak S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
 RA DeSouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
 RL Nature 0:0-0(2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000468; EAA29041.1; -; Genomic_DNA.
 SQ SEQUENCE 22 AA; 2684 MW; 628E72662E7BBA89 CRC64;
 Query Match 16.7%; Score 4; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 NNNN 19

Db 18 NNNN 21

||||

RESULT 15
Q8WSY1 ANOGA
ID Q8WSY1 ANOGA PRELIMINARY; PRT; 22 AA.
AC Q8WSY1
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GASUA; TISSUE=Salivary gland;
RX MEDLINE=22057806; PubMed=12062411; DOI=10.1016/S0014-5793(02)02578-4;
RA Lanfrancotti A., Lombardo F., Santolamazza F., Veneri M.,
RA Castriagnano T., Coluzzi M., Arca' B.;
RT "Novel cDNAs encoding salivary proteins from the malaria vector
RT Anopheles gambiae.";
RL FEBS Lett. 517:67-71(2002).
DR EMBL; AJ419880; CAD12040.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2395 MW; 429DAF6FA0D39C2 CRC64;

Query Match 16.7%; Score 4; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SIFE 12
Db 18 SIFE 21

Search completed: January 20, 2006, 17:55:55
Job time : 84 secs